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## APPL PARTS

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SPEC  
Specification

SPEC NO  
Specification Not in English

TRNA  
Transmittal New Application

CTNF  
Count Non-Final

CTRS  
Count Restriction

EXIN  
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M903  
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M905  
DO/EO Missing Requirement

NFDR  
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NOA  
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## OUTGOING

CTMS
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## INCOMING

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Appeal Brief

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XT/  
Extension of Time filed separate

### Internal

SRNT  
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CLMPTO  
PTO Prepared Complete Claim Set

ECBOX  
Evidence Copy Box Identification

WCLM  
Claim Worksheet

WFEE  
Fee Worksheet

### File Wrapper

FWCLM  
File Wrapper Claim

IIFW  
File Wrapper Issue Information

SRFW  
File Wrapper Search Info

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
17831	ENU01625	AN161C30:45	67-86	483-504	NAP		g2462677	141	48	0.00004	27	39	(Z99568) hypothetical protein. [Schizosaccharomyces pombe]
17832	ENU01626	80..4101	69-89	490-512	NAP		g2909624		152	1.00E-36	44	33	(AL021942) hypothetical protein Rv0565c [Mycobacterium tuberculosis]
17833	ENU01627	AN161C7014: 3929..4417	54-75	481-500	NAP		g13533008	148	35	0.3			hypothetical 53.5 KD protein in GCD14-POS18 intergenic region; hypothetical protein YJL123c - yeast (Saccharomyces cerevisiae) ; (Z49398) ORF YJL123c [Saccharomyces cerevisiae]
17834	ENU01628	AN161S4363: 554..66	37-65	462-483	NAP		g1352891	422	153	5.00E-37	44	40	putative glycosyltransferase HOC1 precursor ; probable membrane protein YJR075w - yeast (Saccharomyces cerevisiae) ; (Z49575) ORF YJR075w [Saccharomyces cerevisiae] ; (L47993) ORF YJR075w [Saccharomyces cerevisiae] ; (U62942) Hoc1p [Saccharomyces cerevisiae] (AL021748) hypothetical [Schizosaccharomyces pombe] (AF072850) cytochrome p450 CYP4C19 [Lytechinus anamesis] (AL023287) probable helicase [Schizosaccharomyces pombe] (AF039713) Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk387c10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cm10f; coded for by C. elegans cDNA cm18g...
17835	ENU01629	AN161C2320: 1370..1858	22-47	444-468	NAP		g2842511	966	177	5.00E-44	50	36	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region ; (AE000443) orf, hypothetical protein [Escherichia coli] "
17836	ENU01630	AN161C347:2	39-60	468-487	NAP		g3452329	194	93	1.00E-18	39	93	(Z98530) ribosomal protein [Schizosaccharomyces pombe]
17837	ENU01631	134..2624	23-56	453-473	NAP		g3116120	136	79	2.00E-14	27	15	
17838	ENU01632	AN161C3163: 1048..555	41-72	457-492	NAP		g2773203	598	215	1.00E-55	61	30	
17839	ENU01633	AN161C3353: 162..656	66-86	492-518	NAP		g2851420	253	79	2.00E-14	33	16	
17840	ENU01634	AN161C1118: 5:8243..7747	52-71	478-506	NAP		g2330823	319	95	2.00E-24	65	65	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17841	ENU01635	...	65-84	497-521	NAP		g2132957		75	3.00E-13	30	31	probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (AL023589) splicesome-associated protein [Schizosaccharomyces pombe] lymphocyte specific helicase - mouse ; (U25691) lymphocyte specific helicase [Mus musculus] (Z98601) diphosphomevalonate decarboxylase [Schizosaccharomyces pombe] (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe] (Z92774) fadD3 [Mycobacterium tuberculosis] (Y17393) prefoldin subunit 2 [Mus musculus] (L47106) kinesin [Neurospora crassa] (AF015825) unknown [Bacillus subtilis] ; (Z99110) yjIB [Bacillus subtilis] (AL023794) putative proline oxidase precursor [Schizosaccharomyces pombe] fruit protein PKIWI501 ; hypothetical protein - kiwi fruit ; (L27810) PKIWI501 [Actinidia delictosa] (D64003) hypothetical protein [Synecocystis sp.] "omega-6 fatty acid desaturase, endoplasmic reticulum (delta-12 desaturase) ; (L26296) delta-12 desaturase [Arabidopsis thaliana] " "(AB018078) oligo-1,4 - 1,4-glucantransferase / amylo-1,6-glucosidase [Saccharomyces cerevisiae] "
17842	ENU01636	ANI61C4567:	48-74	486-505	NAP		g3135996	589	120	8.00E-27	41	32	
17843	ENU01637	ANI61S483:3	27-50	466-485	NAP		g2137490	465	185	2.00E-46	54	27	
17844	ENU01638	ANI61C2329:	27-47	457-488	NAP		g2330786	969	152	2.00E-36	47	40	
17845	ENU01639	ANI61C5098:	56-75	498-517	NAP		g3738207	339	147	5.00E-35	43	50	
17846	ENU01640	ANI61C2362:	28-48	470-490	NAP		g1877292	206	52	9.00E-12	30	32	
17847	ENU01641	ANI61C7547:	44-72	473-507	NAP		g3212116	127	63	0.000000	30	91	
17848	ENU01642	ANI61C6627:	54-71	499-518	NAP		g1947184	579	122	4.00E-41	81	14	
17849	ENU01643	ANI61C1152:	23-54	466-489	NAP		g2612899	147	52	5.00E-10	35	95	
17850	ENU01644	ANI61C7562:	23-46	462-490	NAP		g3192023	187	101	5.00E-21	36	33	
17851	ENU01645	ANI61C2007:	22-49	474-493	NAP		g1170600	140	36	0.14	30	91	
17852	ENU01646	ANI61C4822:	66-93	506-537	NAP		g1001214	443	156	1.00E-37	45	33	
17853	ENU01647	ANI61S344:1	33-54	475-505	NAP		g1169598	954	370	e-102	98	44	
17854	ENU01648	ANI61C5920:	62-81	505-536	NAP		g3986291	544	152	9.00E-41	57	9	

Seq num	Seq id	Primer Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17855	ENNU01649	AN161C9533: 2666..2148	64-83	514-540	NAP		g4185903	922	202	3.00E-62	83	27	(AJ132432) fimbrin [Gibberella pulicaris]
17856	ENNU01650	AN161C4266: 770..1289	42-67	500-519	NAP		g118774	1172	177	5.00E-44	60	21	DNA ligase (polydeoxyribonucleotide synthase (ATP)) ; DNA ligase (ATP) (EC 6.5.1.1) - fission yeast (Schizosaccharomyces pombe) ; (X05107) DNA ligase [Schizosaccharomyces pombe]
17857	ENNU01651	AN161C8612: 1145..625	72-90	528-550	NAP		g2131348	383	56	1.00E-16	39	26	hypothetical protein YDL156w - yeast (Saccharomyces cerevisiae) ; (X97751) D1536 [Saccharomyces cerevisiae] ; (Z74204) ORF YDL156w [Saccharomyces cerevisiae]
17858	ENNU01652	AN161C6664: 1400..876	68-87	531-550	NAP		g4538926	357	124	5.00E-28	43	23	(AL049483) putative phosphatidylserine decarboxylase [Arabidopsis thaliana]
17859	ENNU01653	AN161C7770: 2237..1710	41-65	505-526	NAP		g2494301	1373	271	3.00E-72	78	39	eukaryotic translation initiation factor 2 gamma subunit (EIF-2-gamma) ; (U37354) initiation factor eIF-2 gamma subunit [Schizosaccharomyces pombe]
17860	ENNU01654	AN161C4206: 2519..1992	49-68	508-534	NAP		g3560221	328	143	8.00E-34	43	50	(AL031523) hypothetical protein [Schizosaccharomyces pombe]
17861	ENNU01655	AN161C3455: 1377..1908	22-55	490-511	NAP		g585222	485	182	2.00E-45	60	90	glutathione peroxidase homolog YBR244W ; probable glutathione peroxidase (EC 1.11.1.9) - yeast (Saccharomyces cerevisiae) ; (Z36113) ORF YBR244w [Saccharomyces cerevisiae]
17862	ENNU01656	AN161C3754: 5352..5883	56-75	525-545	NAP		g586542	855	149	1.00E-35	41	29	general amino acid permease AGP2 ; probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae) ; (X75891) YBR1007 [Saccharomyces cerevisiae] ; (Z36001) ORF YBR132c [Saccharomyces cerevisiae] ; YBR1007 gene [Saccharomyces cerevisiae]



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17863	ENU01657	AN161C7497: 932..400	22-41	492-512	NAP		g729611	807	189	9.00E-48			vanadate resistance protein vanadate resistance protein GOG5/VRG4/VAN2 ; vanadate resistance protein VAN2 - yeast (Saccharomyces cerevisiae) ; (L33915)
17864	ENU01658	AN161C9506: 865..743	61-82	531-551	NAP		g3093417	512	173	6.00E-43	49	58	vanadate resistant protein [Saccharomyces cerevisiae] ; (U15599)
17865	ENU01659	AN161C9637: 5288..5822	25-46	498-517	NAP		g731928	393	163	7.00E-40	46	73	Van2p [Saccharomyces cerevisiae] ; (Z72747) ORF YGL225w [Saccharomyces cerevisiae] ; VRG4 gene [Saccharomyces cerevisiae] (AF036546) protein kinase CK2 beta subunit [Candida albicans] hypothetical 27.4 KD protein in HYR1 3'region ; hypothetical protein YIR042c - yeast (Saccharomyces cerevisiae) ; (Z46902) unknown [Saccharomyces cerevisiae].
17866	ENU01660	AN161C8632: 1385..855	50-78	525-544	NAP		g585381	1296	257	4.00E-84	94	68	lactam utilization protein LAMB ; lactam utilization protein lamb - Emmericella nidulans ; (M77283) lamb [Emmericella nidulans] (AL031545) putative coatmer delta subunit [Schizosaccharomyces pombe] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:ID14061) [Arabidopsis thaliana] (AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa] RTA1 protein ; RTA1 protein - yeast (Saccharomyces cerevisiae) ; (Z72998) ORF YGR213c [Saccharomyces cerevisiae] ; (X84736) RTA1 [Saccharomyces cerevisiae]
17867	ENU01661	AN161C1444: 1040..1577	66-85	542-561	NAP		g3581908	589	122	5.00E-49	70	67	
17868	ENU01662	AN161C2252: 70..606	22-52	490-517	NAP		g1351714	103	47	0.00008	22	32	
17869	ENU01663	AN161C2212: 2027..2565	29-51	506-525	NAP		g3549879	768	124	5.00E-28	49	30	
17870	ENU01664	AN161C1102: 7..562..22	45-64	522-543	NAP		g3600039	183	95	4.00E-19	30	23	
17871	ENU01665	AN161C9234: 1247..707	52-71	531-550	NAP		g2970667	215	56	8.00E-15	41	46	
17872	ENU01666	AN161C3224: 374..4922	53-73	538-559	NAP		g1710802	199	75	3.00E-13	33	56	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17873	ENU01667	ANI61C8425: 1..551	22-46	498-530	NAP		g466190	551	213	5.00E-55	54	80	ribosomal large subunit pseudouridine synthase B (pseudouridylylate synthase) (uracil hydrolyase) ; hypothetical protein X13 - Bacillus subtilis ; (L09228) ORFX13 [Bacillus subtilis] ; (Z99116) similar to hypothetical proteins [Bacillus subtilis] (X82490) unnamed protein product [Fusarium oxysporum] (AL023590) Glutathione S-transferase [Schizosaccharomyces pombe] histidine biosynthesis bifunctional amidotransferase / cyclase ; amidotransferase HIS7 (EC 2.4.2.-) / cyclase HIS7 - yeast (Saccharomyces cerevisiae) ; (Z36117) ORF YBR248c [Saccharomyces cerevisiae]
17874	ENU01668	ANI61C461: 58..1409	54-74	539-563	NAP		g2274947	177	79	2.00E-14	28	61	hypothetical 57.2 KD protein in MET8-HPC2 intergenic region ; hypothetical protein YBR214w - yeast (Saccharomyces cerevisiae) ; (Z36083) ORF YBR214w [Saccharomyces cerevisiae]
17875	ENU01669	ANI61C2346: 2599..2045	57-87	550-569	NAP		g3136036	189	68	1.00E-14	33	58	myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe] (Y11113) endoglucanase IV [Hypocrea jecorina] probable membrane protein YPL224c - yeast (Saccharomyces cerevisiae) ; (Z73580) ORF YPL224c [Saccharomyces cerevisiae]
17876	ENU01670	ANI61C6107: 5339..4783	62-94	555-576	NAP		g585255	588	231	2.00E-60	70	29	[Saccharomyces cerevisiae] probable oxidoreductase YJR096w ; aldehyde reductase homolog YJR096w - yeast (Saccharomyces cerevisiae) ; (Z49596) ORF YJR096w [Saccharomyces cerevisiae] (U88308) C32E8.5 gene product [Caenorhabditis elegans] (AF053318) CCR4-associated factor 1 [Homo sapiens]
17877	ENU01671	ANI61C3450: 677..120	72-96	566-587	NAP		g586334	307	77	8.00E-14	37	35	
17878	ENU01672	ANI61C1133: 8..560..3	68-87	563-583	NAP		g2500938	380	127	7.00E-31	46	32	
17879	ENU01673	ANI61C7642: 157..716	62-81	560-579	NAP		g2315274	220	87	7.00E-17	38	52	
17880	ENU01674	ANI61C3041: 202..762	22-46	521-540	NAP		g2133005	317	71	8.00E-19	38	36	
17881	ENU01675	ANI61C8628: 2821..2259	41-60	536-561	NAP		g1176340	313	94	9.00E-21	36	57	
17882	ENU01676	ANI61C6429: 7156..7718	35-56	523-555	NAP		g1825727	407	138	3.00E-32	43	60	
17883	ENU01677	ANI61C7861: 82..644	22-49	522-542	NAP		g4106061	534	169	1.00E-41	58	51	

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17884	ENU01678	ANI61C1228:	45-64	541-569	NAP		g1706503	2105	135	3.00E-31	41	12	DNA polymerase alpha (DNA polymerase I); DNA-directed DNA polymerase (EC 2.7.7.7) - yeast
		1995..1429											(Saccharomyces cerevisiae) ; (Z50161) DNA Polymerase I [Saccharomyces cerevisiae] ; (Z71378) ORF YNL102w [Saccharomyces cerevisiae] (U73857) betaine-aldehyde dehydrogenase [Escherichia coli]
17885	ENU01679	ANI61C9640:	55-78	558-579	NAP		g1657510	1307	201	3.00E-51	52	37	verprolin ; verprolin - yeast
		4633..5199											(Saccharomyces cerevisiae) ; (U19028) Vrp1p [Saccharomyces cerevisiae] ; MDP2 gene [Saccharomyces cerevisiae]
17886	ENU01680	ANI61C7173:	48-68	559-578	NAP		g2507155	179	59	0.000000	34	19	glucose transporter (sugar carrier) ; glucose transport protein STP1 - Arabidopsis thaliana ; (X55350) glucose transporter [Arabidopsis thaliana]
		69..266								02			probable monooxygenase MTCY31.20 ; (Z73101) hypothetical protein Rv0892 [Mycobacterium tuberculosis] lactate 2-monooxygenase (lactate oxidase) ; lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis]
17887	ENU01681	ANI61C7819:	72-91	586-605	NAP		g134976	359	45	0.0004			tropomyosin ; tropomyosin - yeast (Schizosaccharomyces pombe) ; (L04126) tropomyosin [Schizosaccharomyces pombe] ; tropomyosin [Schizosaccharomyces pombe]
		2860..3435											lysophospholipase precursor (phospholipase B) ; lysophospholipase (EC 3.1.1.5) - Penicillium notatum (fragment) ; (X60348) lysophospholipase [Penicillium chrysogenum]
17888	ENU01682	ANI61C652.5:	52-71	562-586	NAP		g1731385	334	96	2.00E-19	37	33	
		55..1132											
17889	ENU01683	ANI61C5538:	22-41	537-558	NAP		g125886	475	77	1.00E-23	38	47	
		424..1004											
17890	ENU01684	ANI61C1189:	36-63	554-574	NAP		g401205	288	86	2.00E-16	41	97	
		8185..8765											
17891	ENU01685	ANI61C8980:	22-48	542-561	NAP		g730338	1174	262	2.00E-69	67	30	
		466..1045											

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17892	ENU01686	ANI61C5264:	60-79	577-599	NAP		g1666269	328	149	2.00E-35	41	74	(Z82021) cytochrome P450 [Agaricus bisporus]
17893	ENU01687	ANI61C1059	25-55	543-566	NAP		g1253399	724	214	3.00E-55			serine/threonine-protein kinase KIN28 ; probable protein kinase KIN28 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (X04423) protein kinase [Saccharomyces cerevisiae] ; (X95644) ORF 2330 [Saccharomyces cerevisiae] ; (Z74156) ORF YDL108w [Saccharomyces cerevisiae] ; protein kinase [Saccharomyces cerevisiae]
17894	ENU01688	ANI61C2075:	22-46	539-563	NAP		g1170905	777	157	6.00E-38	61	50	24 KD metalloproteinase precursor (deuterolysin) ; metalloproteinase (EC 3.4.-.-) 23K - Aspergillus flavus ; (L37524) metalloproteinase [Aspergillus flavus]
17895	ENU01689	ANI61C2888:	24-44	537-567	NAP		g2498527	234	97	9.00E-20	36	21	dimethylglycine dehydrogenase precursor (MEGLYDH) ; dimethylglycine dehydrogenase - rat ; (X55995) dimethylglycine dehydrogenase [Rattus norvegicus] (Z98533) rho gdp dissociation inhibitor. [Schizosaccharomyces pombe]
17896	ENU01690	ANI61C8417:	58-78	585-606	NAP		g2330853	351	119	2.00E-26	45	74	inhibitor. [Schizosaccharomyces pombe]
17897	ENU01691	ANI61C8659:	70-98	602-619	NAP		g3080529	223	101	6.00E-21	37	64	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
17898	ENU01692	ANI61C8489:	23-42	551-573	NAP		g1723237	148	62	2.00E-12	31	12	hypothetical 143.6 KD protein C26A3.09C in chromosome I ; (Z69240) hypothetical protein [Schizosaccharomyces pombe]
17899	ENU01693	ANI61C754:	7	26-46	NAP		g1438796	1015	245	1.00E-64	61	43	"OVCA1=candidate tumor suppressor [human, fetal brain, Peptide, 443 aa]"

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17900	ENNU01694	AN161C6597:	68-87	600-619	NAP		g132744	474	146	3.00E-38			"60S ribosomal protein L17 ; ribosomal protein L23.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (X01694) ribosomal protein L17 [Saccharomyces cerevisiae] ; (X79489) L23 B x-137 [Saccharomyces cerevisiae] ; (Z35848) ORF YBL087c [Saccharomyces cerevisiae] ; (U18916) Rpl17bp: Ribosomal protein, large subunit [Saccharomyces cerevisiae] ; (U15653) ribosomal protein L17B [Saccharomyces cerevisiae] "
17901	ENNU01695	AN161C6603:	36-55	571-590	NAP		g3426129	717	152	2.00E-36	47	13	"(AL031307) leptomycin B resistance protein, ABC transporter [Schizosaccharomyces pombe] "
17902	ENNU01696	AN161C2370:	63-82	598-617	NAP		g3915530	223	76	1.00E-13	25	17	"hypoetical 118.4 KD protein in WRS1-PKH2 intergenic region ; hypoetical protein YOL098c - yeast (Saccharomyces cerevisiae) ; (Z48149) similarity with D. melanogaster insulinase [Saccharomyces cerevisiae] ; (Z74840) ORF YOL098c [Saccharomyces cerevisiae] (AC005623) alien-like protein [Arabidopsis thaliana] (AB011003) UDP-N-acetylglucosamine pyrophosphorylase [Candida albicans] probable 1-acyl-SN-glycerol-3-phosphate acyltransferase (1-AGP acyltransferase) (1-AGPAT) (lysophosphatidic acid acyltransferase) (LPAAT) ; probable sn2-acylglyceride fatty acyltransferase (EC 2.3.1.-) - yeast (Saccharomyces cerevisiae) ; (L13282) acyltransferase [Saccharomyces cerevisiae] ; (Z74100) ORF YDL052c [Saccharomyces cerevisiae]
17903	ENNU01697	AN161C2471:	55-74	589-610	NAP		g3885329	560	210	7.00E-54	47	46	
17904	ENNU01698	AN161C7526:	23-42	557-579	NAP		g3413964	458	161	5.00E-39	55	36	
17905	ENNU01699	AN161C8576:	23-44	560-579	NAP		g464422	491	176	1.00E-43			

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17906	ENU01700	ANI61C1038	22-55	556-578	NAP		g585972	461	161	5.00E-39	48	58	SCO2 protein precursor ; SCO1 protein homolog SCO2 - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0308 [Saccharomyces cerevisiae] ; (Z35893) ORF YBR024w [Saccharomyces cerevisiae] ; ORF YBR0308 [Saccharomyces cerevisiae]
17907	ENU01701	ANI61C9637	72-91	604-629	NAP		g118109	560	214	3.00E-55			[Saccharomyces cerevisiae] peptidyl-prolyl cis-trans isomerase (PPIASE) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
17908	ENU01702	ANI61C8628	22-44	563-582	NAP		g2088561	165	84	9.00E-16	31	60	(U95053) glutamate-cysteine ligase regulatory subunit [Mus musculus] (AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis] (D87078) similar to D.melanogaster puntillo protein (S22026) ; similar to human KIAA0099 protein(D43951) [Homo sapiens]
17909	ENU01703	ANI61C5399	71-92	603-632	NAP		g2808725		48	0.00004			cyanamide hydratase (urea hydro-lyase) ; cyanamide hydratase (EC 4.2.1.69) - fungus (Myrothecium verrucaria) ; (M59078) cyanamide hydratase [Myrothecium verrucaria] (AL022070) mago-nashi homolog [Schizosaccharomyces pombe]
17910	ENU01704	ANI61C4146	22-48	561-583	NAP		g1944416	617	134	5.00E-31	40	21	(AL033389) putative allantoinase permease [Schizosaccharomyces pombe]
17911	ENU01705	ANI61C8125	22-53	560-584	NAP		g117800	730	211	4.00E-54	60	73	60S ribosomal protein L15 ; (Y15321) putative ribosomal protein L15 [Aspergillus niger]
17912	ENU01706	ANI61C9584	22-53	553-586	NAP		g2950474	340	96	2.00E-19	57	97	(U24698) norsolorinic acid reductase [Aspergillus parasiticus]
17913	ENU01707	ANI61C5212	72-97	611-638	NAP		g3850093	294	86	2.00E-16	33	36	
17914	ENU01708	ANI61C1119	68-90	617-636	NAP		g3122672	798	155	5.00E-54	91	77	
17915	ENU01709	ANI61C1135	29-49	576-598	NAP		g1200177	916	85	3.00E-32	42	47	

# Database Statistics

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17916	ENU01710	ANI61C1038	22-54	571-591	NAP		g1730665	121	61	0.000000	24	90	hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region ; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae) ; (Z71633) ORF YNR018w [Saccharomyces cerevisiae]
17917	ENU01711	ANI61C8430:	55-73	609-628	NAP		g2507240	213	88	6.00E-17	39	31	aspartic proteinase 3 precursor (YAP5IN 1) ; aspergillopepsin I (EC 3.4.23.18) YAP3 precursor - yeast (Saccharomyces cerevisiae) ; (U53877) Yap3p: aspartic proteinase [Saccharomyces cerevisiae] ; (X89514) Aspartyl protease [Saccharomyces cerevisiae] ; (Z73292) ORF YLR120c [Saccharomyces cerevisiae] (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
17918	ENU01712	ANI61C4637:	56-76	611-630	NAP		g2276352	429	173	1.00E-42	47	49	succinate dehydrogenase (ubiquinone) iron-sulfur protein precursor (IP) ; (AF042062) succinate dehydrogenase iron-sulphur protein [Mycosphaerella graminicola]
17919	ENU01713	ANI61C9863:	22-44	571-596	NAP		g3334166	904	276	8.00E-74	81	57	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17920	ENU01714	ANI61C9609:	26-47	582-602	NAP		g1351714	695	115	3.00E-26	36	40	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17921	ENU01715	ANI61C9609:	26-47	582-602	NAP		g1351714	695	115	3.00E-26	36	40	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17922	ENU01716	ANI61C6570:	24-52	582-601	NAP		g2388943	659	204	5.00E-52	53	52	egp-binding protein, len:392a a, similar eg. to YBR025C, YBN5_yeast, P38219, hypotheticala l 44.2 Kd protein, (394aa), fasta scores, opt.:1664, E(0):0, (63.7% identity in 391 aa overlap), also sim..."
17923	ENU01717	ANI61C9806:	25-44	584-606	NAP		g3810864	422	66	2.00E-18	36	53	(AL032681) alcohol dehydrogenase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17924	ENU01718	AN161C3200:	47-66	597-630	NAP		g2498268	143	61	0.000000	36	36	copper transport protein CTR3 (copper transporter 3) ; probable membrane protein YLR411w - yeast
		3021..2396								006			(Saccharomyces cerevisiae) ; (U20162) Ctr3p [Saccharomyces cerevisiae] ; (U81482) copper transporter 3 [Saccharomyces cerevisiae] probable eukaryotic translation initiation factor 3 beta subunit (EIF-3 beta) ; (Z70691) eukaryotic translation initiation factor 3 beta subunit [Schizosaccharomyces pombe] (AL022117) putative o-methyltransferase [Schizosaccharomyces pombe] (Z99162) farnesyltransferase beta subunit [Schizosaccharomyces pombe] (AL031545) hypothetical ryanodine receptor domain containing protein [Schizosaccharomyces pombe] signal recognition particle 54 K D protein homolog ; signal recognition particle 54K protein homolog - Aspergillus niger ; (L38317) srpA gene product [Aspergillus niger] ; srpA gene [Aspergillus niger] (AF030296) ubiquitin conjugating enzyme UBC1 [Glomerella cingulata] (AF012091) cystein rich protein [Metarhizium anisopliae] "endo-1,4-beta-xylinase 2 precursor (xylinase 2) (1,4-beta-D-xylin xylanohydrolase 2) ; endo-1,4-beta-xylinase (EC 3.2.1.8) 2 precursor - Emericella nidulans ; (Z49893) xylinase [Emericella nidulans] " hypothetical protein YOL151w - yeast (Saccharomyces cerevisiae) ; (Z48239) orf2 [Saccharomyces cerevisiae] ; (Z74893) ORF YOL151w [Saccharomyces cerevisiae]
17925	ENU01719	AN161C5549:	60-81	622-644	NAP		g1723536	633	110	4.00E-39	42	25	
		191..818											
17926	ENU01720	AN161C1131	35-55	600-619	NAP		g2959364	299	136	1.00E-31	41	70	
		2:847..220											
17927	ENU01721	AN161C4472:	58-79	611-642	NAP		g2408017	229	78	7.00E-22	41	39	
		796..170											
17928	ENU01722	AN161C9766:	48-73	613-632	NAP		g3581910	562	155	2.00E-37	45	48	
		2644..3270											
17929	ENU01723	AN161C1069	22-47	588-607	NAP		g3334345	2295	333	6.00E-91	92	39	
		1:2644..3271											
17930	ENU01724	AN161C1043	63-82	632-652	NAP		g3323498	654	132	1.00E-51	94	80	
		5:4737..5368											
17931	ENU01725	AN161C3265:	67-88	639-658	NAP		g2352898	780	116	1.00E-49	52	50	
		1748..1480											
17932	ENU01726	AN161C1074	46-65	617-639	NAP		g1722902	1116	250	5.00E-98	96	88	
		6:1250..615											
17933	ENU01727	AN161C7309:	63-82	626-657	NAP		g2132023	300	93	3.00E-20	33	55	
		1500..864											



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17934	ENU01728	AN161C3091:	44-64	617-638	NAP		g131622	281	65	4.00E-20			"phosphoribosylglycinamide formyltransferase (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase); ADE8 protein - yeast (Saccharomyces cerevisiae) ; (M36585) ADE8 gene product [Saccharomyces cerevisiae] ; (U32274) Ade8p: glycinamide ribotide transformylase, EC number 2.1.2.2; YDR408C; CAI: 0.12 [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae]"
17935	ENU01729	AN161C468:2	30-49	605-624	NAP		g1351673	423	141	4.00E-33	42	57	hypothetical 37.7 KD protein C1F7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown [Schizosaccharomyces pombe] (Z98974) putative cytochrome p450 [Schizosaccharomyces pombe] hypothetical protein YPL170w - yeast (Saccharomyces cerevisiae) ; (Z73526) ORF YPL170w [Saccharomyces cerevisiae] ; (X96770) P2515 protein [Saccharomyces cerevisiae] hypothetical 128.1 KD protein in OMP2-MSG5 intergenic region ; probable membrane protein YNL054w - yeast (Saccharomyces cerevisiae) ; (U12141) Ynl2467p [Saccharomyces cerevisiae] ; (Z71330) ORF YNL054w [Saccharomyces cerevisiae] (Z97339) hypothetical protein [Arabidopsis thaliana] (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
17936	ENU01730	AN161C7926:	39-58	609-633	NAP		g2388903	558	210	7.00E-54	57	37	
17937	ENU01731	AN161C1107	32-51	607-629	NAP		g2132219	249	72	7.00E-22	40	100	
17938	ENU01732	AN161C6672:	56-76	629-653	NAP		g1730734	144	68	8.00E-11	24	17	
17939	ENU01733	AN161S4240:	23-54	594-621	NAP		g2244937	997	334	3.00E-99	95	40	
17940	ENU01734	AN161C354:1	35-54	619-638	NAP		g3850084	483	133	9.00E-31	41	61	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17941	ENU01735	AN161C1069	49-68	634-653	NAP		g2132301	219	62	0.000000	30	84	hypothetical protein YPR143w - yeast (Saccharomyces cerevisiae) ; (U40829) Note that there is an overlapping ORF on the other strand (27648-27085)
		1:1390..744								004			
17942	ENU01736	AN161C1646: 650..4	72-91	641-676	NAP		g3581866	298	137	6.00E-32	40	76	[Saccharomyces cerevisiae] (AL031541) putative dehydrogenase [Streptomyces coelicolor]
17943	ENU01737	AN161C1050 5:10224..10876	23-55	611-633	NAP		g1083640	186	85	6.00E-16	26	39	cytochrome P450III - rat ; (X79991) cytochrome P450III [Rattus norvegicus] ; (D38381) P450 6beta-2 [Rattus norvegicus] ; cytochrome P450 [Rattus norvegicus]
17944	ENU01738	AN161C1116 0:1150..1803	55-77	646-666	NAP		g3219917	212	64	4.00E-18	28	84	hypothetical 27.4 KD protein C30D10.14 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
17945	ENU01739	AN161C8325: 773..1431	22-45	612-638	NAP		g2131352	336	101	5.00E-21	48	87	hypothetical protein YDL166c - yeast (Saccharomyces cerevisiae) ; (Z67750) putative protein [Saccharomyces cerevisiae] ; (Z74214) ORF YDL166c [Saccharomyces cerevisiae] probable sterigmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emmericella nidulans]
17946	ENU01740	AN161C7771: 2257..2894	30-50	629-646	NAP		g2493387	2647	458	e-128	98	43	Deoxyhypusine synthase ; (U22400) deoxyhypusine synthase [Neurospora crassa]
17947	ENU01741	AN161C8376: 39..700	57-75	657-676	NAP		g1352268	911	325	1.00E-88	77	60	hypothetical 52.3 KD protein C56F8.06C in chromosome I precursor ; (Z69728) unknown
17948	ENU01742	AN161C744:7 3..735	32-54	632-651	NAP		g1723438	219	74	8.00E-13	43	19	[Schizosaccharomyces pombe] (Z95395) hypothetical protein [Schizosaccharomyces pombe] (AL031825) putative membrane transport protein
17949	ENU01743	AN161C9987: 115..777	23-43	624-643	NAP		g2462674	356	122	2.00E-27	32	57	[Schizosaccharomyces pombe]
17950	ENU01744	AN161C2574: 4710..4048	22-54	620-642	NAP		g3702646	276	104	6.00E-22	34	36	[Schizosaccharomyces pombe]
17951	ENU01745	AN161C3010: 256..920	49-69	651-670	NAP		g2131405	462	150	7.00E-36	51	51	[Schizosaccharomyces pombe] hypothetical protein YDR267c - yeast (Saccharomyces cerevisiae) ; (U51030) Ydr267cp [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17952	ENU01746	ANI61C9890:	49-68	652-673	NAP		g549768	133	55	0.000000			hypothetical 61.1 KD protein in YPT52-DBP7 intergenic region ;
		1427..2093								5			hypothetical protein YKR016w - yeast (Saccharomyces cerevisiae) ; (Z28241) ORF YKR016w [Saccharomyces cerevisiae]
17953	ENU01747	ANI61C4162:	23-46	627-647	NAP		g3913152	919	336	1.00E-91	70	66	"alpha-L-arabinofuranosidase precursor (arabinoxylan arabinofuranohydrolase) ; (Z78010) (1,4)-beta-D-arabinoxylan arabinofuranohydrolase [Aspergillus tubingensis]"
		4593..3927											sorbitol utilization protein SOU2 ; (AF002134) Sou2p [Candida albicans] (Z98533) putative ma-directed ma polymerase [Schizosaccharomyces pombe]
17954	ENU01748	ANI61C8530:	43-63	647-668	NAP		g2492755	704	113	5.00E-50	54	72	hypothetical protein YDR440w - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr440wp; CAI: 0.13 [Saccharomyces cerevisiae]
		2774..2107											citrate transport protein - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2039-ORF [Saccharomyces cerevisiae] ; (Z36160) ORF YBR291c [Saccharomyces cerevisiae] ; ORF YBR2039 [Saccharomyces cerevisiae] (Z99292) hypothetical protein [Schizosaccharomyces pombe]
17955	ENU01749	ANI61C7365:	37-56	629-664	NAP		g2330856	841	75	5.00E-17	32	18	[Schizosaccharomyces pombe] M-phase inducer phosphatase ; protein-tyrosine-phosphatase (EC 3.1.3.48) nimT - Emmericella nidulans ; (X64601) NIMT/CDC25 [Emmericella nidulans] (AL023776) hypothetical protein [Schizosaccharomyces pombe]
		1551..882											
17956	ENU01750	ANI61C3463:	67-86	674-699	NAP		g2131494	346	91	8.00E-18	35	38	hypothetical protein 150 [Murine herpesvirus 68] ; (Y09060) serine threonine rich glycoprotein [murine herpesvirus 68] ; (U97553) glycoprotein 150 [murine herpesvirus 68]
		1301..1975											
17957	ENU01751	ANI61C8563:	22-44	632-656	NAP		g626251	280	47	1.00E-11			
		428..1104											
17958	ENU01752	ANI61C319.4	24-51	637-659	NAP		g2414577	431	88	1.00E-34	40	69	
		177..4854											
17959	ENU01753	ANI61C3311:	40-59	660-679	NAP		g1333636	197	43	0.003			
		4708..5389											
17960	ENU01754	ANI61C737.1	25-48	648-667	NAP		g266564	1297	343	e-124	96	41	
		037..353											
17961	ENU01755	ANI61C8708:	32-59	656-675	NAP		g3184056	76	46	0.0002			
		3206..2521											

# Sequence Annotation

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17962	ENU01756	AN150C6889	47-66	665-690	NAP		g2132389		233	1.00E-60	57	73	"phosphate transport protein, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X92441) YOR50-12 [Saccharomyces cerevisiae] ; (Z75130) ORF YOR222w [Saccharomyces cerevisiae]"
		_1:1734..1049											
17963	ENU01757	AN161C70:24	22-45	645-667	NAP		g2496730	369	169	2.00E-41	40	55	hypothetical protein Y4OU precursor ; (AE000089) Y4OU [Rhizobium sp. NGR234]
		89..1802											
17964	ENU01758	AN161C7798:	28-47	656-675	NAP		g2132397	344	134	5.00E-31	44	42	POSS protein - yeast (Saccharomyces cerevisiae) ; (Z73544) ORF YPL188w [Saccharomyces cerevisiae]
		790..101											
17965	ENU01759	AN161C8193:	22-48	642-673	NAP		g1351368	360	100	2.00E-35			RNA polymerase II holoenzyme cyclin-like subunit ; cyclin homolog UME3 - yeast (Saccharomyces cerevisiae) ; (U20635) Sn8p [Saccharomyces cerevisiae] ; (U20221) RNA polymerase II holoenzyme cyclin-like subunit [Saccharomyces cerevisiae] ; (U16248) cyclin [Saccharomyces cerevisiae] ; (Z71301) ORF YNL025c [Saccharomyces cerevisiae] ; RNA polymerase II regulatory protein [Saccharomyces cerevisiae]
		3049..2356											
17966	ENU01760	AN161C5471:	22-41	657-676	NAP		g1703215	283	129	2.00E-29	29	36	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
		2354..1658											
17967	ENU01761	AN161C9593:	22-49	655-677	NAP		g731806	707	270	5.00E-72	56	20	"probable calcium-transporting ATPase 7 ; probable membrane protein YIL048w - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 1151, CAl: 0.17, similar to S30768 S30768 probable ATPase - yeast (saccharomyces cerevisiae) [Saccharomyces cerevisiae]"
		1..698											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17968	ENU01762	ANI61C1070	60-79	696-715	NAP		g1730823	610	136	2.00E-31	38	36	probable mannosyltransferase ALG9; probable membrane protein YNL219c-yeast (Saccharomyces cerevisiae); (Z71495) ORF YNL219c [Saccharomyces cerevisiae]; (X96417) putative mannosyltransferase [Saccharomyces cerevisiae]
17969	ENU01763	ANI61C7105: 1769..1069	22-44	652-680	NAP		g586542	859	95	1.00E-41	46	36	general amino acid permease AGP2; probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae); (X75891) YBR1007 [Saccharomyces cerevisiae]; (Z36001) ORF YBR132c [Saccharomyces cerevisiae]; YBR1007 gene [Saccharomyces cerevisiae] (U70619) heroin esterase [Rhodococcus sp.]
17970	ENU01764	ANI61C3637: 100..802	28-63	669-688	NAP		g2088525	352	83	4.00E-18	37	64	lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (AL035226) major facilitator superfamily protein [Schizosaccharomyces pombe] (AL023589) membrane transporter [Schizosaccharomyces pombe]
17971	ENU01765	ANI61C1020: 706..3	53-76	695-714	NAP		g125935	137	65	5.00E-10	32	19	hypothetical 26.1 KD protein in POP4-SHM1 intergenic region; hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae); (X70529) ORF YBR1729 [Saccharomyces cerevisiae]; (Z36130) ORF YBR261c [Saccharomyces cerevisiae] unknown; (AF046024) UBA3 [Homo sapiens]; (AB012190) Nedd8-activating enzyme hUba3 [Homo sapiens] (AL035396) SRG1-like protein [Arabidopsis thaliana] (AF069492) SONA [Emmericella nidulans]
17972	ENU01766	ANI61C4189: 2709..2005	35-54	674-697	NAP		g4160574	519	63	2.00E-18	33	40	
17973	ENU01767	ANI61C8086: 2503..1797	56-76	701-720	NAP		g3135989	619	183	1.00E-45	39	40	
17974	ENU01768	ANI61C7151: 490..1197	24-45	670-689	NAP		g586379	359	120	6.00E-36	40	98	
17975	ENU01769	ANI61C8423: 208..916	39-59	686-705	NAP		g4507765	660	204	5.00E-52	46	53	
17976	ENU01770	ANI61C2775: 2225..1517	71-91	715-737	NAP		g4454019		45	0.00007			
17977	ENU01771	ANI61C9647: 1724..1014	36-55	681-704	NAP		g3202044	1440	496	e-140	98	65	

# Gene Set

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17978	ENU01772	ANI61C7619:	70-89	711-738	NAP		g729968	889	301	3.00E-81	60	53	"saccharopine dehydrogenase [NADP+, L-glutamate forming] ; saccharopine dehydrogenase (NADP+, L-glutamate-forming) (EC 1.5.1.10) - yeast (Saccharomyces cerevisiae) ; (X77363) saccharopine dehydrogenase (NADP+, L-glutamate forming) [Saccharomyces cerevisiae] ; (Z71665) ORF YNR050c [Saccharomyces cerevisiae]"
		1340..630											
17979	ENU01773	ANI61C1147	57-79	706-726	NAP		g2624697	823	266	5.00E-76	76	53	Pectin Lyase A
		1:36..747											
17980	ENU01774	ANI61C8541:	54-76	704-723	NAP		g1709941	298	106	2.00E-22	27	35	proline-specific permease ; proline transport protein - yeast (Saccharomyces cerevisiae) ; (X95720) O6345 [Saccharomyces cerevisiae] ; (Z75256) ORF YOR348c [Saccharomyces cerevisiae] (AL023518) hypothetical protein [Schizosaccharomyces pombe] "hypothetical 23.7 KD protein C13G6.14 in chromosome I ; hypothetical protein SPAC13G6.14 - fission yeast (Schizosaccharomyces pombe) ; hypothetical protein SPAC24B11.03 - fission yeast (Schizosaccharomyces pombe) ; (Z54308) hypothetical protein [Schizosaccharomyces pombe] ; (Z67757) unknown [Schizosaccharomyces pombe] ; (AF125215) diadenosine 5', 5'''-P1,P6-hexaphosphate hydrolase [Schizosaccharomyces pombe]"
		3665..2954											
17981	ENU01775	ANI61C6911:	35-56	687-707	NAP		g3130055	90	41	0.000000	28	64	RAS-2 protein ; (D16137) NC-ras-2 protein [Neurospora crassa]
		1061..347											
17982	ENU01776	ANI61C578:8	22-41	678-697	NAP		g1175461	212	75	5.00E-13			
		1..798											
17983	ENU01777	ANI61C1120	22-41	680-699	NAP		g2500078	676	151	2.00E-55	68	94	
		8:2075..1355											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17984	ENU01778	ANI61C1029	22-51	680-699	NAP		g1730800	334	120	1.00E-37	37	85	hypothetical 28.8 KD protein in PSD1-SK01 intergenic region ; hypothetical protein YNL168c - yeast (Saccharomyces cerevisiae) ; (X92517) N1696 [Saccharomyces cerevisiae] ; (Z71444) ORF YNL168c [Saccharomyces cerevisiae] (D64052) cytochrome P450 like_TBP [Nicotiana tabacum] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] xanthine dehydrogenase (purine hydroxylase I) ; xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans ; (X82827) xanthine dehydrogenase [Emericella nidulans] hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		4:9723..9004											
17985	ENU01779	ANI61C1253:	68-87	728-748	NAP		g1545805	653	102	9.00E-27	66	44	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] xanthine dehydrogenase (purine hydroxylase I) ; xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans ; (X82827) xanthine dehydrogenase [Emericella nidulans] hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		7171..6449											
17986	ENU01780	ANI61C4046:	58-83	706-741	NAP		g3560142	680	132	3.00E-30	34	38	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] xanthine dehydrogenase (purine hydroxylase I) ; xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans ; (X82827) xanthine dehydrogenase [Emericella nidulans] hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		3414..2689											
17987	ENU01781	ANI61C6939:	61-80	729-748	NAP		g2493965	729	218	5.00E-70	64	15	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] xanthine dehydrogenase (purine hydroxylase I) ; xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans ; (X82827) xanthine dehydrogenase [Emericella nidulans] hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		556..1285											
17988	ENU01782	ANI61C6754:	25-45	693-712	NAP		g1351711	3300	181	9.00E-72	59	18	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] xanthine dehydrogenase (purine hydroxylase I) ; xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans ; (X82827) xanthine dehydrogenase [Emericella nidulans] hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		3042..3771											
17989	ENU01783	ANI61C177:2	43-62	713-732	NAP		g2635242	234	93	2.00E-18	31	61	(Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		2..753											
17990	ENU01784	ANI61C6621:	25-44	696-715	NAP		g2982954	658	139	1.00E-32	42	44	(AE000680) glutamyl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		2002..2734											
17991	ENU01785	ANI61C1038	24-43	689-714	NAP		g3257130	388	109	2.00E-23	35	57	(AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		8:6660..7392											
17992	ENU01786	ANI61C380:1	26-49	698-717	NAP		g2808634	545	150	1.00E-35	46	20	(AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		856..2589											
17993	ENU01787	ANI61C124:7	27-47	700-719	NAP		g3914244	70	2.00E-15				(U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
		..741											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17994	ENU01788	ANI61C3719:	67-90	741-761	NAP		g1352938	479	188	4.00E-47	43	61	hypothetical 39.7 KD protein in HOM6-PMIT4 intergenic region ; hypothetical protein YJR142w - yeast (Saccharomyces cerevisiae) ; (Z49642) ORF YJR142w [Saccharomyces cerevisiae]
17995	ENU01789	ANI61C846:2	22-49	700-719	NAP		g1351369	850	275	3.00E-73	60	41	meiotic MRNA stability protein kinase UME5 ; (U20222) Ssb10p [Saccharomyces cerevisiae] ; RNA polymerase II regulatory protein [Saccharomyces cerevisiae]
17996	ENU01790	ANI61C8292:	22-57	699-720	NAP		g118066	495	186	1.00E-46	41	45	cyclohexanone monooxygenase ; (M19029) cyclohexanone monooxygenase [Acinetobacter sp.]
17997	ENU01791	ANI61C2524:	60-80	738-759	NAP		g2493572	414	175	2.00E-43	41	45	putative CDP-diacylglycerol--serine O-phosphatidyltransferase (phosphatidylserine synthase) ; (Z86109) unknown [Saccharomyces pastorianus]
17998	ENU01792	ANI61C1071	32-51	713-737	NAP		g2842695	79	58	0.000000	23	17	hypothetical 150.9 KD protein C6G9_04 in chromosome I ; (Z81317) hypothetical protein [Schizosaccharomyces pombe]
17999	ENU01793	ANI61C3292:	63-83	749-769	NAP		g2330659	222	59	2.00E-14	29	16	(Z98595) putative snf2 family helicase [Schizosaccharomyces pombe]
18000	ENU01794	ANI61S1000:	52-71	738-759	NAP		g117619		76	3.00E-13	30	37	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18001	ENU01795	AN161C5352:	57-83	748-768	NAP		g3123159	493	202	1.00E-51	45	60	hypothetical 40.4 KD TRP-ASP repeats containing protein C14B1.4 in chromosome III ; (Z37139) similar to guanine nucleotide binding protein; cDNA EST EMBL:T00917 comes from this gene; cDNA EST CEMSE07F comes from this gene; cDNA EST EMBL:T00918 comes from this gene; cDNA EST EMBL:D70900 comes from this gene; cD...
		28..781											
18002	ENU01796	AN161C6476:	68-89	750-781	NAP		g2804298	680	92	6.00E-31	37	39	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous] (AC000133) ORF [Emerticella nidulans]
		6018..6773											
18003	ENU01797	AN161C1116	61-80	749-775	NAP		g1870210	1452	481	e-135	98	53	(AL031174) beta-transducin [Schizosaccharomyces pombe]
		6:120..876											
18004	ENU01798	AN161C1060	65-87	758-779	NAP		g3393019	791	194	5.00E-81	60	53	putative seryl-TRNA synthetase YHR011W (serine--TRNA ligase) (SERRS) ; serine--TRNA ligase homolog - yeast (Saccharomyces cerevisiae) ; (U10400) Yhr011wp [Saccharomyces cerevisiae]
		4:70..826											
18005	ENU01799	AN161C8864:	58-77	751-772	NAP		g731635	551	189	2.00E-47	44	53	"(AL031532) yeast gtr2 homolog, novel small GTPase subfamily protein [Schizosaccharomyces pombe]"
		2659..1903											
18006	ENU01800	AN150C2350	23-58	720-744	NAP		g3560242		251	2.00E-67	55	75	putative flavin-containing monooxygenase MTV014.14 ; (AL021646) hypothetical protein Rv3170 [Mycobacterium tuberculosis] (AF097728) pyruvate carboxylase [Aspergillus terreus]
		0_1:82..845											
18007	ENU01801	AN161C1420:	22-47	724-743	NAP		g3913051	244	76	3.00E-13	30	55	RAS-related protein RAB-11B ; GTP-binding protein Rab11b - mouse ; (L26528) Rab11b [Mus musculus]
		1..764											
18008	ENU01802	AN161C6541:	22-44	723-744	NAP		g3806120	3163	392	e-108	89	19	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii]"
		1379..2143											
18009	ENU01803	AN161C1003	22-56	726-750	NAP		g1172815	699	251	6.00E-74	78	91	
		4:100..870											
18010	ENU01804	AN150C6358	47-73	756-775	NAP		g1437475		151	3.00E-42	40	80	
		_1:803..33											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18011	ENU01805	ANI61C8273:	72-91	771-803	NAP		g1346665	128	53	0.000002	35	33	"N-terminal acetyltransferase 2 (amino-terminal, alpha-amino, acetyltransferase 2) ; protein N-acetyltransferase (EC 2.3.1.-) NAT2 - yeast (Saccharomyces cerevisiae) ; (X85807) ORF G6630 [Saccharomyces cerevisiae] ; (Z72932) ORF YGR147c [Saccharomyces cerevisiae] "
		4655..3882											probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (Y17243) cytochrome P450 [Gibberella fujikuroi] (AL021839) myb family DNA binding protein [Schizosaccharomyces pombe] phosphoribosylaminoimidazole carboxylase (AIR carboxylase) (AIRC) ; (U70673) phosphoribosylaminoimidazole carboxylase [Filiobasidiella neoformans] hypothetical 36.2 KD protein in HAM1-PEM2 intergenic region ; hypothetical protein YJR070c - yeast (Saccharomyces cerevisiae) ; (Z49570) ORF YJR070c [Saccharomyces cerevisiae] ; (L47993) ORF YJR070c [Saccharomyces cerevisiae] unknown ; (D87432) Similar to Schistosoma mansoni amino acid permease (L25068). [Homo sapiens] (D17548) protein-tyrosine phosphatase [Saccharomyces cerevisiae] (X98493) ACC oxidase [Nicotiana tabacum] (X63998) aminopeptidase yscII [Saccharomyces cerevisiae] (AL023796) cyclin C homologue [Schizosaccharomyces pombe]
18012	ENU01806	ANI61C3339:	54-73	756-786	NAP		g2132957	768	271	5.00E-72	53	49	
		3593..2819											
18013	ENU01807	ANI61C3910:	51-70	765-784	NAP		g4127832	220	106	2.00E-22	32	46	
		207..982											
18014	ENU01808	ANI61C1094	43-62	743-778	NAP		g2894269	225	68	8.00E-11	44	29	
		2:150..216											
18015	ENU01809	ANI61C9734:	54-73	758-790	NAP		g2500019	1081	123	5.00E-29	48	39	
		2103..1324											
18016	ENU01810	ANI61C9817:	35-54	748-773	NAP		g1352887	525	157	7.00E-43	51	70	
		902..122											
18017	ENU01811	ANI61C8177:	35-54	755-774	NAP		g4507053	223	85	5.00E-16	34	45	
		14..795											
18018	ENU01812	ANI61C7083:	38-58	762-781	NAP		g459243	155	86	3.00E-16	33	29	
		90..875											
18019	ENU01813	ANI61C1049	37-57	758-780	NAP		g2826769		83	2.00E-15			
		4:4220..5005											
18020	ENU01814	ANI61C1857:	39-58	765-783	NAP		g3368	2245	207	8.00E-53	41	28	
		2322..2414											
18021	ENU01815	ANI61C5906:	27-46	753-772	NAP		g3192038	395	129	3.00E-29	32	74	
		1318..531											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18022	ENU01816	ANI61C9151:	22-53	751-769	NAP		g2500768	963	190	5.00E-66	61	66	Septin homolog SPN2 ; (U29888)
		4849..4060											septin homolog [Schizosaccharomyces pombe]
18023	ENU01817	ANI61C9777:	58-78	782-805	NAP		g2665711		82	1.00E-19			(AF035413) AgaG [Agrobacterium tumefaciens]
18024	ENU01818	1870..1082 ANI61C9875:	52-71	783-806	NAP		g1705594	1074	327	6.00E-89	67	47	peroxisome assembly protein CAR1 (peroxin-2) ; car1 protein - Podospora anserina ; (X87329) peroxisome assembly factor [Podospora anserina]
		79..875											hypothetical protein YLR189c - yeast (Saccharomyces cerevisiae) ; (U17246)
18025	ENU01819	ANI61C6977:	22-46	759-778	NAP		g1077411	721	240	8.00E-67	56	20	Ylr189cp [Saccharomyces cerevisiae] (AJ009657) Mu3 subunit of clathrin-associated protein complex AP-3 [Drosophila melanogaster]
		1666..868											"asparaginyl-TRNA synthetase, mitochondrial precursor (asparagine--TRNA ligase) (ASNRS) ; hypothetical protein YCR024c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR024c, len:492 [Saccharomyces cerevisiae]"
18026	ENU01820	ANI61C1134:	22-43	759-778	NAP		g3341417		62	2.00E-20			
		3715..2917											
18027	ENU01821	ANI61C1485:	25-44	761-782	NAP		g135160	639	165	3.00E-40	40	51	
		1557..2356											
18028	ENU01822	ANI61C5728:	24-46	773-792	NAP		g3925768	675	115	9.00E-34	46	70	(AL034352) putative GTP-binding protein [Schizosaccharomyces pombe]
		4582..3771											(AF095899) PDI related protein A [Aspergillus niger]
18029	ENU01823	ANI61C8692:	56-75	793-824	NAP		g3873259	1526	257	5.00E-68	58	56	mitochondrial import receptor subunit TOM40 (MOM38 protein) (translocase of outer membrane 40 KD subunit) ; mitochondrial import receptor MOM38 - Neurospora crassa ; (X56883) outer membrane protein [Neurospora crassa] ; outer membrane protein MOM38 [Neurospora crassa]
		967..157											
18030	ENU01824	ANI61C7436:	58-77	807-827	NAP		g127218	924	257	5.00E-68	57	66	
		2475..3286											
18031	ENU01825	ANI61C3438:	22-45	772-791	NAP		g1168396	833	298	2.00E-80	58	50	actin interacting protein 2 ; AIP2 protein - yeast (Saccharomyces cerevisiae) ; (U35667) Aip2p [Saccharomyces cerevisiae] ; (Z67750) putative protein [Saccharomyces cerevisiae] ; (Z74226) ORF YDL178w [Saccharomyces cerevisiae]
		1120..309											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18032	ENU01826	ANI61C1214:	24-52	780-799	NAP		g130806	249	56	0.000000	35	22	pre-mRNA processing RNA helicase PRP5 ; pre-mRNA processing protein PRP5 - yeast (Saccharomyces cerevisiae) ; (M33191) PRP5 [Saccharomyces cerevisiae] ; (Z36106) ORF YBR237w [Saccharomyces cerevisiae]
18033	ENU01827	ANI61C5721:	22-51	769-799	NAP		g2498971	369	56	4.00E-28	36	54	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans]
18034	ENU01828	ANI61C5721:	22-51	769-799	NAP		g2498971	369	56	4.00E-28	36	54	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans]
18035	ENU01829	ANI61C9612:	22-53	767-799	NAP		g4263703	221	101	2.00E-23	33	53	(AC006223) hypothetical protein [Arabidopsis thaliana]
18036	ENU01830	ANI61C1628:	31-53	793-816	NAP		g1710663	2331	428	e-119	72	23	putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) ; (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe]
18037	ENU01831	ANI61C7971:	22-51	783-813	NAP		g3947884	625	146	2.00E-34	48	70	body component, putative gamma-tubulin interacting protein, yeast SCP98 homolog [Schizosaccharomyces pombe]
18038	ENU01832	ANI61C1061:	52-70	810-845	NAP		g4588080	616	175	3.00E-43	35	56	(AF095286) guanine deaminase GDA [Homo sapiens]
18039	ENU01833	ANI61C5959:	51-70	827-849	NAP		g115699	1548	226	2.00E-90	58	57	"catalase (PXP-9) ; catalase (EC 1.11.1.6), peroxisomal - yeast (Candida tropicalis) ; (X13978) catalase (AA 1 - 485) [Candida tropicalis] ; (X06660) catalase (AA 1 - 485) [Candida tropicalis] ; peroxisomal catalase [Candida tropicalis] "
18040	ENU01834	ANI61C9843:	55-74	837-856	NAP		g2414656	694	234	7.00E-61	47	54	(Z99261) putative aminotransferase [Schizosaccharomyces pombe]

# Gene Ontology

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
18041	ENU01835	ANI61C1438:	24-45	807-826	NAP	g2127591	137	57	0.000000	29	81	02	N-acetylphosphinothricin-tripetide-deacetylase - Streptomyces viridochromogenes ; (X65195) N-acetylphosphinothricin-tripetide-deacetylase [Streptomyces viridochromogenes]
		1368..522											
18042	ENU01836	ANI61C1600:	24-43	811-831	NAP	g2293194	289	89	2.00E-32				(AF008220) yfER [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
		1195..346											(AF102147) putative dimethyladenosine transferase [Homo sapiens]
18043	ENU01837	ANI61C6951:	26-45	816-835	NAP	g4050050	648	159	8.00E-72	54	82		(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
		582..1433											sporulation protein SPS19 (sporulation-specific protein SPX19) ; sporulation protein SPS19 - yeast (Saccharomyces cerevisiae) ; (X78898) NI362 [Saccharomyces cerevisiae] ; (Z71479) ORF YNL202w [Saccharomyces cerevisiae]
18044	ENU01838	ANI61C9308:	32-55	817-842	NAP	g3395556	676	66	2.00E-32	51	59		
		2353..1501											
18045	ENU01839	ANI61C7122:	57-77	845-867	NAP	g730864	506	152	3.00E-38	53	71		
		49..878											
18046	ENU01840	ANI61C1011	68-87	860-879	NAP	g2494910	1455	255	3.00E-67	47	33		hypothetical 91.7 KD TRP-ASP repeats containing protein in NUP116-FAR3 intergenic region ; probable membrane protein YMR049c - yeast (Saccharomyces cerevisiae) ; (Z49703) unknown [Saccharomyces cerevisiae] (Z75526) Weak similarity to Staphylococcus autolysin gene (TR-G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene [Caenorhabditis elegans] (AC004850) vacuolar assembly protein VPS41 homolog (SS3) [Homo sapiens] mutS (E. coli) homolog 3 ; (U61981) hMSH3 [Homo sapiens] (U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes]
		9:2048..1195											
18047	ENU01841	ANI61C122:	1 47-69	840-859	NAP	g3874039	295	90	2.00E-17	42	27		
		400..546											
18048	ENU01842	ANI61C8569:	40-65	834-853	NAP	g4309891	317	124	7.00E-28	37	33		
		66..921											
18049	ENU01843	ANI61C2388:	49-69	843-863	NAP	g4505249	1372	278	4.00E-74	48	25		
		1763..2619											
18050	ENU01844	ANI61C3304:	22-45	814-836	NAP	g517205	305	149	3.00E-35	33	47		
		3423..2567											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18051	ENU01845	AN161C924:4	70-92	867-890	NAP		g3810847	341	161	8.00E-39	39	37	(AL032684) zinc finger protein [Schizosaccharomyces pombe]
18052	ENU01846	AN161C8857: 9..911	29-48	824-854	NAP		g2492894	1809	331	5.00E-90	56	13	adenylate cyclase (ATP pyrophosphate-lyase) (adenyl cyclase) ; adenylate cyclase (EC 4.6.1.1) - Podospora anserina ; (L43413) adenyl cyclase [Podospora anserina]
18053	ENU01847	AN161C4219: 925..57	44-68	850-869	NAP		g2132252	703	74	1.00E-12	28	40	hypothetical protein YPL263c - yeast (Saccharomyces cerevisiae) ; (Z73619) ORF YPL263c [Saccharomyces cerevisiae]
18054	ENU01848	AN161C5719: 921..50	49-79	856-878	NAP		g1717749	522	153	1.00E-45	41	32	"potassium transport protein ; (Z69369) SPAC3F10.02c, potassium transport gene, len: 841, co nfiict with PIR:S50225 potassium transport protein homolog at position 4549 causes frameshift near N-terminus [Schizosaccharomyces pombe]"
18055	ENU01849	AN161C6777: 874..1	50-69	854-881	NAP		g1175428	583	229	3.00E-59	41	89	(Z54140) conserved hypothetical protein [Schizosaccharomyces pombe]
18056	ENU01850	AN161C8505: 2230..1356	59-79	870-891	NAP		g3080508	510	168	4.00E-41	45	68	(AL022598) UDP-galactose transporter homologue [Schizosaccharomyces pombe]
18057	ENU01851	AN161C8544: 103..977	72-93	880-904	NAP		g3136060	281	145	5.00E-34	34	59	(AL023592) zinc finger protein [Schizosaccharomyces pombe]
18058	ENU01852	AN161C7094: 1117..236	42-61	863-882	NAP		g113382	323	50	0.00002	36	58	alcohol dehydrogenase III ; alcohol dehydrogenase (EC 1.1.1.1) III - Emericella nidulans ; (X02764) alcohol dehydrogenase 3 [Emmericella nidulans] (U94348) acetyl-coenzyme A synthetase [Pyrobaculum aerophilum] (U38783) orf of unknown function; Method: conceptual translation supplied by author
18059	ENU01853	AN161C5249: 176..1059	26-45	848-867	NAP		g4100125	317	89	3.00E-34	40	37	[Schizosaccharomyces pombe]
18060	ENU01854	AN161C1107 8:47..931	33-57	856-875	NAP		g1145409	110	76	3.00E-13	26	42	(Z69254) alpha-galactosidase [Hypoocrea jecorina]
18061	ENU01855	AN161C1082 1:1936..1052	43-62	857-885	NAP		g1580818	1121	439	e-122	67	39	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
18062	ENU01856	AN161C1077 5:2172..1288	42-62	865-884	NAP		g3850084	543	86	2.00E-35	44	72	

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18063	ENU01857	ANI61C5563:	25-45	846-868	NAP		g3873847	153	89	3.00E-17	35	29	(Z82256) cDNA EST EMBL:D67325 comes from this gene; cDNA EST EMBL:C13315 comes from this gene; cDNA EST EMBL:D37596 comes from this gene; cDNA EST EMBL:D69512 comes from this gene; cDNA EST EMBL:C11315 comes from this gene; cDN...
		970..85											
18064	ENU01858	ANI61C9914:	59-78	883-902	NAP		g1723213	499	146	2.00E-34	40	54	hypothetical 51.5 KD protein C3H8.02 in chromosome I ; (Z69086) unknown
		1844..2729											[Schizosaccharomyces pombe]
18065	ENU01859	ANI61C4664:	24-43	854-874	NAP		g3080538	623	182	2.00E-45	48	61	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
		653..1545											[Schizosaccharomyces pombe]
18066	ENU01860	ANI61C1025	22-53	855-875	NAP		g3915186	197	103	2.00E-21	39	57	ubiquitin-conjugating enzyme E2-21 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) (peroxin-4) ; (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]
		5:1471..2366											(Z99295) pre-mrna splicing factor [Schizosaccharomyces pombe]
18067	ENU01861	ANI61C7946:	52-74	888-907	NAP		g2414602	434	85	8.00E-16	37	56	(X98931) heat shock protein 70 [Emmericella nidulans]
		2004..1107											myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
18068	ENU01862	ANI61C1054	34-56	873-892	NAP		g2764949	1252	334	3.00E-96	97	43	(L48797) toxin pump [Cochliobolus carbonum]
		8:1613..720											(AF010145) hexose transporter [Aspergillus parasiticus]
18069	ENU01863	ANI61C5778:	39-58	871-901	NAP		g2500938	988	238	4.00E-62	41	52	hypothetical 40.7 KD protein in OPDE 3'region (ORF2) ; hypothetical protein 2 - Pseudomonas aeruginosa ; (Z14064) ORF2 [Pseudomonas aeruginosa]
		1808..2712											hypothetical 37.7 KD protein C1F7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast [Schizosaccharomyces pombe] ; (Z67998) unknown [Schizosaccharomyces pombe]
18070	ENU01864	ANI61C2559:	67-86	905-930	NAP		g1063421		99	4.00E-20			
		227..1131											
18071	ENU01865	ANI61C257:1	22-53	861-886	NAP		g2306977	1117	124	1.00E-41	56	42	
		317..410											
18072	ENU01866	ANI61C5632:	22-47	868-887	NAP		g732227	502	80	4.00E-32	42	79	
		31..938											
18073	ENU01867	ANI61C1078	54-73	900-919	NAP		g1351673	521	174	7.00E-43	42	66	
		4:1116..209											

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18074	ENU01868	AN161C1004	67-86	921-940	NAP		g2842513	139	49	4.00E-14	25	90	(AL021748) superoxide dismutase [Schizosaccharomyces pombe]
18075	ENU01869	AN161C562:8	71-91	925-944	NAP		g134297	482	155	4.00E-47	40	70	SCJ1 protein; SCJ1 protein - yeast (Saccharomyces cerevisiae); (X58679) SCJ1 [Saccharomyces cerevisiae]; (Z49809) unknown [Saccharomyces cerevisiae]; heat shock protein [Saccharomyces cerevisiae]
18076	ENU01870	AN161C1004	67-86	921-940	NAP		g2842513	139	49	4.00E-14	25	90	(AL021748) superoxide dismutase [Schizosaccharomyces pombe]
18077	ENU01871	AN161C924:2	72-91	911-946	NAP		g1706692	1046	206	1.00E-52	52	61	C-24(28) sterol reductase; probable transport protein ERG4 - yeast (Saccharomyces cerevisiae); (Z72534) ORF YGL012w [Saccharomyces cerevisiae]
18078	ENU01872	AN161C7696: 18..936	39-59	896-915	NAP		g2598593		39	0.034			(Y15369) MtN12 [Medicago truncatula]
18079	ENU01873	AN161C1754: 4729..3810	57-78	909-934	NAP		g3368		96	8.00E-26			(X63998) aminopeptidase yscII [Saccharomyces cerevisiae]
18080	ENU01874	AN161C6862: 22-46	882-905	NAP			g1791305	610	149	1.00E-57	43	70	(U83489) sepin B [Emmericella nidulans]
18081	ENU01875	AN150C1_17 41:3..929	24-43	889-908	NAP		g1703202		168	4.00E-41	38	68	sterigmatocystin biosynthesis regulatory protein; sterigmatocystin synthesis transcriptional regulator aflR - Emmericella nidulans; (U34740) pathway specific transcription factor [Emmericella nidulans]
18082	ENU01876	AN161C352:9 95..69	23-42	888-907	NAP		g1176004	480	192	4.00E-48	39	82	hypothetical 40.4 KDa protein in PES4-HIS2 intergenic region; (D50617) YFR024C [Saccharomyces cerevisiae]
18083	ENU01877	AN161C4038: 71-93	936-957	NAP			g2160185	299	101	8.00E-21	26	42	(AC000132) Similar to S. pombe ISP4 (gb D83992). [Arabidopsis thaliana]
18084	ENU01878	AN161C1100 6:1241..312	32-53	897-919	NAP		g585251		77	1.00E-13			Polyketide synthase HETM; hetm protein - Anabaena sp. (PCC 7120); (L22883) polyketide synthase [Anabaena sp.]
18085	ENU01879	AN161C8862: 22-54	888-910	NAP			g3006183	381	97	9.00E-38	37	67	(AL022304) trp-ast repeats containing protein [Schizosaccharomyces pombe]
18086	ENU01880	AN161C1020 9:2555..1619	34-59	907-926	NAP		g2330840	417	118	1.00E-41	38	90	(Z98531) hypothetical protein [Schizosaccharomyces pombe]





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18095	ENNU01889	AN161C7499:	69-87	418-435	NAP		g2127839	180	65	2.00E-10	32	82	"deoxycytidine triphosphate deaminase homolog - Methanococcus jannaschii ; (U67553) deoxycytidine triphosphate deaminase, putative (dcd)
		1412..1003											[Methanococcus jannaschii]"
18096	ENNU01890	AN161C3183:	32-51	388-407	NAP		g400513		33	0.0007			NADH-ubiquinone oxidoreductase B22 subunit (complex I-B22) (CI-B22) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine ; (X64836) NADH-ubiquinone oxidoreductase complex B22 subunit [Bos taurus]
		568..985											gamma-adaptin - smut fungus (Ustilago maydis) ; (Z46804) gamma-adaptin [Ustilago maydis]
18097	ENNU01891	AN161C1610:	36-56	395-414	NAP		g1078673	1228	40	0.006	31	13	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
		1312..1732											(AL031603) 60s ribosomal protein [Schizosaccharomyces pombe]
18098	ENNU01892	AN161C4480:	22-44	382-401	NAP		g2465151	111	53	0.000001	40	74	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) ; (U34740) putative p450 monooxygenase [Emeticella nidulans]
		445..24											hypothetical protein YPL088w - yeast (Saccharomyces cerevisiae) ; (U43281) Lpg20p [Saccharomyces cerevisiae]
18099	ENNU01893	AN161C6633:	66-83	434-452	NAP		g3646455	432	61	0.000000	77	53	Scyralone dehydratase ; (D86079) scyralone dehydratase [Colletotrichum lagenarium]
		880..1308											hypothetical 66.5 KD protein in ALG9-RAP1 intergenic region ; probable membrane protein YNL218w - yeast (Saccharomyces cerevisiae) ; (Z71494) ORF YNL218w [Saccharomyces cerevisiae]
18100	ENNU01894	AN161C2205:	30-49	400-419	NAP		g2493389	179	56	0.000000	39	21	(AC005169) hypothetical protein [Arabidopsis thaliana]
		4095..4526											(M77661) putative pol polypeptide [Magnaporthe grisea]
18101	ENNU01895	AN161C6093:	31-49	409-426	NAP		g2132183	760	138	3.00E-32	50	42	
		2385..2822											
18102	ENNU01896	AN161C1021	53-72	429-448	NAP		g3024608	488	138	3.00E-44	63	69	
		1:862..1299											
18103	ENNU01897	AN161C1106	56-75	433-452	NAP		g1730822	804	157	3.00E-38	52	24	
		5:3087..3525											
18104	ENNU01898	AN161C1828:	55-72	434-453	NAP		g3687238	493	176	7.00E-44	57	53	
		420..860											
18105	ENNU01899	AN161C3632:	30-51	416-435	NAP		g538067	189	97	6.00E-20	36	10	
		9..456											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18106	ENU01900	AN161C1108:	58-77	445-463	NAP		g731968	426	141	2.00E-33	50	45	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region ; hypothetical protein YJL213w - yeast
		4975..4527											(Saccharomyces cerevisiae) ; (Z34098) ORF [Saccharomyces cerevisiae] ; (Z49488) ORF YJL213w [Saccharomyces cerevisiae]
18107	ENU01901	AN161C4859:	71-90	462-481	NAP		g731347		56	7.00E-17			Metal resistance protein YCF1 (yeast cadmium factor 1) ; (L35237) metal resistance protein [Saccharomyces cerevisiae]
		2706..2254											(AF026204) No definition line found [Caenorhabditis elegans]
18108	ENU01902	AN161C3691:	40-59	432-451	NAP		g2435542	89	45	0.0004	37	70	"60S ribosomal protein YL16B ; ribosomal protein L6.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U22382) Rpl16bp: 60S ribosomal protein YL16B [Saccharomyces cerevisiae] "
18109	ENU01903	AN161C9317:	25-44	419-443	NAP		g1346942	399	125	2.00E-28	50	84	"Interferon-induced GTP-binding protein MX ; Mx resistance protein homolog - perch (fragment) ; (M27252) [Perca fluviatilis gene with homology to murine Mx genes, partial cds.], gene product [Perca fluviatilis] " (AL023518) hypothetical protein [Schizosaccharomyces pombe]
		5033..4573											[Schizosaccharomyces pombe] hypothetical 31.6 KD protein C2E12.03C in chromosome I ; (Z69726) unknown [Schizosaccharomyces pombe]
18110	ENU01904	AN161C1116	63-83	472-491	NAP		g127568	292	82	3.00E-15	31	51	(U31884) aromatic L-amino acid decarboxylase [Rattus norvegicus]
		4:4277..4747											Nitrate reductase 3 (NR) ; (U20450) nitrate reductase [Zea mays] (AF088906) clock-controlled gene-9 protein [Neurospora crassa]
18111	ENU01905	AN161C1389:	72-98	481-501	NAP		g3130056	206	80	7.00E-15	37	22	
		74..545											
18112	ENU01906	AN161C3296:	61-80	479-500	NAP		g1723416	297	104	4.00E-22	39	50	
		747..266											
18113	ENU01907	AN161C3109:	41-58	470-488	NAP		g975309	802	103	2.00E-31	49	29	
		2704..3193											
18114	ENU01908	AN161C3335:	36-55	465-484	NAP		g1352497	1224	112	5.00E-28	42	18	
		2067..2558											
18115	ENU01909	AN150C844_	27-46	460-479	NAP		g3746895		63	0.000000			
		1:539..45											

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18116	ENU01910	ANI61C1026	53-72	494-513	NAP		g465665	310	135	2.00E-31	41	68	"hypothetical 27.1 KD protein UFD4-CAP1 intergenic region ; hypothetical protein YKL009w - yeast (Saccharomyces cerevisiae) ; (S53418) ribosomal protein L10 homolog [Saccharomyces cerevisiae=yeast, Peptide, 236 aa] [Saccharomyces cerevisiae] ; (Z28009) ORF YKL009w [Saccharomyces cerevisiae] "
18117	ENU01911	ANI61C9065	58-76	502-521	NAP		g1491795	503	159	2.00E-38	41	18	"(U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus] "
18118	ENU01912	ANI61C1043	51-68	498-517	NAP		g4107287	459	50	0.000000			(AL035076) putative allantoin permease [Schizosaccharomyces pombe]
18119	ENU01913	ANI61C3562	55-73	505-524	NAP		g4586977	3318	176	1.00E-43	47	7	(AB018382) Mok13; Mok13 is homologous to Mok1 which is an alpha-glucan synthase [Schizosaccharomyces pombe]
18120	ENU01914	ANI61C5666	49-67	512-531	NAP		g3122291	661	161	4.00E-48	70	49	Inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) (PPASE) ; (AJ001000) inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) [Pichia pastoris] hypothetical 16.6 KD protein in ATL 5'region (ORF3) ; (D17366) ORF3 [Staphylococcus aureus] ; (L41499) ORF3 [Staphylococcus aureus] "(U21319) similar to alcohol dehydrogenase, highest similarity to B. japonicum FIXR protein (SP:FIXR_BRAJA_P05406) [Caenorhabditis elegans] "
18121	ENU01915	ANI61C3340	68-87	541-560	NAP		g1723227	109	39	0.017			(AC000133) ORF [Emmericella nidulans]
18122	ENU01916	ANI61C7507	50-69	528-547	NAP		g687834	45	39	0.023			"origin recognition complex protein, subunit 2 ; (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe] ; (AL049474) origin recognition complex protein, subunit 2. [Schizosaccharomyces pombe] "
18123	ENU01917	ANI61C1802	24-44	505-524	NAP		g1870209	332	104	3.00E-22	41	32	
18124	ENU01918	ANI61C4995	54-71	537-556	NAP		g2498711	230	99	2.00E-20	34	31	

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18125	ENU01919	ANI61C4995:	54-71	537-556	NAP		g2498711	230	99	2.00E-20	34	31	"origin recognition complex protein, subunit 2 ; (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe] ; (AL049474) origin recognition complex protein, subunit 2. [Schizosaccharomyces pombe]"
18126	ENU01920	ANI61C8394:	24-43	507-526	NAP		g117804	244	119	1.00E-26			cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Saccharomyces cerevisiae) ; (X03215) cytochrome b2 precursor [Saccharomyces cerevisiae] ; (Z46729) cytochrome b2 precursor [Saccharomyces cerevisiae] ; (AL022070) hsp gprp homolog [Schizosaccharomyces pombe] ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
18127	ENU01921	ANI61C7977:	62-81	545-564	NAP		g2950485	313	137	5.00E-32	45	73	"High affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
18128	ENU01922	ANI61C7152:	41-58	525-545	NAP		g3123032	275	125	2.00E-28	32	30	66 kDa stress protein p66 [Physarum polycephalum]
18129	ENU01923	ANI61C3573:	37-61	523-542	NAP		g1709181	434	45	0.000000	27	27	"High affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
18130	ENU01924	ANI61C8580:	31-52	522-541	NAP		g2808541	871	108	2.00E-23	39	25	(Y16261) CRO1 protein [Podospira anserina]
18131	ENU01925	ANI61C8962:	65-84	559-578	NAP		g1351916	1951	272	1.00E-72	68	22	"AMP deaminase (myoadenylate deaminase) ; AMP deaminase (EC 3.5.4.6) - yeast (Saccharomyces cerevisiae) ; (Z46659) AMD1 gene, len: 810, CAl: 0.19, AMP deaminase [Saccharomyces cerevisiae]"
18132	ENU01926	ANI61C1026	38-57	548-567	NAP		g2440196	487	147	6.00E-35	48	64	(Z99532) myo-inositol transporter [Schizosaccharomyces pombe]

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18133	ENU01927	ANI61C6374:	59-78	570-588	NAP		g140499	649	184	5.00E-46	57	67	"putative 30.7 KD methyltransferase in TSM1-ARE1 intergenic region ; hypothetical protein YCR047c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR047c, len:275 [Saccharomyces cerevisiae]"
18134	ENU01928	ANI61C8578:	55-73	585-604	NAP		g2493143	440	121	4.00E-27	71	88	Vacuolar ATP synthase 16 KD proteolipid subunit ; (U02877) vacuolar ATPase subunit c [Candida tropicalis] (Z99126) putative mannosyl transferase [Schizosaccharomyces pombe] (U78597) kinesin light chain [Plectonema boryanum] probable peroxisomal membrane protein PMP20 (allergen ASP F 3) ; (U58050) peroxisomal-like protein [Aspergillus fumigatus] cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035537) cell division control protein 7 [Schizosaccharomyces pombe]
18135	ENU01929	ANI61C3426:	51-70	583-602	NAP		g2398816	312	103	9.00E-22	30	46	"5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (methionine synthase, vitamin-B12 independent isozyme) (cobalamin-independent methionine synthase) (delta-P8 protein) ; 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - yeast (Saccharomyces cerevisiae) ; (U18839) Met6p- 5-methyltetrahydropteroyl triglutamate--homocysteine methyltransferase [Saccharomyces cerevisiae] ; (U32508) N5-methyltetrahydrofolate homocysteine methyltransferase [Saccharomyces cerevisiae]"
18136	ENU01930	ANI61C1156:	37-61	572-591	NAP		g2645229	156	67	9.00E-11	32	40	
18137	ENU01931	ANI61C5927:	63-81	604-623	NAP		g3914384	536	90	5.00E-45	65	86	
18138	ENU01932	ANI61C823:	68-87	614-633	NAP		g1168817	236	60	1.00E-18	33	16	
18139	ENU01933	ANI61C5908:	71-90	628-647	NAP		g730018	1750	317	4.00E-86	77	26	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18140	ENU01934	ANI61C3096:	49-67	608-627	NAP		g3929350	3103	259	1.00E-68	65	22	Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (multifunctional beta-oxidation protein) [contains: 2-enoyl-CoA hydratase ; D-3-hydroxyacyl CoA dehydrogenase ] ; multifunctional beta-oxidation protein - Neurospora crassa ; (X80052)
		2148..1528											multifunctional beta-oxidation protein [Neurospora crassa]
18141	ENU01935	ANI61C6914:	51-71	610-629	NAP		g4501859	550	101	4.00E-44			"acyl-Coenzyme A dehydrogenase, short/branched chain precursor ; acyl-CoA dehydrogenase, short/branched chain specific precursor (SBCAD) (2-methyl branched chain acyl-CoA dehydrogenase) (2-MEBCAD) ; short/branched chain acyl-CoA dehydrogenase (EC 1.3.-.-) precursor - human ; (U12778) acyl-CoA dehydrogenase [Homo sapiens] " (AF034089) calcineurin subunit B [Neurospora crassa]
18142	ENU01936	ANI61C1103	49-68	612-631	NAP		g2645886	627	210	5.00E-54	87	92	quininate permease (quininate transporter) ; quininate transport protein - Emericella nidulans ; (X13525) quininate permease [Emericella nidulans]
		7.5341..4717											(AL031262) hypothetical protein [Schizosaccharomyces pombe]
18143	ENU01937	ANI61C8512:	47-67	611-631	NAP		g131768	252	73	9.00E-16	32	31	cytochrome B ; ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Emericella nidulans mitochondrion (SGC3) ; (J01389) apocytochrome b [Emericella nidulans]
		26..652											(AB009078) L-2,3-butanediol dehydrogenase [Brevibacterium saccharolyticum]
18144	ENU01938	ANI61C6933:	39-58	608-627	NAP		g3417428	214	75	3.00E-13	31	29	casein kinase II beta chain (CK II) ; (X74274) casein kinase II beta subunit [Schizosaccharomyces pombe]
		1260..629											
18145	ENU01939	ANI61C3548:	33-56	593-623	NAP		g117840	1057	320	5.00E-87	98	54	
		918..286											
18146	ENU01940	ANI61C7842:	28-45	604-623	NAP		g4062842	290	80	1.00E-14	41	69	
		137..774											
18147	ENU01941	ANI61C4563:	50-71	631-649	NAP		g729881	641	226	1.00E-58	58	85	
		1004..363											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18148	ENU01942	ANI61C9471: 43..685	64-83	645-664	NAP		g1718099	846	254	5.00E-67	76	54	vacuolar ATP synthase subunit AC39 (V-ATPase AC39 subunit) (V-ATPase 41 kDa subunit) ; (U36470) vacuolar ATPase 41 kDa subunit [Neurospora crassa]
18149	ENU01943	ANI61C2909: 756..108	45-62	628-651	NAP		g1723727	481	115	1.00E-31	62	42	hypothetical 41.0 kDa protein in YIP1-CBP4 intergenic region ; hypothetical protein YGR173w - yeast (Saccharomyces cerevisiae) ; (Z72958) ORF YGR173w [Saccharomyces cerevisiae]
18150	ENU01944	ANI61C6178: 682..24	32-51	625-648	NAP		g2894179	356	148	4.00E-35	43	65	(AJ223998) PCZA361.15 [Amycolatopsis orientalis]
18151	ENU01945	ANI61C1138: 3..2574..1916	53-72	650-669	NAP		g3810873	144	55	0.000000	32	45	(AB010465) lactonohydrolase [Fusarium oxysporum]
18152	ENU01946	ANI61C8219: 742..81	50-69	650-669	NAP		g1902911		89	4.00E-17			(D83988) reductase [Colletotrichum lagenarium]
18153	ENU01947	ANI61C7493: 4028..3367	67-84	667-686	NAP		g2494090	208	62	1.00E-11	37	55	hypothetical 33.3 kDa protein in PERR-ARGF intergenic region ; (AE000134) putative lyase/synthase [Escherichia coli]
18154	ENU01948	ANI61C1055: 7..133..538	31-50	635-653	NAP		g3023956	885	189	1.00E-47	42	16	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
18155	ENU01949	ANI61C3688: 4356..3691	39-58	643-662	NAP		g2983787	238	86	3.00E-16	39	46	"(AE000737) fructose-1,6-bisphosphate aldolase class II [Aquifex aeolicus]"
18156	ENU01950	ANI61C8586: 1110..441	39-58	647-666	NAP		g3004863	967	262	2.00E-69	57	27	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
18157	ENU01951	ANI61C2388: 4438..5116	56-75	673-692	NAP		g1170278	510	194	5.00E-49	56	62	ATP phosphoribosyltransferase ; ATP phosphoribosyltransferase (EC 2.4.2.17) - yeast (Candida albicans) ; (X83871) ATP phosphoribosyltransferase [Candida albicans]
18158	ENU01952	ANI61C508: 005..4326	69-88	687-706	NAP		g825440	927	183	2.00E-82	92	87	(L42299) RAS [Aspergillus fumigatus]



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18159	ENU01953	AN161C2966:	50-67	677-697	NAP		g127568	224	112	2.00E-24	37	58	"interferon-induced GTP-binding protein MX ; Mx resistance protein homolog - perch (fragment) ; (M27252) [Perca fluviatilis gene with homology to murine Mx genes, partial cds.] gene product [Perca fluviatilis]"
		2334..1644											
18160	ENU01954	AN161C7836:	51-70	687-705	NAP		g2687850	659	116	4.00E-45	45	34	(Y15839) fatty acid transporter protein [Cochiobolus heterostrophus]
		1578..882											
18161	ENU01955	AN161C1016	36-55	671-690	NAP		g1526987	423	110	3.00E-45	49	89	(U13050) pectate lyase D [Fusarium solani f. sp. pisi]
		8:767..70											
18162	ENU01956	AN161C2322:	66-85	706-725	NAP		g4481956	290	100	8.00E-28	51	36	(AL035637) putative uracil kinase-cytosine deaminase-bifunctional enzyme [Schizosaccharomyces pombe] (X89453) DRPLA [Rattus norvegicus]
		429..1130											
18163	ENU01957	AN161C7012:	49-68	689-709	NAP		g995557		36	0.21			NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 22K chain precursor - Neurospora crassa
		843..141											
18164	ENU01958	AN161C1806:	27-46	671-695	NAP		g280478	446	117	2.00E-39	55	96	putative potassium transport protein C1F5.12 ; (Z68136) unknown [Schizosaccharomyces pombe]
		1112..402											
18165	ENU01959	AN161C6073:	22-45	675-694	NAP		g1351299	260	126	1.00E-28	36	24	sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
		1834..1120											
18166	ENU01960	AN161C3790:	68-87	721-741	NAP		g1711561	304	122	3.00E-27	31	41	microtubule-associated protein YTM1 ; hypothetical protein YOR272w - yeast (Saccharomyces cerevisiae) ; (X89633) hypothetical protein [Saccharomyces cerevisiae] ; (Z75180) ORF YOR272w [Saccharomyces cerevisiae] ; (U92821) microtubule-associated protein [Saccharomyces cerevisiae]
		843..128											
18167	ENU01961	AN161C905:	60-79	731-750	NAP		g2494905	618	178	4.00E-44	48	49	
		33..1165											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	at Score	Blast Score	Blast Prob	% id	% cvrg	Description
18168	ENU01962	ANI61C6665:	47-66	723-744	NAP	g1723254	673	130	1.00E-29	55	63		probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase ; (Z69369) putative phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerases [Schizosaccharomyces pombe]
18169	ENU01963	ANI61C2704:	70-89	754-773	NAP	g115595	225	67	4.00E-16	34	69		F-actin capping protein alpha subunit ; actin-capping protein alpha chain - yeast (Saccharomyces cerevisiae) ; (X61398) Capping Protein Alpha Subunit [Saccharomyces cerevisiae] ; (Z28007) ORF YKL007 <sup>w</sup> [Saccharomyces cerevisiae] ; (S59773) CAP1 [Saccharomyces cerevisiae] transposase - fungus (Cochliobolus carbonum) (AL023794) hypothetical protein [Schizosaccharomyces pombe] unknown ; (AF075599) ubiquitin conjugating enzyme 12 [Homo sapiens] ; (AB012191) Nedd8-conjugating enzyme hUbc12 [Homo sapiens] (Z97050) iUvD [Mycobacterium tuberculosis] hypothetical 49.5 KD protein in UBP3-PET122 intergenic region ; hypothetical protein YER152c - yeast (Saccharomyces cerevisiae) ; (U18917) Yer152cp [Saccharomyces cerevisiae] (AF080235) reductase homolog [Streptomyces cyanogenus]
18170	ENU01964	ANI50C1415	22-50	722-741	NAP	g2133335		221	5.00E-57	42	47		
18171	ENU01965	ANI61C7152:	72-91	778-797	NAP	g3192028	312	113	1.00E-24	36	85		
18172	ENU01966	ANI61C1188:	41-60	752-771	NAP	g4507791	510	148	8.00E-47	56	96		
18173	ENU01967	ANI61C1125	70-89	787-806	NAP	g2213526	342	121	7.00E-27	33	42		
18174	ENU01968	ANI61C1023	61-83	781-798	NAP	g731527	265	67	3.00E-23	37	51		
18175	ENU01969	ANI61C3627:	40-59	767-786	NAP	g4240421		97	3.00E-22				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18176	ENU01970	ANI61C3268:	71-90	801-821	NAP		g121146	1021	293	1.00E-78	66	47	geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - Neurospora crassa ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]
18177	ENU01971	ANI61C9212:	65-84	791-816	NAP		g1168269	414	131	5.00E-30	41	76	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) ; (L23430) endo-1,5-alpha-L-arabinase [Aspergillus niger] ; endo-1,5-alpha-L-arabinase [Aspergillus niger]" transcription initiation protein SPT6 ; SPT6 protein - yeast (Saccharomyces cerevisiae) ; (M34391) SPT6 protein [Saccharomyces cerevisiae] ; (Z72899) ORF YGR116w [Saccharomyces cerevisiae]
18178	ENU01972	ANI61C1330:	66-84	800-819	NAP		g134854	907	123	4.00E-41	37	17	(U58946) transposase [Aspergillus awamori] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AC005824) unknown protein [Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
18179	ENU01973	ANI61C8126:	66-86	804-823	NAP		g1805251	1222	311	4.00E-84	55	47	(X91867) CPC3 protein [Neurospora crassa]
18180	ENU01974	ANI61C9741:	67-85	805-824	NAP		g1020413	119	83	2.00E-15	26	42	catalase ; catalase (EC 1.11.1.6) - Haemophilus influenzae (strain Rd KW20) ; (U32774) catalase (hkte) [Haemophilus influenzae Rd] (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]
18181	ENU01975	ANI61C9072:	37-57	780-799	NAP		g3860264	344	68	5.00E-22	39	54	
18182	ENU01976	ANI61C8695:	63-82	809-830	NAP		g1351702	765	129	2.00E-29	36	40	
18183	ENU01977	ANI61C1015:	66-85	816-835	NAP		g3355628	557	111	1.00E-37	35	15	
18184	ENU01978	ANI50C1469	36-55	785-808	NAP		g1168784		83	7.00E-30	37	45	
18185	ENU01979	ANI61C3072:	28-47	781-804	NAP		g4454690		54	0.000001			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18186	ENU01980	ANI61C1073	70-87	828-847	NAP		g1351671	165	83	3.00E-15			hypothetical 25.4 KD protein C1F7.10 in chromosome I ; hypothetical protein SPAC1F7.10 - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown
		4:1983..1164											
18187	ENU01981	ANI61C4097:	56-75	814-834	NAP		g586299	630	203	2.00E-51	50	67	[Schizosaccharomyces pombe] hypothetical oxidoreductase in RPB5-CD28 intergenic region ; probable membrane protein YBR159w - yeast (Saccharomyces cerevisiae) ; (Z36028) ORF YBR159w [Saccharomyces cerevisiae]
		234..1054											
18188	ENU01982	ANI61C6237:	71-91	836-855	NAP		g732189	735	157	9.00E-38	37	61	hypothetical 49.1 KD protein in SSB2-SPX18 intergenic region ; hypothetical protein YNL207w - yeast (Saccharomyces cerevisiae) ; (X78898) N1342 [Saccharomyces cerevisiae] ; (Z71483) ORF YNL207w [Saccharomyces cerevisiae]
		1362..2188											"GTP-binding protein YPT1 ; GTP-binding protein ypt1 - Neurospora crassa ; (S51252) NCYPT1=putative small GTP-binding protein [Neurospora crassa] ; small GTP-binding protein [Neurospora crassa] " (AL035210) halotolerance protein [Schizosaccharomyces pombe]
18189	ENU01983	ANI61C1754:	22-44	790-809	NAP		g466171	827	215	3.00E-79	89	96	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emericella nidulans] (Z98602) putative siroheme synthase [Schizosaccharomyces pombe]
		3010..2181											(AL021815) putative cis-muconate cycloisomerase [Schizosaccharomyces pombe]
18190	ENU01984	ANI61C9551:	26-45	812-831	NAP		g4160397	782	257	5.00E-68	49	76	
		5918..5071											
18191	ENU01985	ANI61C7226:	42-61	839-858	NAP		g2498971	2547	599	e-171	99	58	
		967..1825											
18192	ENU01986	ANI61C7492:	49-68	851-880	NAP		g2330809	571	217	7.00E-57	50	96	
		456..1329											
18193	ENU01987	ANI61C6496:	42-61	868-887	NAP		g2879855	954	179	2.00E-44	48	45	
		695..61											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18194	ENU01988	ANI61C1410:	58-77	891-910	NAP		g3024813	280	125	3.00E-28	3		"Vanillyl-alcohol oxidase (aryl-alcohol oxidase) (4-allylphenol oxidase) ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With Isoeugenol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With Isoeugenol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With P-Cresol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 2-Nitro-P-Cresol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 2-Nitro-P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 4-(1-Heptyl)phenol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 4-(1-Heptyl)phenol "
18195	ENU01989	ANI61C9556:	36-57	869-888	NAP		g3451313	242	65	1.00E-15	34	77	(AL031324) conserved hypothetical protein [Schizosaccharomyces pombe]
18196	ENU01990	ANI61C298:	60-79	897-916	NAP		g3024443	464	160	1.00E-38	38	92	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Zalerion arboricola ; (U33266) pyrroline carboxylate reductase [Zalerion arboricola]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18197	ENU01991	ANI61C8349:	64-83	903-922	NAP	g3738171	507	145	3.00E-40	44	87	87	"(AL031856) atp synthase gamma chain, mitochondrial precursor [Schizosaccharomyces pombe]"
		420..1320											probable NADP-dependent oxidoreductase P1 ; zeta-crystallin homolog - Arabidopsis thaliana ; (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
18198	ENU01992	ANI61C8021:	70-89	913-932	NAP	g2498731	206	50	2.00E-18	39	64	64	RTM1 protein ; RTM1 protein - yeast (Saccharomyces cerevisiae) ; (U02618) RTM1 gene product [Saccharomyces cerevisiae]
18199	ENU01993	ANI61C3602:	22-46	881-900	NAP	g730689	261	75	1.00E-12	32	89	89	(AJ006852) alternative NADH-dehydrogenase [Yarrowia lipolytica] lipoamide acyltransferase component precursor of branched-chain alpha-keto acid dehydrogenase complex (E2) (Dihydrolipoamide branched chain transacylase) (BCKAD E2 subunit) ; dihydrolipoamide transacylase precursor - mouse ; (L42996) acyltransferase [Mus musculus] ; branched chain alpha-ketoacid dehydrogenase:subunit=E2 [Mus musculus]
18200	ENU01994	ANI61C9410:	53-72	912-931	NAP	g3718005	1054	387	e-107	62	52	52	(D64005) nitrilase [Synechocystis sp.]
18201	ENU01995	ANI61C9218:	46-65	915-934	NAP	g1709438	621	242	3.00E-63				(D45894) thiamine-4 [Neurospora crassa] (AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis] (AL049522) hypothetical protein [Schizosaccharomyces pombe] (L02869) VPS17 [Saccharomyces cerevisiae]
18202	ENU01996	ANI61C3555:	61-80	937-956	NAP	g1001835	320	145	5.00E-34	33	79	79	Extensin precursor (cell wall hydroxyproline-rich glycoprotein) ; hydroxyproline-rich glycoprotein precursor - common tobacco ; (X13885) extensin (AA 1-620) [Nicotiana tabacum]
18203	ENU01997	ANI61C8559:	50-75	929-948	NAP	g4432914	896	128	1.00E-51	59	46	46	
18204	ENU01998	ANI61C9802:	72-89	952-972	NAP	g2909465	235	100	2.00E-20	29	96	96	
18205	ENU01999	ANI61C7233:	47-64	930-949	NAP	g4539600	403	88	5.00E-31	52	70	70	
18206	ENU02000	ANI61C5362:	42-62	931-948	NAP	g173177	577	210	1.00E-53	40	52	52	
18207	ENU02001	ANI61C1208:	25-44	913-933	NAP	g119714	150	53	0.000002	29	33	33	
		4167..5117											

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Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18208	ENU02002	ANI61C1065	43-62	933-952	NAP		g1708797	445	96	4.00E-19	39	22		LET1 protein - yeast (Kluyveromyces marxianus var. lactis) ; (X70373) LET1 [Kluyveromyces lactis]
18209	ENU02003	ANI61C1708:	27-46	924-943	NAP		g3661614	2806	579	e-164	88	41		(AF093142) aconitase [Aspergillus terreus]
18210	ENU02004	ANI61C859:1	70-90	968-987	NAP		g1169587	994	294	6.00E-99	60	65		"fructose-2,6-bisphosphatase ; fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.46) - yeast (Saccharomyces cerevisiae) ; (Z49430) ORF YJL155c [Saccharomyces cerevisiae]"
18211	ENU02005	ANI50C721_1:18..977	38-57	936-955	NAP		g2239208		132	4.00E-30	35	30		(Z97209) hypothetical protein [Schizosaccharomyces pombe]
18212	ENU02006	ANI61C9205: 45-64	963-982	NAP			g140459	376	49	4.00E-14	51	74		"hypothetical 30.7 KD protein in RVS161-ADP1 intergenic region ; hypothetical protein YCR010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR010c, len:283 [Saccharomyces cerevisiae]"
18213	ENU02007	ANI61C1116	46-66	967-986	NAP		g1938424	274	85	3.00E-34	41	21		(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
18214	ENU02008	ANI61C7920: 69-87	994-1015	NAP			g112790	456	199	3.00E-50	33	90		3-dehydroshikimate dehydratase (DHS dehydratase) ; 3-dehydroshikimate dehydratase - Neurospora crassa ; (X14603) DHS dehydratase [Neurospora crassa] ; (M10139) 3-dehydroshikimate dehydratase [Neurospora crassa]
18215	ENU02009	ANI50C1679	39-62	967-986	NAP		g2228748		90	3.00E-17	23	52		(U93867) RNA polymerase III subunit [Homo sapiens]
18216	ENU02010	ANI61C142:1	72-94	1002-1022	NAP		g2735428		54	0.000002				(U94913) H-K-ATPase alpha 2b subunit [Rattus norvegicus]

# Sequence Information

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18217	ENU02011	AN161C5215:	39-58	977-996	NAP		g4093186	247	71	2.00E-11	30	91	"(AF106583) contains similarity to domains present in ubiquitin-regulatory proteins (Pfam: PF00789, Score=79.3, E=7.8e-20, N=1), C2H2-type zinc finger domain (Pfam: PF00096, Score=9.5, E=6.2, N=1) and ubiquitin-associated domains (Pfam: PF00... "(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18218	ENU02012	AN161C1002	44-64	986-1008	NAP		g1167523	219	62	1.00E-20	26	24	"hypothetical 76.1 KD protein in UNG1-OST6 intergenic region ; hypothetical protein YML020w - yeast (Saccharomyces cerevisiae) ; (Z46659) unknown orf, len: 664, CAI: 0.13 [Saccharomyces cerevisiae] "
18219	ENU02013	AN161C9368:	45-64	1001-1021	NAP		g2497103	512	138	4.00E-39	42	43	(U81606) mixed-linked glucanase precursor [Cochliobolus carbonum] vegetatibe incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserna] "glutamate decarboxylase, 67 KD isoform (GAD-67) (67 KD glutamic acid decarboxylase) ; glutamate decarboxylase (EC 4.1.1.15) 1 - cat ; (M18629) glutamic acid decarboxylase [Felis catus] "
18220	ENU02014	AN161C6615:	22-53	982-1001	NAP		g2326188	654	235	5.00E-61	46	92	splicing factor U2AF homolog - mouse ; (X64587) orf [Mus musculus] putative transcriptional regulatory protein in MKK2-COX11 intergenic region ; hypothetical protein YPL133c - yeast (Saccharomyces cerevisiae) ; (U43703) Lpil2p [Saccharomyces cerevisiae]
18221	ENU02015	AN161C5217:	49-68	1010-1029	NAP		g3023956	264	90	1.00E-22	33	21	hypothetical 63.5 KD protein C3H1.06C in chromosome I ; (Z68144) putative major facilitator superfamily transporter [Schizosaccharomyces pombe]
18222	ENU02016	AN161C3697:	40-59	1006-1024	NAP		g416884	658	253	1.00E-66	40	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18223	ENU02017	AN161C6281:	70-90	1045-1065	NAP		g110998	451	178	2.00E-49	42	61	
18224	ENU02018	AN161C3002:	63-82	1041-1061	NAP		g1730882	529	152	5.00E-54	41	69	
18225	ENU02019	AN161C1025	64-83	1044-1063	NAP		g1351690	393	73	2.00E-19	30	55	
18226	ENU02020	AN161C1002	44-64	1036-1055	NAP		g1167523	219	62	1.00E-20	26	25	



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18227	ENU02021	AN161C6760:	63-85	1055-1075	NAP		g538067	1738	217	8.00E-56	36	24	[M77661] putative pol polypeptide [Magnaporthe grisea]
18228	ENU02022	AN161C1099	42-61	1039-1058	NAP		g3912972	328	125	9.00E-29	33	94	[alcohol dehydrogenase II (ADH 1) ; (AF008244) alcohol dehydrogenase II [Pichia stipitis]
18229	ENU02023	AN161C3608:	44-63	1045-1064	NAP		g2408068	769	159	3.00E-77	51	67	(Z99165) hypothetical protein [Schizosaccharomyces pombe]
18230	ENU02024	AN161C4301:	42-61	1046-1065	NAP		g2791498	176	111	8.00E-24	35	97	(AL021246) hypothetical protein Rv2458 [Mycobacterium tuberculosis]
18231	ENU02025	AN161C8515:	49-66	1054-1073	NAP		g543962	525	173	2.00E-42	45	88	cell division control protein 16 ; cdc16 protein - fission yeast [Schizosaccharomyces pombe] ; (Schizosaccharomyces pombe) ; (X71605) cdc16 [Schizosaccharomyces pombe] ; (Z98981) cell division control protein 16 [Schizosaccharomyces pombe]
18232	ENU02026	AN161C9037:	39-58	1047-1077	NAP		g2385382	586	116	3.00E-52	42	97	(AJ001428) D-mandelate dehydrogenase [Rhodotorula graminis] ; (AJ001429) D-mandelate dehydrogenase [Rhodotorula graminis]
18233	ENU02027	AN161C3359:	70-88	1091-1110	NAP		g1351714	236	81	2.00E-14	27	62	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
18234	ENU02028	AN161C2496:	63-82	1084-1103	NAP		g140489	700	158	3.00E-69			"GNS1 protein ; probable membrane protein YCR034w - yeast [Saccharomyces cerevisiae] ; (X56909) YCR521 [Saccharomyces cerevisiae] ; (S78624) YCR521 [Saccharomyces cerevisiae=yeast, Peptide, 347 aa] [Saccharomyces cerevisiae] ; (X59720) YCR034w, len:347 [Saccharomyces cerevisiae] ; (AF012655) v-snare bypass mutant [Saccharomyces cerevisiae]"
18235	ENU02029	AN161C9101:	63-82	1084-1104	NAP		g3114719	587	109	2.00E-49	43	16	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18236	ENU02030	ANI61C8453:	60-81	1106-1125	NAP	g1352980	846	215	8.00E-85	50	30	ATP-dependent RNA helicase DOB1 (MRNA transport regulator MTR4); SKI2 protein homolog YJL050w - yeast (Saccharomyces cerevisiae); (Z49325) ORF YJL050w [Saccharomyces cerevisiae] transposase - fungus (Cochliobolus carbonum) (U51327) versicolorin B synthase [Aspergillus parasiticus]; (U51328) versicolorin B synthase [Aspergillus parasiticus]
18237	ENU02031	ANI61C119:1	22-56	1069-1088	NAP	g2133335	329	53	0.000003	27	64	(U74468) indole-3-acetaldehyde dehydrogenase [Ustilago maydis] calcium/calmodulin-dependent protein kinase (CMPK); Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans; (M74120) calmodulin-dependent protein kinase [Emericella nidulans]; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans] sterigmatocystin 7-O-methyltransferase precursor; (L25835) O-methyltransferase [Aspergillus flavus]; (L25834) O-methyltransferase [Aspergillus parasiticus]; (L22091) O-methyltransferase [Aspergillus parasiticus]
18238	ENU02032	ANI61C360:2	60-83	1120-1139	NAP	g1293655	589	132	4.00E-30	37	53	(AL031128) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=404.95; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P46821; 2-match_description=microtubule-associated protein ... (Z25485) ACRI-protein [Saccharomyces cerevisiae] (Z99165) hypothetical protein [Schizosaccharomyces pombe]
18239	ENU02033	ANI61C7661:	58-75	1123-1142	NAP	g1658175	809	279	1.00E-86	45	72	(U74468) indole-3-acetaldehyde dehydrogenase [Ustilago maydis] calcium/calmodulin-dependent protein kinase (CMPK); Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans; (M74120) calmodulin-dependent protein kinase [Emericella nidulans]; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans] sterigmatocystin 7-O-methyltransferase precursor; (L25835) O-methyltransferase [Aspergillus flavus]; (L25834) O-methyltransferase [Aspergillus parasiticus]; (L22091) O-methyltransferase [Aspergillus parasiticus]
18240	ENU02034	ANI61C7147:	54-72	1125-1144	NAP	g3122300	1980	602	0	98	82	(U74468) indole-3-acetaldehyde dehydrogenase [Ustilago maydis] calcium/calmodulin-dependent protein kinase (CMPK); Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans; (M74120) calmodulin-dependent protein kinase [Emericella nidulans]; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans] sterigmatocystin 7-O-methyltransferase precursor; (L25835) O-methyltransferase [Aspergillus flavus]; (L25834) O-methyltransferase [Aspergillus parasiticus]; (L22091) O-methyltransferase [Aspergillus parasiticus]
18241	ENU02035	ANI61C1107	44-63	1117-1136	NAP	g2498702	196	109	3.00E-23	33	30	(U74468) indole-3-acetaldehyde dehydrogenase [Ustilago maydis] calcium/calmodulin-dependent protein kinase (CMPK); Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans; (M74120) calmodulin-dependent protein kinase [Emericella nidulans]; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans] sterigmatocystin 7-O-methyltransferase precursor; (L25835) O-methyltransferase [Aspergillus flavus]; (L25834) O-methyltransferase [Aspergillus parasiticus]; (L22091) O-methyltransferase [Aspergillus parasiticus]
18242	ENU02036	ANI61C7320:	49-68	1129-1148	NAP	g3355742		47	0.0003			(AL031128) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=404.95; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P46821; 2-match_description=microtubule-associated protein ... (Z25485) ACRI-protein [Saccharomyces cerevisiae] (Z99165) hypothetical protein [Schizosaccharomyces pombe]
18243	ENU02037	ANI61C6437:	22-40	1130-1147	NAP	g396595	782	236	7.00E-81	61	96	(Z25485) ACRI-protein [Saccharomyces cerevisiae] (Z99165) hypothetical protein [Schizosaccharomyces pombe]
18244	ENU02038	ANI61C7645:	22-46	1130-1149	NAP	g2408062	531	164	1.00E-39	35	58	(Z25485) ACRI-protein [Saccharomyces cerevisiae] (Z99165) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18245	ENU02039	ANI61C2531:	62-81	1179-1198	NAP		g2833229	626	116	4.00E-52	36	70	Laccase (benzenedio: oxygen oxidoreductase) (urishiol oxidase) (diphenol oxidase)
18246	ENU02040	ANI61C6864:	32-51	1151-1170	NAP		g854534	764	184	1.00E-45	45	39	(X87634) oxidative stress resistance [Saccharomyces cerevisiae]
18247	ENU02041	ANI61C292:9	70-89	1199-1218	NAP		g2853081	416	99	2.00E-28	38	96	(AL021768) ATP binding protein-like [Arabidopsis thaliana]
18248	ENU02042	ANI61C2972:	52-71	1194-1213	NAP		g4507229	1009	242	e-102	47	74	"Succinic semialdehyde dehydrogenase ; (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens] ; (AL031230) d173M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24) [Homo sapiens] " calcium-transporting ATPase 2 (vacuolar CA2+-ATPase) ; Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae) ; (U03060) calcium ATPase [Saccharomyces cerevisiae] ; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
18249	ENU02043	ANI61C1069	39-58	1185-1204	NAP		g728904	1065	177	1.00E-43	47	31	(AL022072) possible transmembrane protein [Schizosaccharomyces pombe]
18250	ENU02044	ANI61C7104:	51-70	1204-1223	NAP		g2950489	309	69	8.00E-11	45	53	Tetracycline resistance protein (transposon TN4351 / TN4400) ; NADP-requiring oxidoreductase - Bacteroides fragilis ; (M37699) tetracycline resistance protein [Transposon Tn4351]
18251	ENU02045	ANI61C3347:	44-63	1198-1217	NAP		g401172	183	107	2.00E-22	28	96	(AL049559) hypothetical protein [Schizosaccharomyces pombe]
18252	ENU02046	ANI61C9152:	24-46	1188-1206	NAP		g4581522	614	153	2.00E-36	32	42	hypothetical 43.5 KD protein in RPB9-ALG2 intergenic region ; hypothetical protein YGL067w - yeast (Saccharomyces cerevisiae) ; (Z72589) ORF YGL067w [Saccharomyces cerevisiae]
18253	ENU02047	ANI61C1022	22-42	1187-1206	NAP		g1723847	313	159	4.00E-38	32	93	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18254	ENU02048	ANI61C8681:	45-64	1219-1238	NAP		g2499619	179	68	7.00E-15	32	21	probable serine/threonine-protein kinase YMR216C; probable membrane protein YMR216c - yeast (Saccharomyces cerevisiae); (Z49809) unknown [Saccharomyces cerevisiae]
18255	ENU02049	ANI61C3355:	22-41	1195-1215	NAP		g418150	856	122	1.00E-56			GABA-specific permease (GABA-specific transport protein); GABA transport protein - yeast (Saccharomyces cerevisiae); (X66472) GABA-specific permease [Saccharomyces cerevisiae]; (X99000) GABA transporter protein [Saccharomyces cerevisiae]; (Z74258) ORF YDL210w [Saccharomyces cerevisiae]; GABA transport protein [Saccharomyces cerevisiae]
18256	ENU02050	ANI61C6437:	60-79	1241-1260	NAP		g2497127	440	182	3.00E-45	32	90	hypothetical 48.4 KD protein in ARP9-IMP2 intergenic region; probable membrane protein YMR034c - yeast (Saccharomyces cerevisiae); (Z49213) unknown [Saccharomyces cerevisiae]
18257	ENU02051	ANI61C1135	69-89	1256-1275	NAP		g2213553	595	183	3.00E-45	39	56	[Schizosaccharomyces pombe] (Z97052) hypothetical protein
18258	ENU02052	ANI61C7225:	64-82	1257-1276	NAP		g2497946	1369	279	e-120	62	77	"PRPD protein; (U73857) similar to yqjP of B. subtilis [Escherichia coli]; (AE000140) orf, hypothetical protein [Escherichia coli]"
18259	ENU02053	ANI61C4189:	39-59	1237-1256	NAP		g2978332	172	57	0.000000	33	51	(AB012140) arylsterase [Acetobacter pasteurianus]
18260	ENU02054	ANI61C4716:	50-69	1252-1271	NAP		g3183362	339	103	3.00E-21	38	74	hypothetical 48.0 KD protein C1B3.08 in chromosome I; (Z98598) hypothetical protein [Schizosaccharomyces pombe]
18261	ENU02055	ANI61C1046	33-52	1237-1255	NAP		g4038592	308	154	1.00E-36	30	32	(Y10403) RNA-directed RNA polymerase [Lycopersicon esculentum]
18262	ENU02056	ANI61C2205:	27-46	1231-1250	NAP		g3850125	458	131	8.00E-30	32	75	(AL033391) hypothetical membrane protein [Candida albicans]
18263	ENU02057	ANI61C7041:	25-44	1238-1257	NAP		g171124	387	78	1.00E-25	29	74	(M20319) aminotriazole resistance protein [Saccharomyces cerevisiae]
18264	ENU02058	ANI61C9605:	43-62	1263-1283	NAP		g3341974	931	360	9.00E-99	47	92	(AB012604) squalene synthase [Candida utilis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18265	ENU02059	ANI61C8226:	67-87	1298-1317	NAP	g4584836	424	424	150	1.00E-35	33	54	(A1238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
18266	ENU02060	ANI61C8226:	67-87	1298-1317	NAP	g4584836	424	150	1.00E-35	33	33	54	(A1238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
18267	ENU02061	ANI61C1064	47-66	1280-1299	NAP	g2565329	694	278	7.00E-77	45	88		(AF025290) cAMP-dependent protein kinase catalytic subunit [Ustilago maydis]
18268	ENU02062	ANI61C4192:	24-43	1261-1279	NAP	g4160579	227	99	5.00E-20	37	49		(AL035218) hypothetical protein [Schizosaccharomyces pombe]
18269	ENU02063	ANI61C5216:	48-68	1288-1307	NAP	g2661608	1696	246	e-118	53	69		(AL009197) hypothetical ctp synthase [Schizosaccharomyces pombe]
18270	ENU02064	ANI61C2416:	23-43	1296-1315	NAP	g2239198	636	178	1.00E-62	55	99		(Z97209) putative tricarboxylate transport protein protein [Schizosaccharomyces pombe]
18271	ENU02065	ANI61C7568:	53-72	1339-1361	NAP	g1709181	503	136	9.00E-39	34	70		"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
18272	ENU02066	ANI61C1128	23-48	1317-1336	NAP	g2132491	152	44	5.00E-11	34	68		Probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr284cp [Saccharomyces cerevisiae]
18273	ENU02067	ANI61C1016	22-41	1326-1345	NAP	g1169782	556	206	5.00E-60	37	91		Fusca protein FUS6 ; (L26498) FUS6 [Arabidopsis thaliana]
18274	ENU02068	ANI61C3255:	44-63	1348-1367	NAP	g3023683	1913	560	e-180	90	86		Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; 6beta-hydroxyhyoscyamine epoxidase (EC 1.14.11.14) - Aspergillus oryzae ; (D63941) enolase [Aspergillus oryzae] ; (D64113) enolase [Aspergillus oryzae] ; enolase [Aspergillus oryzae] putative tarrate transporter ; (U32375) membrane protein [Agrobacterium vitis]
18275	ENU02069	ANI61C1080	62-81	1389-1408	NAP	g4033481	233	63	2.00E-21	30	84		(AB018313) KIAA0770 protein [Homo sapiens]
18276	ENU02070	ANI61C7689:	71-90	1408-1426	NAP	g3882261	375	98	8.00E-25	31	54		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18277	ENU02071	ANI61C9422:	40-63	1379-1398	NAP		g4406656	214	102	4.00E-21	29	45	(AF131820) Unknown [Homo sapiens]
18278	ENU02072	124..1524 ANI61C3006:	40-59	1388-1407	NAP		g2493484	1127	342	e-110	53	81	glycerol kinase (ATP:glycerol 3-phosphotransferase) (glycerokinase) (GK) ; (U48403) glycerol kinase [Mus musculus]
18279	ENU02073	ANI61C6597:	44-63	1393-1413	NAP		g417699	1559	321	e-171			"histone deacetylase RPD3 (transcriptional regulatory protein RPD3) ; transcription regulator RPD3 - yeast (Saccharomyces cerevisiae) ; (S66438) RPD3 [Saccharomyces cerevisiae, Peptide, 433 aa] [Saccharomyces cerevisiae] ; (X83226) global transcriptional regulator [Saccharomyces cerevisiae] ; (Z71606) ORF YNL330c [Saccharomyces cerevisiae]"
18280	ENU02074	ANI61C1223:	24-45	1374-1393	NAP		g3023717	1095	437	e-121	58	86	ESA1 protein ; hypothetical protein YOR244w - yeast (Saccharomyces cerevisiae) ; (Z75152) ORF YOR244w [Saccharomyces cerevisiae] (U39201) acetolactate synthase [Magnaporthe grisea] (AF027868) Yoan [Bacillus subtilis] ; (Z29114) similar to hypothetical proteins [Bacillus subtilis] (U73857) galactoside O-acetyltransferase [Escherichia coli] (AL032671) predicted using GeneFinder [Caenorhabditis elegans] (AC004473) Contains similarity to golliath protein gblM97204 from D. melanogster. [Arabidopsis thaliana] Isotrichodermin C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides] (AF041050) 4-coumarate:CoA ligase [Populus tremuloides] (Z98529) conserved hypothetical protein [Schizosaccharomyces pombe]
18281	ENU02075	ANI61C1029	69-87	1431-1450	NAP		g1072104	2199	628	e-180	70	68	
18282	ENU02076	6:9675..8253 ANI61C7367:	47-64	1420-1439	NAP		g2619026	699	153	8.00E-73	43	96	
18283	ENU02077	ANI61C1141	45-65	1436-1454	NAP		g1657538	206	51	3.00E-14	40	26	
18284	ENU02078	4:1586..135 ANI50C5820	72-89	1467-1486	NAP		g3873654		43	0.005			
18285	ENU02079	3_1:2193..737 ANI61C8228:	57-80	1452-1471	NAP		g3249088	134	76	6.00E-13	25	27	
18286	ENU02080	ANI61C1073	41-59	1448-1467	NAP		g3915140	448	73	2.00E-19	33	74	
18287	ENU02081	ANI61C8810:	23-40	1443-1462	NAP		g3258637	442	128	3.00E-50	37	64	
18288	ENU02082	3452..1970 ANI61C3730:	52-71	1484-1501	NAP		g3859776		62	0.000000	41	38	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18289	ENU02083	ANI61C3730:	72-91	1510-1529	NAP		g2648302	239	115	6.00E-25	43	49	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"
18290	ENU02084	ANI61C2434:	23-41	1481-1500	NAP		g1661227	633	234	1.00E-60	32	62	(U75973) NAA-G-peptidase; NAALADase; prostate specific membrane antigen; PSM; PSMA [Rattus norvegicus] ; (AF040256) glutamate carboxypeptidase II [Rattus norvegicus]
18291	ENU02085	ANI61C1714:	24-43	1496-1515	NAP		g547880	693	102	7.00E-58	43	78	LYSINE-specific permease ; (U00007) lysine-specific permease [Escherichia coli] ; Lys permease [Escherichia coli] (AF017990) Fkbp39p
18292	ENU02086	ANI61C5953:	24-43	1512-1532	NAP		g3406742	509	157	2.00E-37	45	72	[Schizosaccharomyces pombe] ; (AL035548) Peptidyl Prolyl cis-trans isomerase [Schizosaccharomyces pombe]
18293	ENU02087	ANI61C1758:	24-45	1514-1533	NAP		g464369	566	118	7.00E-26	26	35	phenol 2-monooxygenase (phenol hydroxylase) ; (L04488) phenol hydroxylase [Trichosporon cutaneum] (X98309) ARI protein [Drosophila melanogaster] ; (X98310) ARI protein [Drosophila melanogaster]
18294	ENU02088	ANI61C1052:	69-87	1591-1608	NAP		g2058299	938	317	e-105	44	95	[Drosophila melanogaster] phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]
18295	ENU02089	ANI61C3068:	24-43	1582-1601	NAP		g130117	639	137	3.00E-39	35	80	Dicarboxylic amino acid permease ; dicarboxylic amino acid permease DIP5 - yeast (Saccharomyces cerevisiae) ; (X95802) dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae] ; (Z73621) ORF YPL265w [Saccharomyces cerevisiae]
18296	ENU02090	ANI61C4335:	45-64	1624-1643	NAP		g1706439	651	220	1.00E-65	35	81	ML03 protein ; (L42551) ORF [Schizosaccharomyces pombe] ; (Z98270) Mlo3p [Schizosaccharomyces pombe]
18297	ENU02091	ANI61C5680:	53-73	1638-1657	NAP		g2498564	186	60	0.000000	39	42	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18298	ENU02092	ANI61C1080	32-51	1618-1637	NAP	g4033481	233	63	4.00E-22	29	90		putative tartrate transporter ; (U232375) membrane protein [Agrobacterium vitis]
18299	ENU02093	ANI61C85111	53-72	1672-1691	NAP	g2494913	923	369	e-101	40	98		hypothetical 57.3 KD TRP-ASP repeats containing protein in POM152-REC114 intergenic region ; hypothetical protein YMR131c - yeast (Saccharomyces cerevisiae) ; (Z48622) unknown [Saccharomyces cerevisiae] "(U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici] "
18300	ENU02094	ANI61C7716	34-53	1655-1674	NAP	g799150	1915	531	e-150	54	69		probable membrane protein YDR294c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr294cp [Saccharomyces cerevisiae] hypothetical protein YDL037c - yeast (Saccharomyces cerevisiae) ; (Z71781) unknown [Saccharomyces cerevisiae] ; (Z74085) ORF YDL037c [Saccharomyces cerevisiae] (AF041049) 4-coumarate:CoA ligase [Populus tremuloides] (AF036097) flavocytochrome b subunit [Bos taurus] (D86086) canalicular multispecific organic anion transporter [Rattus norvegicus] (Y16045) leucine-rich repeat protein [Arabidopsis thaliana] Uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe] (Y16834) hexose transporter [Candida albicans] hypothetical 87.0 KD protein in PAN1-PR1 intergenic region ; hypothetical protein YIR007w - yeast (Saccharomyces cerevisiae)
18301	ENU02095	ANI61C5161	53-72	1680-1700	NAP	g2132493	1168	379	e-104	51	86		
18302	ENU02096	ANI61C1048	63-83	1692-1713	NAP	g2131317		40	0.04				
18303	ENU02097	ANI61C5282	56-74	1705-1724	NAP	g3258635	526	219	3.00E-61	32	99		
18304	ENU02098	ANI61C1054	41-60	1693-1713	NAP	g2921400	606	257	1.00E-74	33	90		
18305	ENU02099	ANI61C1542	47-66	1713-1731	NAP	g1405353	614	100	3.00E-55	35	30		
18306	ENU02100	ANI61C7473	71-90	1762-1781	NAP	g2760084	228	126	4.00E-28	31	49		
18307	ENU02101	ANI61C1883	68-87	1760-1779	NAP	g2492816	1271	176	e-114	50	84		
18308	ENU02102	ANI61C1014	68-88	1821-1852	NAP	g3336839	795	100	4.00E-78	40	95		
18309	ENU02103	ANI61C9693	71-90	1864-1883	NAP	g731909	427	85	2.00E-30	36	31		



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18310	ENU02104	ANI61C5240:	67-86	1924-	NAP		g1613878	1680	499	e-140	45	49	(U72236) <i>Moda</i> [Dicyostelium discoideum]
18311	ENU02105	755..2676	46-63	1924-	NAP		g3877738	122	44	0.003			(Z74473) predicted using GeneFinder [Caenorhabditis elegans]
18312	ENU02106	11354..10547	50-69	1995-	NAP		g3702646	601	135	4.00E-63	34	73	(AL031825) putative membrane transport protein
18313	ENU02107	ANI61C1125:	52-71	2051-	NAP		g129307	885	272	e-101	39	93	[Schizosaccharomyces pombe] L- amino acid oxidase precursor (LAO) ; L- amino- acid oxidase (EC 1.4.3.2)
18314	ENU02108	ANI61C9178:	35-54	2034-	NAP		g3417415	462	102	2.00E-48	44	50	precursor - Neurospora crassa (AL031261) phosphoserine phosphatase [Schizosaccharomyces pombe]
18315	ENU02109	ANI61C466:4	53-76	2060-	NAP		g2501570	395	137	1.00E-36	35	71	hypothetical 51.4 KD protein in RAR1-SCJ1 intergenic region ; hypothetical protein YMR210w - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae] probable membrane protein YDL074c - yeast (Saccharomyces cerevisiae) ; (Z74122) ORF YDL074c
18316	ENU02110	ANI61C1122	34-53	2050-	NAP		g2132428	356	153	4.00E-36	28	40	[Saccharomyces cerevisiae] (AL034490) hypothetical proten [Schizosaccharomyces pombe]
18317	ENU02111	ANI61C1062	24-45	2080-	NAP		g4008552	334	100	4.00E-26	35	57	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum]"
18318	ENU02112	ANI61C7956:	63-82	2145-	NAP		g119830	757	661	0	47	36	"hypothetical 77.5 KD protein in PRP1-STE3 intergenic region ; hypothetical protein YKL179c - yeast (Saccharomyces cerevisiae) ; (X74151) previously orf13 and orf14 [2], now merged; homologous to human CENP-E [Saccharomyces cerevisiae] ; (Z28179) ORF YKL179c
18319	ENU02113	ANI61C4756:	22-57	2132-	NAP		g549740	469	113	4.00E-41	28	94	[Saccharomyces cerevisiae]" (AL021747) hypothetical protein [Schizosaccharomyces pombe]
18320	ENU02114	ANI61C6804:	61-80	2201-	NAP		g2842464	260	63	0.000000	26	93	
		3811..6011		2219						008			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18321	ENU02115	AN161S2760:	43-62	2188-2207	NAP		g2072788	89	1.00E-16	27	20		(U64574) cell cycle inhibitor Nif1 [Schizosaccharomyces pombe]; (AL035065) cell cycle inhibitor nif1. [Schizosaccharomyces pombe]
18322	ENU02116	AN161C3865:	38-57	2198-2217	NAP		g1350600	3129	1186	0	77	88	Ribonucleoside-diphosphate reductase large chain (ribonucleotide reductase); CDC22 protein - fission yeast (Schizosaccharomyces pombe); (Z67998) Cdc22p [Schizosaccharomyces pombe]
18323	ENU02117	AN161C2081:	54-73	2213-2235	NAP		g125935	437	195	1.00E-48	28	70	lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (M59935) negative-acting regulatory protein [Emmericella nidulans]; (M77664) repressor protein [Emmericella nidulans]
18324	ENU02118	AN161C9003:	63-85	2272-2291	NAP		g168082	1305	439	e-140	40	78	Maltose permease MAL3T (maltose transport protein MAL3T); maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae); (Z26167) ORF YBR298c [Saccharomyces cerevisiae]
18325	ENU02119	AN161C594:	67-86	2369-2388	NAP		g585446	772	120	1.00E-83	37	70	hypothetical 175.8 K D protein in GND1-IK11 intergenic region; hypothetical protein YHR186c - yeast (Saccharomyces cerevisiae); (U00030) Yhr186cp [Saccharomyces cerevisiae] (X86780) polyketide synthase [Streptomyces hygroscopicus] probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae); (Z73573) ORF YPL217c [Saccharomyces cerevisiae]
18326	ENU02120	AN161C1055	52-71	2415-2434	NAP		g731756	867	236	6.00E-79	37	42	"probable glucan 1,3-beta-glucosidase precursor (exo-1,3-beta-glucanase); (Z70721) putative 1,3-beta-d-glucanohydrolase [Schizosaccharomyces pombe] "
18327	ENU02121	AN161C8706:	66-85	2452-2472	NAP		g987102	493	132	2.00E-62	36	8	
18328	ENU02122	AN161C1003	72-90	2497-2516	NAP		g2133002	2342	503	e-141	45	65	
18329	ENU02123	AN161C1125	72-91	2498-2516	NAP		g1706727	841	332	7.00E-90	42	48	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18330	ENU02124	ANI61C1003	72-90	2497-	NAP		g2133002	2342	503	e-141	45	65	probable membrane protein YPL217c-yeast (Saccharomyces cerevisiae) ; (Z73573) ORF YPL217c [Saccharomyces cerevisiae]
18331	ENU02125	ANI61C9304	24-47	2476-2495	NAP		g2132957	207	51	0.000000	42	14	probable membrane protein YOR378w-yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae]
18332	ENU02126	ANI61C3630	62-81	2518-2537	NAP		g1002380		39	0.14			(U24189) RRM-type RNA binding protein [Caenorhabditis elegans]
18333	ENU02127	ANI61C648	2	58-77	NAP		g4502897	719	222	1.00E-80	40	47	cleft lip and palate associated transmembrane protein 1 ; (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] ; (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens]
18334	ENU02128	ANI61C7559	67-86	2707-2727	NAP		g2853114	361	92	1.00E-17	26	25	(AL021766) hypothetical protein [Schizosaccharomyces pombe]
18335	ENU02129	ANI61C220	2	49-69	NAP		g3913731	1354	504	e-156	42	82	probable mannosyl-oligosaccharide glucosidase (processing A-glucosidase I) ; (Z98603) hypothetical protein [Schizosaccharomyces pombe]
18336	ENU02130	ANI61C8057	45-66	2887-2906	NAP		g4176548	1115	288	e-109	54	57	(AL035259) putative Ca-calmodulin-dependent serine-threonine-protein kinase [Schizosaccharomyces pombe]
18337	ENU02131	ANI61C1412	66-85	203-223	NAP		g133186	400	111	6.00E-25	71	65	Guanyl-specific ribonuclease PB1 ; ribonuclease T1 (EC 3.1.27.3) - Penicillium brevicompactum ; RNase [Penicillium brevicompactum]
18338	ENU02132	ANI61C1055	30-50	163-189	NAP		g2493874	127	64	9.00E-11	42	94	cytochrome C oxidase assembly protein COX17 ; COX17 protein - yeast (Saccharomyces cerevisiae) ; (L75948) approximately 300 nucleotides distal from helicase gene [Saccharomyces cerevisiae] ; (Z73114) ORF YLL009c [Saccharomyces cerevisiae]

# Database Information

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18339	ENU02133	AN161C1360:	22-50	164-183	NAP		g2833211	238	46	0.000000	62	50	NADH-ubiquinone oxidoreductase 10.5 KD subunit (complex I) (CI); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 10.5K chain - Neurospora crassa ; (X69929) NUO-10.5 [Neurospora crassa]
		1556..1353								07			
18340	ENU02134	AN161C480:4	55-77	202-222	NAP		g99521	416	137	1.00E-32	91	45	nad5 intron 1 protein 459 - Sugar beet mitochondrion (fragment) ; (X55786) ORF459 [Beta vulgaris] (AC000104) EST gb T45093 comes from this gene. [Arabidopsis thaliana] phenol hydroxylase - imperfect fungus (Trichosporon beigelii) "(AE000352) orf, hypothetical protein [Escherichia coli]"
		32..223											
18341	ENU02135	AN161C7399:	23-42	172-192	NAP		g1903364		44	0.0002			"mitochondrial 60S ribosomal protein L33 (YML33) ; ribosomal protein L30, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49704) MprJ33p [Saccharomyces cerevisiae]"
		82..293											
18342	ENU02136	AN161C8581:	70-89	232-251	NAP		g102033	98	42	0.0007			30S ribosomal protein S15 (BS18) ; (Z80835) ribosomal protein S15 [Bacillus subtilis] ; (Z99112) ribosomal protein S15 (BS18) [Bacillus subtilis] (AL031179) splicing factor [Schizosaccharomyces pombe]
		4554..4777											
18343	ENU02137	AN161C3361:	24-43	187-206	NAP		g1789035	162	62	4.00E-10	46	84	"DNA-directed RNA polymerases I, II, and III 7.7 KD polypeptide (ABC10-alpha) ; DNA-directed RNA polymerase (EC 2.7.7.6) chain ABC10 alpha - yeast (Saccharomyces cerevisiae) ; (U23378) RNA polymerase I, II and III subunit ABC10 alpha [Saccharomyces cerevisiae] ; (U10397) Rpb12p: RNA polymerase II subunit [Saccharomyces cerevisiae]"
		1117..893											
18344	ENU02138	AN161C5161:	51-70	215-235	NAP		g1710603	169	62	6.00E-10	38	87	(AC000133) pyrC [Emmericella nidulans]
		5997..5772											
18345	ENU02139	AN161C3149:	31-49	197-218	NAP		g2507327	156	51	0.000001	44	86	
		77..306											
18346	ENU02140	AN161C7173:	71-90	241-267	NAP		g3395591	176	70	2.00E-12			
		1312..1550											
18347	ENU02141	AN161C4095:	53-72	231-250	NAP		g3647370	210	80	3.00E-15	50	84	
		457..696											
18348	ENU02142	AN161C8881:	59-79	240-259	NAP		g730606	134	56	0.000000	45	88	
		2362..2604								05			
18349	ENU02143	AN161C1355:	59-78	230-261	NAP		g1870226	531	187	2.00E-47	98	86	
		1288..1532											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18350	ENU02144	AN161S4306:	22-55	190-225	NAP		g2315135	415	166	3.00E-41	100	100	(AB003522) beta subunit of coupling factor one [Arabidopsis thaliana]
18351	ENU02145	AN161S3217:	35-56	215-242	NAP								
18352	ENU02146	AN161C1479:	22-50	215-235	NAP		g4586031	147	56	0.000000	59	94	(AC007109) unknown protein [Arabidopsis thaliana]
18353	ENU02147	AN161C7312:	53-76	252-271	NAP		g1352897	133	56	0.000000			(AC007109) unknown protein [Arabidopsis thaliana]
		2010..2265											hypothetical 11.3 KD protein in MIR1-STE18 intergenic region ; probable membrane protein YJR085c - yeast (Saccharomyces cerevisiae) ; (Z49585) ORF YJR085c [Saccharomyces cerevisiae] ; (L47993) ORF YJR085c [Saccharomyces cerevisiae]
		3506..3246											Rub1
18354	ENU02148	AN161C9353:	39-62	247-266	NAP		g4139493	187	87	4.00E-17	64	92	(AF047427) unknown [Pasteurella haemolytica]
18355	ENU02149	AN161C5287:	31-55	234-261	NAP		g3978168	135	55	0.000000			(U12823) hemolysin [Acanthamoeba polyphaga]
18356	ENU02150	AN161C1253:	26-49	242-261	NAP		g607954	218	66	6.00E-11	62	80	Chloroplast 50S ribosomal protein L23 ; (X65615) ribosomal protein L23 [Sinapis alba]
18357	ENU02151	AN161S4051:	22-53	223-258	NAP		g1350634	490	195	7.00E-50	100	100	(AJ223315) rAsp f7 [Aspergillus fumigatus]
18358	ENU02152	AN161C1068	49-68	270-289	NAP		g2879888	453	155	5.00E-38	75	84	(X95503) zinc finger protein [Mus musculus] ; (X95504) zinc finger protein [Mus musculus]
18359	ENU02153	AN161C563:2	53-72	275-296	NAP		g2326720	48	34	0.27	32	12	"Thioredoxin ; thioredoxin - Emericella nidulans ; thioredoxin [Aspergillus nidulans, Peptide, 109 aa] "
18360	ENU02154	AN161C6455:	23-44	249-268	NAP		g267125	269	96	8.00E-20	53	87	"Keratin, type I cytoskeletal 47 KD ; (X04805) keratin B1 [Xenopus laevis] "
18361	ENU02155	AN161C3233:	48-69	284-305	NAP		g1346341		32	1.5			(AC004680) unknown protein [Arabidopsis thaliana]
18362	ENU02156	AN161C1135	26-45	253-284	NAP		g3420051	477	189	5.00E-48	74	91	[Arabidopsis thaliana]
		8:3396..3096											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18363	ENU02157	ANI61C4231:	31-51	264-292	NAP		g3334316	170	59	0.00000001			"DNA-directed RNA polymerases I, II, and III 8.3 KD polypeptide (ABC10-beta) ; (D89596) RNA polymerase II subunit Rpb10 [Schizosaccharomyces pombe] ; (U80219) RNA polymerases I-III common subunit Rpb10 [Schizosaccharomyces pombe] ; (AF027818) RNA polymerases I, II and III subunit Rpb10 [Schizosaccharomyces pombe] ; (Z98598) dna-directed ma polymerases i, ii, and iii 8.3 kd polypeptide(abc10-beta).dna-directed ma polymerases i, ii, and iii 8.3 kd polypeptide(abc10-beta). [Schizosaccharomyces pombe]" (AC000133) ORF [Emericella nidulans]
18364	ENU02158	ANI61C5142:	47-66	289-309	NAP		g1870220	97	41	0.002			suppressor of Ty (S.cerevisiae) 4 homolog 1 ; transcription initiation protein SPT4 homolog 1 ; (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] ; (U38818) SPT4H [Homo sapiens] ; (U38817) SPT4H [Homo sapiens] ; (U43154) Supt4h [Mus musculus] ; (U96809) chromatin structural protein homolog [Mus musculus]
18365	ENU02159	ANI61C2477:	22-57	262-287	NAP		g4507311		92	1.00E-18			ribosomal protein L38 ; 60S ribosomal protein L38 ; ribosomal protein L38 - rat ; ribosomal protein L38 - human ; (X57007) ribosomal protein L38 [Rattus rattus] ; (Z26876) ribosomal protein [Homo sapiens]
18366	ENU02160	ANI61C5703:	61-80	307-326	NAP		g4506645	167	61	0.0000000002			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18367	ENU02161	ANI61C914:1	22-55	272-291	NAP		g731363	131	57	0.000000			PET100 protein precursor ; probable membrane protein YDR079w - yeast (Saccharomyces cerevisiae) ; (X82086)
		532..1221								03			1 putative transmembrane spans [Saccharomyces cerevisiae] ; (Z46796) unknown [Saccharomyces cerevisiae] ; (Z74375) ORF YDR079w [Saccharomyces cerevisiae] ; (U91943) cytochrome c oxidase-specific assembly factor [Saccharomyces cerevisiae]
18368	ENU02162	ANI61C1597: 24-50		271-294	NAP		g2656010	201	76	5.00E-14	29	71	(Z99165) hypothetical protein [Schizosaccharomyces pombe]
		238..550											(AC007195) putative blue copper-binding protein II [Arabidopsis thaliana]
18369	ENU02163	ANI61C4533: 24-52		267-295	NAP		g4589971	572	221	1.00E-57	97	98	"Histone H3.2, minor; histone H3.3-like protein - Arabidopsis thaliana ; (X60429) histone H3.3 like protein [Arabidopsis thaliana] ; (X60429) histone H3.3 like protein [Arabidopsis thaliana] ; (U09458) histone H3.2 [Medicago sativa] ; (U09460) histone H3.2 [Medicago sativa] ; (U09461) histone H3.2 [Medicago sativa] ; (U09464) histone H3.2 [Medicago sativa] ; (U09465) histone H3.2 [Medicago sativa] ; (X79714) histone H3 [Lolium temulentum] ; (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] ; (AF024716) histone 3 [Gossypium hirsutum] ; (AB015760) histone H3 [Nicotiana tabacum] ; (AF093633) histone H3 [Oryza sativa] ; (AF109910) histone H3 [Porteresia coarctata] ; (AL035708) histone H3.3 [Arabidopsis thaliana] ; (AL035708) Histone H3 [Arabidopsis thaliana] " (AC000133) mt2 [Emmericella nidulans]
		799..857											
18370	ENU02164	ANI61C466:4 65-84		318-337	NAP		g417103	338	141	1.00E-33			
		309..3995											
18371	ENU02165	ANI61C5625: 23-50		270-295	NAP		g1870224	569	224	2.00E-58	98	99	
		900..586											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18372	ENU02166	ANI61C1062	31-50	282-303	NAP		g465533	166	46	0.00008	32	87	hypothetical 11.5 KD protein in HTB2-NTH2 intergenic region ; hypothetical protein YBL001c - yeast
		2:5429..5743											(Saccharomyces cerevisiae) ; (Z26494) unknown [Saccharomyces cerevisiae] ; (Z35762) ORF YBL001c [Saccharomyces cerevisiae] ; ORF YBL0105 [Saccharomyces cerevisiae] (U12823) hemolysin [Acanthamoeba polyphaga]
18373	ENU02167	ANI61C1253:	29-53	273-303	NAP		g607954	218	57	2.00E-11	57	91	Conidiation-specific protein 6 ; (L26036) conidiation protein [Neurospora crassa]
		6112..5796					g461773	98	46	0.00006	34	91	(U12823) hemolysin [Acanthamoeba polyphaga]
18374	ENU02168	ANI61C5247:	22-50	276-296	NAP								cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]
		3049..2733											hypothetical protein YDR286c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr286cp [Saccharomyces cerevisiae] "(S53434) L46=ribosomal protein [Kluyveromyces marxianus, Peptide, 51 aa] [Kluyveromyces marxianus]" epoxide hydrolase [Rattus norvegicus]
18375	ENU02169	ANI61C1253:	29-53	273-303	NAP		g607954	218	57	2.00E-11	57	91	(AC005278) Similar to gb U85207 smRNP core Sm protein homolog Sm-X5 from Mus musculus. EST gb AA612141 comes from this gene. [Arabidopsis thaliana]
		6112..5796											(Z98595) 60s ribosomal protein 122 [Schizosaccharomyces pombe]
18376	ENU02170	ANI61C3429:	22-50	278-297	NAP		g117803	132	78	2.00E-14	44	15	
		379..62											
18377	ENU02171	ANI61C592:9	22-53	279-300	NAP		g2131413	70	49	0.000009	23	92	
		05..1225											
18378	ENU02172	ANI61C7935:	22-54	282-302	NAP		g263485	139	33	0.6			
		802..902											
18379	ENU02173	ANI61C1965:	62-86	323-343	NAP		g228278	148	56	0.000000	31	95	
		393..70								07			
18380	ENU02174	ANI61C8199:	24-49	287-306	NAP		g3850571	286	100	5.00E-21	57	95	
		2534..2210											
18381	ENU02175	ANI61C7018:	24-43	288-310	NAP		g4581479	335	104	2.00E-22	60	74	
		469..141											



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18382	ENU02176	AN161C107:1	22-54	286-308	NAP		g1723740	99	50	0.000004	31	82	hypothetical 12.4 KD protein in NAB1A-GPI1 intergenic region ; hypothetical protein YGR215w - yeast (Saccharomyces cerevisiae) ; (Z73000) ORF YGR215w [Saccharomyces cerevisiae]
18383	ENU02177	AN161C1034	27-46	292-315	NAP		g586501	138	64	4.00E-10	35	92	hypothetical 13.2 KD protein in ORC2-TIP1 intergenic region ; hypothetical protein YBR062c - yeast (Saccharomyces cerevisiae) ; (Z25931) ORF YBR062c [Saccharomyces cerevisiae]
18384	ENU02178	AN161C2076: 1448..1116	37-56	295-327	NAP		g3850102	437	161	1.00E-39	67	77	(AL033388) putative golgi membrane protein-sorting protein [Schizosaccharomyces pombe]
18385	ENU02179	AN161C4334: 606..943	22-51	297-317	NAP		g2132826	91	56	0.000000	34	93	probable membrane protein YOL026c - yeast (Saccharomyces cerevisiae) ; (Z74768) ORF YOL026c [Saccharomyces cerevisiae]
18386	ENU02180	AN161C6137: 3737..4075	35-53	312-331	NAP		g2131721	217	64	1.00E-17	52	91	[Saccharomyces cerevisiae] hypothetical protein YHR004c-a - yeast (Saccharomyces cerevisiae) ; (Z80875) Mtr11p [Saccharomyces cerevisiae] ; (U10555) Mtr11p [Saccharomyces cerevisiae]
18387	ENU02181	AN161C4486: 475..137	72-92	350-369	NAP		g1175403	164	60	0.000000	36	54	hypothetical 19.0 KD protein C31A2.08 in chromosome I ; hypothetical protein SPAC31A2.08 - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe]
18388	ENU02182	AN161C5870: 684..1024	60-79	334-358	NAP		g2281089	152	74	3.00E-13	54	81	(AC002333) Sm protein F isolate [Arabidopsis thaliana]
18389	ENU02183	AN161C3916: 2424..2765	61-88	339-360	NAP		g3183357		41	0.002			hypothetical 13.4 KD protein C17H9.07 in chromosome I ; (Z28597) hypothetical protein [Schizosaccharomyces pombe]
18390	ENU02184	AN161C3209: 50..393	70-89	351-371	NAP		g2498272	267	98	2.00E-20	46	77	Cyanate lyase (cyanate hydrolase) (cyanase) ; (U59481) cyanate lyase [Synechococcus PCC7942] ; (AB000100) cyanase [Synechococcus sp.]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18391	ENU02185	ANIG1C8982:	33-51	317-336	NAP		g2983605	238	100	4.00E-21	46	72	(AE000725) ribose 5-phosphate isomerase B [Aquitex aeolicus]
18392	ENU02186	7793..7448 ANIG1C1601:	56-77	341-361	NAP		g1351714		52	0.000002			putative transporter C11D3.18C; (Z68166) unknown
18393	ENU02187	2298..1951 ANIG1C5803:	22-43	309-327	NAP		g3183399	125	55	0.000000	28	91	[Schizosaccharomyces pombe] hypothetical 13.9 KD protein C2E11.03C in chromosome I; (AL031181) very hypothetical protein [Schizosaccharomyces pombe]; (AL035064) very hypothetical protein [Schizosaccharomyces pombe]
18394	ENU02188	1:1334..986 ANIG1C1064	29-54	314-335	NAP		g731777	149	61	1.00E-10	38	97	"hypothetical 11.0 KD protein in FAA3-MAS3 intergenic region; hypothetical protein YIL008w - yeast (Saccharomyces cerevisiae); (Z38113) orf. len: 99, CAl=0.21 [Saccharomyces cerevisiae]"
18395	ENU02189	872..523 ANIG1C4009:	52-71	342-359	NAP		g2276355	328	101	2.00E-21	60	80	(Z97992) putative small ribonuclear protein [Schizosaccharomyces pombe]
18396	ENU02190	562..657 ANIG1C6138:	35-68	322-343	NAP		g1363744	260	41	0.004	38	45	hypothetical protein YLR435w - yeast (Saccharomyces cerevisiae); (U21094) Ylr435wp [Saccharomyces cerevisiae] (AC000133) ORF [Emicella nidulans]
18397	ENU02191	4:431..79 ANIG1C1127	42-62	329-352	NAP		g1870220	685	234	2.00E-61	98	87	hypothetical 10.7 KD protein C17C9.09C in chromosome I; (Z73099) hypothetical protein [Schizosaccharomyces pombe]
18398	ENU02192	1347..993 ANIG1C9645:	54-74	347-366	NAP		g1723568		48	0.00002			[Schizosaccharomyces pombe] small nuclear ribonucleoprotein polypeptide E; U1 and U2 small nuclear ribonucleoprotein E (SNRNP-E); small nuclear ribonucleoprotein E-human; (X12466) snRNP E protein (AA 1-92) [Homo sapiens]; (L19064) small nuclear ribonucleoprotein E [Gallus gallus]; (X65702) SmE protein [Gallus gallus]; (M37716) small nuclear RNA protein (snRNP E) [Homo sapiens]
18399	ENU02193	4:3168..3523 ANIG1C1000	26-45	307-339	NAP		g4507129	169	68	2.00E-11			

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18400	ENU02194	ANIG1C9311:	44-63	341-360	NAP		g1175442	759	138	1.00E-32	58	39	hypothetical protein C22F3.01 in chromosome I ; hypothetical protein SPAC22F3.01 - fission yeast (Schizosaccharomyces pombe) (fragment) ; (Z54285) unknown [Schizosaccharomyces pombe]
		3740..3382											Lectin precursor (agglutinin); lectin precursor - rice ; (M24504) lectin [Oryza sativa]
18401	ENU02195	ANIG1C8065:	65-84	364-383	NAP		g113509	78	68	2.00E-11	35	45	60S ribosomal protein L35
		714..354											
18402	ENU02196	ANIG1C5436:	34-59	334-353	NAP		g2833359	268	45	0.0002	57	73	"40S ribosomal protein S15 (S12) ; ribosomal protein S12, cytosolic - Podospora anserina ; (Z23267) cytoplasmic ribosomal protein S12 [Podospora anserina]"
		564..925											(AL035263) weak similarity to chick phosphatidylethanolamine site rol acetyltransferase
18403	ENU02197	ANIG1C4673:	28-57	329-350	NAP		g464706	506	108	1.00E-37	78	76	[Schizosaccharomyces pombe] putative protein transport protein SEC61 gamma subunit ; hypothetical protein SPAC4G8.02c - fission yeast (Schizosaccharomyces pombe) ; (Z56276) putative protein transport protein sec61-gamma subunit [Schizosaccharomyces pombe]
		38..402											nuclear transport factor 2 (NTF-2) (nuclear transport factor P10) ; hypothetical protein YER009w - yeast (Saccharomyces cerevisiae) ; (U18778) Ntf2p: Nuclear Transport Factor 2 [Saccharomyces cerevisiae]
18404	ENU02198	ANIG1C7221:	50-72	353-372	NAP		g4176531	1107	89	1.00E-17	34	18	(AL032684) putative ubiquitin-protein ligase [Schizosaccharomyces pombe]
		1542..1906											hypothetical 23.0 KD protein in SNF2-CPA1 intergenic region ; hypothetical protein YOR294w - yeast (Saccharomyces cerevisiae) ; (Z75202) ORF YOR294w [Saccharomyces cerevisiae]
18405	ENU02199	ANIG1C9819:	31-56	337-356	NAP		g1351034	167	47	0.000000	52	95	
		4967..4600											
18406	ENU02200	ANIG1C3164:	69-88	368-394	NAP		g731437	244	53	2.00E-15	44	81	
		630..263											
18407	ENU02201	ANIG1C4957:	60-79	368-393	NAP		g3810851	851	96	1.00E-19	33	15	
		460..85											
18408	ENU02202	ANIG1C6549:	63-84	378-397	NAP		g3183481	299	92	1.00E-18	51	56	
		905..529											

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18409	ENU02203	ANI61C1235:	24-43	341-362	NAP		g114663	685	167	4.00E-41	97	88	"ATP synthase protein 9, mitochondrial precursor (LIPID-binding protein); (M30144) mitochondrial ATP synthase precursor [Emmericella nidulans]"
18410	ENU02204	ANI61C2997:	61-89	381-400	NAP		g1362228	448	161	2.00E-39	60	54	pac2 protein - fission yeast (Schizosaccharomyces pombe); (D43748) Pac2p [Schizosaccharomyces pombe]; (Z98979) camp independent regulatory protein
18411	ENU02205	ANI61C7253:	51-70	375-394	NAP		g3005841	341	143	7.00E-34	54	80	[Schizosaccharomyces pombe] (AJ002026) rAsp f 13 [Aspergillus fumigatus]
18412	ENU02206	ANI61C8384:	67-86	392-411	NAP		g3451473	587	121	2.00E-27	50	41	(AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe]
18413	ENU02207	ANI61C6419:	69-88	389-414	NAP		g2492777	314	99	9.00E-21	40	35	hypothetical ZINC-type alcohol dehydrogenase-like protein in pre-SET4 intergenic region; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae); (Z54141) unknown [Saccharomyces cerevisiae] (Z97050) hypothetical protein Rv0163 [Mycobacterium tuberculosis]
18414	ENU02208	ANI61C1015:	63-91	390-410	NAP		g2213500	173	85	3.00E-16	39	76	[Mycobacterium tuberculosis] (X99300) unknown epidymal protein [Mus musculus]
18415	ENU02209	ANI61C2495:	24-55	343-371	NAP		g1430862	90	61	0.000000	26	91	(Z99259) small nuclear ribonucleoprotein
18416	ENU02210	ANI61C9745:	30-56	358-377	NAP		g2414614	177	43	0.000000	50	60	[Schizosaccharomyces pombe]
18417	ENU02211	ANI61C2576:	22-53	351-370	NAP		g2501450	201	76	7.00E-17	46	94	ubiquitin-like protein SMT3; SMT3 protein - yeast (Saccharomyces cerevisiae); (U27233) Smt3p [Saccharomyces cerevisiae]; (U33057) suppressor of MIF2 mutations; CAI: 0.31 [Saccharomyces cerevisiae]
18418	ENU02212	ANI61C1557:	55-75	386-406	NAP		g1175395	290	80	5.00E-15	43	84	hypothetical 14.1 KD protein C31A2.02 in chromosome I; hypothetical protein SPAC31A2.02 - fission yeast (Schizosaccharomyces pombe); (Z50113) unknown [Schizosaccharomyces pombe] (AC000133) ORF [Emmericella nidulans]
18419	ENU02213	ANI61C1098:	22-54	349-373	NAP		g1870220	169	81	3.00E-15	39	97	

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18420	ENU02214	ANI61C727:1	45-64	362-397	NAP		g1708982	550	129	1.00E-29	52	23	Ammonium transporter MEP3 ; ammonium transport protein MEP3 - yeast (Saccharomyces cerevisiae) ; (U40829) Similar to B. subtilis membrane protein NrgA (Swiss Prot. accession number Q07429) [Saccharomyces cerevisiae] "(AB007633) Myo3 [Schizosaccharomyces pombe] ; (Z98762) SPAC4A8.05c, myosin heavy chain, len:2104aa, similar eg. to MYO2_DICD1, P08799, myosin ii heavy chain; non muscle, (2116aa), fasta scores, opt: 2488, E0.0, (29.5% identit y in 2167 aa overlap), PS00017 ATP/GTP-bind...
18421	ENU02215	ANI61C7854: 785..1181	45-72	376-399	NAP		g2828348	362	64	5.00E-10			
18422	ENU02216	ANI61C5660: 1057..1454	68-88	396-423	NAP		g3023324	414	133	5.00E-31	48	76	"ATP synthase D chain, mitochondrial ; (AF019223) F1Fo-ATP synthase subunit 7 [Kluveromyces lactis] " DNA-directed RNA polymerase II 13.3 KD polypeptide (RPB11) (RPB14) ; (D85818) RNA polymerase II subunit RPB14 [Mus musculus] (AF099136) vacuolar ATP synthase subunit F [Neurospora crassa] (X89714) rhamnogalacturonan acetyltransferase [Aspergillus aculeatus] (Z28052) ORF YKL053c-a [Saccharomyces cerevisiae] ; (Z28054) ORF YKL053c-a [Saccharomyces cerevisiae]
18423	ENU02217	ANI61C9131: 580..181	54-73	389-411	NAP		g2500634	198	56	3.00E-12	52	70	(AL031326) putative protein [Arabidopsis thaliana] "ribosomal protein L11.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z72870) ORF YGR085c [Saccharomyces cerevisiae] " (AC007196) unknown protein [Arabidopsis thaliana] (AB011378) MAT-2 protein [Fusarium oxysporum]
18424	ENU02218	ANI61C6203: 9440..9041	52-73	381-409	NAP		g4426615	398	73	2.00E-15	57	75	
18425	ENU02219	ANI61C5382: 1245..845	22-50	356-379	NAP		g1004217	840	127	6.00E-31	64	47	
18426	ENU02220	ANI61C1044 2:1486..1886	36-58	374-394	NAP		g2980812	86	37	0.003			
18427	ENU02221	ANI61C4350: 2224..1823	69-89	408-428	NAP		g3451060		34	0.38			
18428	ENU02222	ANI61C9613: 1012..610	55-77	390-415	NAP		g71107	635	154	2.00E-42	76	63	
18429	ENU02223	ANI61C1800: 1807..2209	31-50	372-391	NAP		g4582434	207	36	1.00E-11	54	87	
18430	ENU02224	ANI61C7401: 1335..930	46-65	389-409	NAP		g3168589	206	59	4.00E-19	38	93	

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18431	ENU02225	ANI61C6584:	35-56	380-401	NAP		g4322266	1653	245	1.00E-64	82	28	(AF077355) protein phosphatase 2A regulatory B subunit [Neurospora crassa]
		1988..2396											
18432	ENU02226	ANI61C5101:	27-51	377-394	NAP		g3676762	443	105	7.00E-32	71	90	(AF087136) RS6/L7A ribosomal protein homolog
		3160..3569											[Schizosaccharomyces pombe]
18433	ENU02227	ANI61C4456:	43-62	388-411	NAP		g1082211	148	57	1.00E-10	31	3	"ankyrin 3, long form - human ; (U13616) ankyrin G [Homo sapiens]"
		102..512											Oleate-induced peroxisomal protein
18434	ENU02228	ANI61C5487:	52-71	400-421	NAP		g131668	218	59	0.000000	49	85	POX18 (lipid-transfer protein) (PXP-18) ; POX18 protein - yeast (Candida tropicalis) ; lipid transfer protein - imperfect fungus (Candida tropicalis) ; (X53633) POX18 [Candida tropicalis] ; (M24440) peroxisomal protein [Candida tropicalis]
		414..3											"probable 60S ribosomal protein L27 ; ribosomal protein L27.e.A, cytosolic - yeast (Saccharomyces cerevisiae) ; (U10400) Rpl27p: Probable 60S ribosomal protein L27 [Saccharomyces cerevisiae]"
18435	ENU02229	ANI61C1012	57-76	407-429	NAP		g730548	446	112	1.00E-24	76	55	Acetamidase ; amds protein - Emericella nidulans ; (M16371) acetamidase enzyme [Emericella nidulans]
		1:661..1075											ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae) ; (Z73153) ORF YLL048c [Saccharomyces cerevisiae]
18436	ENU02230	ANI61C7031:	49-68	404-423	NAP		g113701	702	99	1.00E-20			(AF047694) glutaredoxin [Vernicia fordii]
		561..145											hypothetical 35.7 KD protein in DNL4-SLG1 intergenic region ; hypothetical protein YOR006c - yeast (Saccharomyces cerevisiae) ; (U43491) hypothetical protein UND313 [Saccharomyces cerevisiae] ; (Z74914) ORF YOR006c [Saccharomyces cerevisiae]
18437	ENU02231	ANI61C1047	39-61	395-414	NAP		g3915963	1420	152	9.00E-37	60	8	
		0:6088..5671											
18438	ENU02232	ANI61C3552:	25-44	383-402	NAP		g3249567	200	52	4.00E-14	50	87	
		725..306											
18439	ENU02233	ANI61C8615:	22-40	379-399	NAP		g2833220	579	101	1.00E-32	68	33	
		3216..2797											

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18440	ENU02234	ANI61C1677: 47-67	47-67	396-425	NAP		g418574	520	106	8.00E-23	38	45	mitochondrial carrier protein YMC1 precursor ; (X67122) mitochondrial carrier protein [Saccharomyces cerevisiae]
18441	ENU02235	ANI61C662:8 26-47	26-47	382-406	NAP		g3850125	193	94	6.00E-19	35	27	(AL033391) hypothetical membrane protein [Candida albicans]
18442	ENU02236	ANI61C1479: 45-64	45-64	405-425	NAP		g627570	180	68	3.00E-11			phosphorylation regulatory protein HP-10 - human
18443	ENU02237	ANI61C3138: 24-52	24-52	386-405	NAP		g2493096	103	57	0.000000	30	96	"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] " (AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis] (AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe]
18444	ENU02238	ANI61C7858: 60-79	60-79	414-441	NAP		g2293314		69	2.00E-11			(Y08703) SlyA protein [Sinorhizobium meliloti]
18445	ENU02239	ANI61C394:1 71-91	71-91	434-453	NAP		g3006160	456	165	2.00E-40	51	33	(AL022070) hypothetical protein [Schizosaccharomyces pombe]
18446	ENU02240	ANI61C1107 2:909..1333	33-53	397-415	NAP		g1926396		33	1.2			"probable transporter FEN2 ; probable membrane protein YCR028c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR028c, len:512 [Saccharomyces cerevisiae] "
18447	ENU02241	ANI61C506:1 28-48	28-48	391-411	NAP		g2950478	276	79	1.00E-14	39	82	(AB005295) HY5 [Arabidopsis thaliana] ; (AB005456) HY5 [Arabidopsis thaliana]
18448	ENU02242	ANI61C3144: 22-43	22-43	385-406	NAP		g140479	260	102	1.00E-21	39	27	protein transport protein SEC9 ; SEC9 protein - yeast (Saccharomyces cerevisiae) ; (L34336) Sec9 [Saccharomyces cerevisiae] ; (Z72794) ORF YGR009c [Saccharomyces cerevisiae]
18449	ENU02243	ANI61S1388: 58-78	58-78	425-444	NAP		g2244709	136	46	0.0001	33	78	
18450	ENU02244	ANI61C7468: 39-58	39-58	405-426	NAP		g730733	368	83	9.00E-16	50	15	

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18451	ENU02245	ANI61C9311:	38-57	398-425	NAP		g731668	517	74	6.00E-13	31	31	SSF1 protein ; SSF1 protein - yeast (Saccharomyces cerevisiae) ; (U00061) Ssf1p [Saccharomyces cerevisiae] ; (U18113) Ssf1p [Saccharomyces cerevisiae]
18452	ENU02246	ANI61C8081:	67-86	436-455	NAP		g1710760	218	56	4.00E-10	84	73	probable 40S ribosomal protein S28 (S33) ; (Z70691) ribosomal protein S28 [Schizosaccharomyces pombe] ; (AL031545) probable 40s ribosomal protein 28s [Schizosaccharomyces pombe]
18453	ENU02247	ANI61C6597:	72-94	434-461	NAP		g1923256	980	169	1.00E-41	53	46	(U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]
18454	ENU02248	ANI61C1463:	50-69	420-440	NAP		g1073534	224	72	8.00E-14	37	40	iucB protein - Escherichia coli ; (X76100) iucB [Escherichia coli]
18455	ENU02249	ANI61C1898:	37-64	409-428	NAP		g2271497	316	84	4.00E-16	45	39	(AF009672) unknown [Acinetobacter sp. ADP1]
18456	ENU02250	ANI61C7592:	25-44	394-416	NAP		g1176485	251	101	3.00E-21	42	96	hypothetical 16.2 KD protein in IME2-MEF2 intergenic region ; probable membrane protein YJL104w - yeast (Saccharomyces cerevisiae) ; (X85021) orf 8 [Saccharomyces cerevisiae] ; (Z49379) ORF YJL104w [Saccharomyces cerevisiae]
18457	ENU02251	ANI61C5414:	24-43	381-416	NAP		g731459	168	73	1.00E-12	38	84	hypothetical 17.1 KD protein in SAH1-ME14 intergenic region ; hypothetical protein YER044c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer044cp [Saccharomyces cerevisiae] (AL049474) similar to glycosylphosphatidylinositol anchor [Schizosaccharomyces pombe]
18458	ENU02252	ANI61C9241:	67-88	430-460	NAP		g4538668	98	45	0.0002	32	73	Lipoic acid synthetase precursor (LIP-SYN) (lipoate synthase) ; lipoic acid synthase (EC 2.8.1.-) precursor - yeast (Saccharomyces cerevisiae) ; (Z75104) ORF YOR196c [Saccharomyces cerevisiae]
18459	ENU02253	ANI61C1281:	60-79	434-453	NAP		g417254	1206	211	2.00E-54	69	35	(Z92669) hypothetical protein Rv0223c [Mycobacterium tuberculosis]
18460	ENU02254	ANI61C1100:	51-74	410-444	NAP		g1871596	180	78	2.00E-14	29	29	



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18461	ENU02255	ANI61C3253:	72-92	444-465	NAP		g1703247	561	221	2.00E-57	70	39	"fructose-bisphosphate aldolase ; (L42380) fructose 1,6 biphosphate-aldolase [Neurospora crassa]"
18462	ENU02256	ANI61C426:5	72-91	441-467	NAP		g729580	697	200	5.00E-51	61	20	"1,4-alpha-glucan branching enzyme (glycogen branching enzyme) ; 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - yeast (Saccharomyces cerevisiae) ; (U18530) 1,4-alpha-glucan branching enzyme [Saccharomyces cerevisiae]"
18463	ENU02257	ANI61C9851:	59-80	435-454	NAP		g3128287	134	63	9.00E-10	33	86	(AF010496) hypothetical protein [Rhodobacter capsulatus]
18464	ENU02258	ANI61C2552:	63-82	440-459	NAP		g2131439	192	83	9.00E-16	34	28	hypothetical protein YDR348c - yeast (Saccharomyces cerevisiae) ; (U51032) Ydr348cp [Saccharomyces cerevisiae]
18465	ENU02259	ANI61C8575:	23-46	400-419	NAP		g4507485		38	0.05			thrombospondin 1 ; (X14787) precursor polypeptide (AA -31 to 1139) [Homo sapiens]
18466	ENU02260	ANI61C9787:	53-75	427-449	NAP		g1175439	258	55	3.00E-14	38	15	hypothetical 107.1 KD protein C24H6.11C in chromosome 1 ; hypothetical protein SPAC24H6.11c - fission yeast (Schizosaccharomyces pombe) ; (Z54142) hypothetical protein [Schizosaccharomyces pombe]
18467	ENU02261	ANI61C1796:	38-58	415-435	NAP		g118513	517	155	1.00E-37	54	39	Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASA DH) ; aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - yeast (Saccharomyces cerevisiae) ; (X15649) aspartic semi-aldehyde dehydrogenase (AA 1-365) [Saccharomyces cerevisiae] ; (Z50046) Hom2p [Saccharomyces cerevisiae]
18468	ENU02262	ANI61C9323:	62-81	425-459	NAP		g793875	274	111	3.00E-24	42	98	(Z49149) 100% identity in 135 aa ov with the CSE1 protein from S. cerevisiae. This ORF is incomplete. [Saccharomyces cerevisiae] ; HRC135 gene [Saccharomyces cerevisiae]
18469	ENU02263	ANI61C1144	69-97	434-467	NAP		g1805251	235	87	8.00E-17	36	26	(U58946) transposase [Aspergillus awamori]

# Sequence Description

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18470	ENU02264	ANI61C1465	22-50	399-420	NAP		g133131	116	48	0.00004	37	79	"mitochondrial 60S ribosomal protein L31 precursor (YML31) ; ribosomal protein YmL31 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X15099) precursor rpL31 protein [Saccharomyces cerevisiae] ; (Z28138) ORF YKL138c [Saccharomyces cerevisiae]"
18471	ENU02265	ANI61C6213	60-81	438-458	NAP		g1723832	368	72	3.00E-17	58	62	hypothetical 15.9 KD protein in OLE1-DUP1 intergenic region ; probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae) ; (Z72576) ORF YGL054c [Saccharomyces cerevisiae]
18472	ENU02266	ANI61C3405	35-59	415-434	NAP		g1170186	200	54	0.000000	34	19	probable ATP-dependent RNA helicase DBP4 (helicase CA4) (helicase UF1) ; probable RNA helicase CA4 - yeast (Saccharomyces cerevisiae) ; (Z49308) ORF YJL033w [Saccharomyces cerevisiae]
18473	ENU02267	ANI61C3640	71-91	451-472	NAP		g1805251	1188	93	8.00E-19	37	26	(U58946) transposase [Aspergillus awamori]
18474	ENU02268	ANI61C7618	63-84	444-464	NAP		g1710803	714	92	1.00E-18	31	23	Retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRF588; EMBL:SCRTG2X:M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae] ; (M97691) Rtg2p [Saccharomyces cerevisiae] ; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]
18475	ENU02269	ANI61C2182	38-57	418-440	NAP		g731298	256	105	2.00E-22	37	24	probable transporter SEO1 ; probable membrane protein YAL067c - yeast (Saccharomyces cerevisiae) ; (U12980) Seo1p: putative membrane protein [Saccharomyces cerevisiae]
18476	ENU02270	ANI61C6415	65-84	449-468	NAP		g3873405		43	0.002			(U17129) unknown [Rhodococcus erythropolis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18477	ENU02271	ANI61C9683:	71-92	452-475	NAP		g465011	1037	261	1.00E-69	97	43	Uricase (urate oxidase) ; urate oxidase (EC 1.7.3.3) - Emericella nidulans ; (X72210) urate oxidase [Emericella nidulans]
18478	ENU02272	ANI61C3079:	27-53	413-432	NAP		g171183	383	129	1.00E-29	45	34	(M61194) CDC14 [Saccharomyces cerevisiae]
18479	ENU02273	ANI61C7257:	30-49	407-436	NAP		g1723218	294	107	2.00E-23	51	83	hypothetical 19.5 KD protein C3H8.07C in chromosome I ; (Z69086) unknown [Schizosaccharomyces pombe]
18480	ENU02274	ANI61C6494:	22-50	409-428	NAP		g1850768	177	88	4.00E-17	47	89	(AB001289) YNL157W homolog [Schizosaccharomyces pombe]
18481	ENU02275	ANI61C497:	31-49	414-438	NAP		g3023637	2950	213	4.00E-55	68	12	probable ATP-dependent RNA helicase HRH1 (DEAH box protein 8) ; probable RNA helicase 1 - human ; (D50487) RNA helicase (HRH1) [Homo sapiens]
18482	ENU02276	ANI61C1049	39-69	428-447	NAP		g3024439	1855	234	2.00E-61	84	35	26S PROTEASE regulatory subunit 6B homolog ; (U15601) 26S proteasome subunit [Aspergillus niger]
18483	ENU02277	ANI61C3576:	26-54	416-435	NAP		g3169068	276	56	5.00E-18	67	84	(AL023704) putative transcription factor ita small subunit [Schizosaccharomyces pombe]
18484	ENU02278	ANI61C2679:	64-84	443-473	NAP		g2132651	286	127	3.00E-29	42	25	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
18485	ENU02279	ANI61C1083	24-48	403-435	NAP		g3265058	703	165	2.00E-40	91	84	(AF060232) monoubiquitin/carboxy extension protein fusion [Botryotinia fuckeliana]
18486	ENU02280	ANI61C3200:	70-91	462-481	NAP		g1078650	546	136	9.00E-42	81	61	"peptidylprolyl isomerase (EC 5.2.1.8) a, cytosolic - fungus (Fusarium sporotrichioides)"
18487	ENU02281	ANI61C5329:	61-80	451-472	NAP		g131768	605	68	3.00E-11			quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]

Seq num	Seq id	Contig	Source	5 pos	Primer 3 pos	Primer 414-434	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18488	ENU02282	ANI61C7023:	22-49				NAP	g465702	221	83	2.00E-20	42	64		probable ribosomal protein B0303.15 in chromosome III; ribosomal protein L11 homolog - <i>Caenorhabditis elegans</i> ; (M77697) ribosomal protein L11 [ <i>Caenorhabditis elegans</i> ] (AC000133) G4P04 [Emmericella nidulans]
18489	ENU02283	ANI61C1355:	60-79				NAP	g1870214	839	267	4.00E-74	98	68		hypothetical protein YPR100w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U32445) Note that there is a 357 codon ORF contained within this ORF on the other strand [ <i>Saccharomyces cerevisiae</i> ] "Lysyl-TRNA synthetase, cytoplasmic (lysine--TRNA ligase) (LYSRS) ; lysine--TRNA ligase (EC 6.1.1.6) - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (J04186) lysyl-TRNA synthetase [ <i>Saccharomyces cerevisiae</i> ] ; (Z68196) Krs1p [ <i>Saccharomyces cerevisiae</i> ] ; (Z74333) ORF YDR037w [ <i>Saccharomyces cerevisiae</i> ] "
18491	ENU02285	ANI61C2432:	25-44				NAP	g135139	698	241	3.00E-63	75	25		3-Isopropylmalate dehydratase (isopropylmalate isomerase) (alpha-IPM isomerase) (IPMI) ; (D63833) 3-isopropylmalate dehydratase [ <i>Rhizopus niveus</i> ] ; alpha-isopropylmalate isomerase [ <i>Rhizopus niveus</i> ] (AJ001732) r-Asp f 4 [ <i>Aspergillus fumigatus</i> ] (AC004077) putative urease accessory protein [ <i>Arabidopsis thaliana</i> ] ; (AC004481) putative urease accessory protein [ <i>Arabidopsis thaliana</i> ] (Z81071) predicted using Genefinder; ribonucleoprotein E (SW:P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene; ...
18492	ENU02286	ANI61C1783:	52-72				NAP	g2492643	621	195	1.00E-49	66	19		
18493	ENU02287	ANI61C4724:	56-78				NAP	g3005839	485	125	2.00E-28	53	52		
18494	ENU02288	ANI61C7180:	51-70				NAP	g3128220	721	195	2.00E-49	62	55		
18495	ENU02289	ANI61C9804:	71-95				NAP	g3876465	129	39	0.0005	63	80		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18496	ENU02290	ANI61C5930:	24-59	424-443	NAP		g3646479	526	70	1.00E-11	37	91	(AJ010981) putative transposase [Talaromyces stipitatus]
18497	ENU02291	ANI61C7029:	64-84	464-483	NAP		g1169238	935	169	1.00E-41	56	30	"glutamate decarboxylase (GAD) ; glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia ; (L16797) glutamate decarboxylase [Petunia hybrida] ; (L16977) glutamate decarboxylase [Petunia hybrida]"
18498	ENU02292	ANI61C8332:	33-52	432-452	NAP		g3378330	347	131	4.00E-30	40	79	(AF079317) unknown [Sphingomonas aromaticivorans]
18499	ENU02293	ANI61C9046:	46-66	441-466	NAP		g731511	805	189	1.00E-47	63	58	hypothetical 29.7 KD protein in RSP5-PAK1 intergenic region ; hypothetical protein YER126c - yeast (Saccharomyces cerevisiae) ; (U18916) Yer126cp [Saccharomyces cerevisiae]
18500	ENU02294	ANI61C1064	22-46	417-442	NAP		g4490325	104	58	0.000000	25	70	(AL035656) hypothetical protein [Arabidopsis thaliana]
18501	ENU02295	ANI61C7541:	42-61	443-462	NAP		g1730544	909	163	3.00E-53	73	53	Prohibitin ; prohibitin - yeast (Saccharomyces cerevisiae) ; (Z72917) ORF YGR132c [Saccharomyces cerevisiae]
18502	ENU02296	ANI61C3317:	32-51	433-452	NAP		g729318	784	106	1.00E-28	49	35	"2,2-dialkylglycine decarboxylase (DGD) ; (J05282) 2,2-dialkylglycine decarboxylase structural protein [Pseudomonas cepacia]"
18503	ENU02297	ANI61C5842:	68-99	463-488	NAP		g2909465	226	78	3.00E-14			(AL021930) hypothetical protein Ry0276 [Mycobacterium tuberculosis]
18504	ENU02298	ANI61C1473:	72-91	471-493	NAP		g3747050	380	115	1.00E-25	68	85	(AF093540) ribosomal protein L26 [Zea mays]
18505	ENU02299	ANI61C2300:	64-83	464-486	NAP		g462565	294	71	3.00E-12	32	31	Mannose-6-phosphate isomerase (phosphomannose isomerase) (PMI) (phosphohexomutase) ; mannose-6-phosphate isomerase (EC 5.3.1.8) - yeast (Candida albicans) ; (X82024) mannose-6-phosphate isomerase [Candida albicans]
18506	ENU02300	ANI61C5903:	33-54	433-455	NAP		g2132260	318	86	2.00E-16	46	37	hypothetical protein YPR040w - yeast (Saccharomyces cerevisiae) ; (Z68111) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]

# Gene Ontology

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18507	ENU02301	ANI61C7819:	23-42	425-445	NAP		g4235093	357	118	2.00E-27	43	19	(AF108944) beta-xylosidase [Aspergillus niger]
18508	ENU02302	2..466 ANI61C4975:	68-88	473-492	NAP		g1749584	415	157	6.00E-38	45	74	(D89188) unnamed protein product [Schizosaccharomyces pombe]
18509	ENU02303	2990..2524 ANI61C2732:	72-94	461-496	NAP		g1722894	465	187	3.00E-47	56	47	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-L-arabinofuranosidase (arabinosidase); xylosidase/arabinosidase - Bacteroides ovatus (strain V975) ; (U04957) xylosidase/arabinosidase [Bacteroides ovatus] ; xylosidase-arabinosidase [Bacteroides ovatus]"
18510	ENU02304	ANI61C1138:	22-41	428-447	NAP		g1931638	414	145	2.00E-34	42	12	(U95973) transcription factor rush-alpha isolog [Arabidopsis thaliana]
18511	ENU02305	8699..9166 ANI61C2853:	34-53	436-459	NAP		g731448	70	43	0.001	31	62	hypothetical 18.3 KD protein in GAL83-YPT8 intergenic region ; hypothetical protein YER030w - yeast (Saccharomyces cerevisiae) ; (U18778) Yer030wp [Saccharomyces cerevisiae] probable stermatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emmentella nidulans]
18512	ENU02306	ANI61C3640:	67-87	459-493	NAP		g2493387	267	96	1.00E-19	38	27	(AL034353) putative acetyltransferase [Schizosaccharomyces pombe]
18513	ENU02307	ANI61C1140:	48-67	452-474	NAP		g3925776	258	108	3.00E-23	39	94	(AF047464) Trp1 [Schizosaccharomyces pombe]
18514	ENU02308	668..1136 ANI61C1115	62-81	470-489	NAP		g2896142	984	85	2.00E-16	40	15	(AF047464) Trp1 [Schizosaccharomyces pombe]
18515	ENU02309	5:3351..3820 ANI61C2532:	24-46	432-451	NAP		g3006140	622	220	6.00E-57	68	60	(AL022299) ribosomal protein [Schizosaccharomyces pombe]; (AJ001133) ribosomal protein L7 [Schizosaccharomyces pombe]
18516	ENU02310	ANI61C8155:	64-84	468-492	NAP		g1572791	63	42	0.003			(U70852) weak similarity to neutral endopeptidases [Caenorhabditis elegans]
18517	ENU02311	ANI61C5147:	69-100	477-498	NAP		g4580321		36	0.12			(AF095903) unknown [Sinorhizobium meliloti]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18518	ENU02312	ANI61C8277:	68-87	478-497	NAP		g134975	495	101	3.00E-31	52	23	Heat shock protein STI1 ; stress-induced protein STI1 - yeast (Saccharomyces cerevisiae) ; (M28486)
		1289..818											heat shock protein STI1 [Saccharomyces cerevisiae] ; (X87331)
													STI1 heat shock protein [Saccharomyces cerevisiae] ; (Z74935)
													ORF YOR027w [Saccharomyces cerevisiae]
18519	ENU02313	ANI61C4165:	22-55	432-452	NAP		g548437	364	146	7.00E-35	47	18	OSH1 protein ; SWH1 protein (version 1) - yeast (Saccharomyces cerevisiae) ; (L28920) Osh1p [Saccharomyces cerevisiae]
		5..478											(AF039376) polypeptide [Arabidopsis arenosa]
18520	ENU02314	ANI61C102:1	28-46	435-460	NAP		g2865437	214	83	1.00E-15			hypothetical 34.1 KD protein C11D3.03C in chromosome I ; (Z68166) unknown
		415..1889											[Schizosaccharomyces pombe]
18521	ENU02315	ANI61C1075	23-44	435-455	NAP		g1351700	696	137	7.00E-42	57	46	CUT8 protein ; (D31772) ORF [Schizosaccharomyces pombe] ; (Z73099) protein kinase
		2:1531..1057											[Schizosaccharomyces pombe]
18522	ENU02316	ANI61C8453:	59-81	464-491	NAP		g729231	249	108	2.00E-23	33	60	[Schizosaccharomyces pombe]
		1035..561											oxobutanate hydroxymethyl-transferase [Arabidopsis thaliana]
18523	ENU02317	ANI61C2468:	54-74	461-486	NAP		g3702336	566	134	4.00E-31	46	45	hypothetical zinc finger protein ZK686.4 in chromosome III ; ZK686.4
		374..848											protein - Caenorhabditis elegans ; (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]
18524	ENU02318	ANI61C2736:	35-60	448-467	NAP		g466044	150	72	2.00E-12	28	37	(Z97050) hypothetical protein Rv0163 [Mycobacterium tuberculosis]
		518..44											[AL023859] putative tRNA splicing endonuclease gamma subunit [Schizosaccharomyces pombe]
18525	ENU02319	ANI61C9206:	22-43	436-455	NAP		g2213500	133	66	2.00E-10	35	91	(AF079317) unknown [Sphingomonas aromaticivorans]
		3099..3574											
18526	ENU02320	ANI61C1049	25-47	439-458	NAP		g3218411	386	98	4.00E-20	31	55	
		4:875..1350											
18527	ENU02321	ANI61C7100:	59-78	472-493	NAP		g3378265	1233	150	3.00E-45	67	35	
		517..41											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18528	ENU02322	ANI61C1087	63-85	475-497	NAP		g1934614	269	109	1.00E-23	36	14	(U93874) cytochrome P450 102 [Bacillus subtilis] ; (Z99117) similar to cytochrome P450 / NADPH-cytochrome P450 reductase [Bacillus subtilis]
18529	ENU02323	ANI61C35:18	41-60	456-475	NAP		g2498971	502	66	2.00E-10			putative sterigmatocystin biosynthesis monoxygenase STCW ; (U34740) putative FAD-containing monoxygenase [Emmericella nidulans] "(U40939) Similar to dihydroflavonol-4-reductase (maize, petunia, tomato). [Caenorhabditis elegans] "
18530	ENU02324	ANI61C8224: 1960..1483	66-84	467-501	NAP		g1072179	109	40	0.009			(U61841) cutinase G-box binding protein [Fusarium solani f. sp. pisi] "(AF125459) contains similarity to enoyl-CoA hydratases/isomerases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans] "(Z95556) fadD35 [Mycobacterium tuberculosis] (AE001038) enoyl-CoA hydratase (fad-3) [Archaeoglobus fulgidus] probable serine/threonine-protein kinase YOL045W ; hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae) ; (Z74788) ORF YOL045w [Saccharomyces cerevisiae]
18531	ENU02325	ANI61C2974: 648..169	51-70	464-486	NAP		g1438949	424	69	1.00E-18	42	28	hypothetical 16.9 KD protein in ALD6-PDR12 intergenic region ; hypothetical protein YPL059w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe13p [Saccharomyces cerevisiae]
18532	ENU02326	ANI61C3312: 1079..601	30-49	447-466	NAP		g4226133		34	0.00006			
18533	ENU02327	ANI61C7634: 551..72	40-68	458-477	NAP		g2113938	551	105	2.00E-30	51	25	
18534	ENU02328	ANI61C2961: 41..520	62-81	480-499	NAP		g2649635	292	124	4.00E-28	40	61	
18535	ENU02329	ANI61C9447: 1448..1928	63-82	481-501	NAP		g2499624	662	187	4.00E-47	68	12	
18536	ENU02330	ANI61C7555: 3253..3734	46-66	455-485	NAP		g3025275	375	102	2.00E-38	59	94	



Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer 491	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18537	ENU02331	ANI61C465:6	51-70	467-491	NAP	NAP		g4557817	1328	187	5.00E-47	57	30	3-oxoacid CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor (succinyl-CoA:3-ketoacid-CoA transferase) (OXCCT) ; (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]
18538	ENU02332	ANI61C1508: 42-62	698..216	458-482	NAP	NAP		g1363392	267	113	8.00E-25	36	24	beta-glucosidase/xylosidase - Erwinia chrysanthemi
18539	ENU02333	ANI61C4557: 57-84	485..3	474-497	NAP	NAP		g3451474	563	224	3.00E-58	63	25	(AL031349) conserved hypothetical protein [Schizosaccharomyces pombe]
18540	ENU02334	ANI61C2769: 44-63	109..591	465-484	NAP	NAP		g729079	644	134	4.00E-31	61	41	"Carboxy-cis,cis-muconate cyclase (3-carboxy-cis,cis-muconate lactonizing enzyme) (CMLE) ; carboxy-cis,cis-muconate cyclase (EC 5.5.1.5) - Neurospora crassa ; (L27538) 3-carboxy-cis,cis-muconate cyclase [Neurospora crassa] "
18541	ENU02335	ANI61C323:4	22-41	444-463	NAP	NAP		g549686	238	119	1.00E-26	39	16	Manganese resistance protein; hypothetical protein YKL064w - yeast (Saccharomyces cerevisiae) ; (X75781) B969 [Saccharomyces cerevisiae] ; (Z28064) ORF YKL064w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] (AB025252) reverse transcriptase [Magnaporthe grisea] (D87924) ORF 6 [Actinomyadura hibiscus]
18542	ENU02336	ANI61C1029	60-79	482-501	NAP	NAP		g4586458	163	85	2.00E-16	35	55	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe]
18543	ENU02337	ANI61C1099	25-42	446-466	NAP	NAP		g2580447		86	2.00E-16		80	tuberos scleros protein 2 - human
18544	ENU02338	ANI61C2925: 70-89	3:1728..1245	492-511	NAP	NAP		g3650394	157	75	2.00E-13	33	80	(AL031540) uroporphyrin methyltransferase
18545	ENU02339	ANI61C349:7	23-53	445-464	NAP	NAP		g631482	273	68	4.00E-11		32	[Schizosaccharomyces pombe]
18546	ENU02340	ANI61S1334: 61-82	145..6662	484-503	NAP	NAP		g3581882	492	197	5.00E-50	59	32	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
18547	ENU02341	ANI61C9558: 65-84	6029..6513	488-507	NAP	NAP		g3395556	695	156	8.00E-38	50	48	[Schizosaccharomyces pombe]

Seq num	Seq id	Contig	Source	5 pos	Primer	3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
18548	ENU02342	ANI61C1812:	46-67	468-488	NAP			g2440206	412	122	2.00E-27	42	20		(Z99532) putative integral membrane protein [Schizosaccharomyces pombe]
18549	ENU02343	ANI61C5509:	27-46	451-470	NAP			g140400	1065	201	3.00E-51	65	50		"hypothetical 37.2 KD protein in CHA1-PRD1 intergenic region ; hypothetical protein YCL059c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL059c, len:316 [Saccharomyces cerevisiae]"
18550	ENU02344	ANI61C6930:	26-46	450-469	NAP			g2160183	316	47	0.000000	47	42		"(AC000132) Identical to A. thaliana U2 SnRNP-specific A' protein (gb X69137). ESTs gb ATTS0705, gb ATTS0339 come from this gene. [Arabidopsis thaliana]"
18551	ENU02345	ANI61C9624:	22-57	446-466	NAP			g2842472	174	83	1.00E-15	31	65		(AL021747) preg-like protein. [Schizosaccharomyces pombe]
18552	ENU02346	ANI61C1031	22-56	445-466	NAP			g731810	335	92	2.00E-18	65	94		"probable 60S ribosomal protein YIL052C ; ribosomal protein L34.c.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 121, CAI: 0.77, RL34_RAT P11250 60S ribosomal protein L34 [Saccharomyces cerevisiae]"
18553	ENU02347	ANI61C6624:	68-87	491-512	NAP			g1749648	32	2.5					"(D89220) similar to Saccharomyces cerevisiae glutathion-dependent formaldehyde dehydrogenase, SWISS-PROT Accession Number P32771 [Schizosaccharomyces pombe]"
18554	ENU02348	ANI61C2275:	69-88	493-513	NAP			g731935	374	138	2.00E-32	52	24		hypothetical 66.4 KD protein in SMC3-MRPL8 intergenic region ; hypothetical protein YIL069c - yeast (Saccharomyces cerevisiae) ; (Z34288) HRE594 [Saccharomyces cerevisiae] ; (X88851) hypothetical protein [Saccharomyces cerevisiae] ; (Z49344) ORF YIL069c [Saccharomyces cerevisiae]

# Database Description

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
18555	ENU02349	ANI61C1036	50-69	462-495	NAP		g128478	171	93	1.00E-18	38	75	Nodulation protein L ; nodulation protein nodL - Rhizobium leguminosarum bv. viciae plasmid pRL1J1 ; (Y00548) nodL [Rhizobium leguminosarum] ; (X17557) nodL [Rhizobium leguminosarum] (Z99295) hypothetical protein [Schizosaccharomyces pombe]
18556	ENU02350	ANI61C7084	30-53	455-475	NAP		g2414606	252	81	4.00E-15			"splicing factor, arginine/serine-rich 2 ; splicing factor, arginine/serine-rich 2 (splicing factor SC35) (SC-35) (splicing component, 35 KD) (PR264 protein) ; splicing factor SC35 - human ; (M90104) splicing factor [Homo sapiens]"
18557	ENU02351	ANI61C4309	43-63	469-488	NAP		g4506899	173	53	0.000001	42	68	hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] (U94183) unknown [Glomerella cingulata] (Z28283) ORF YKR057w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18558	ENU02352	ANI61C9235	57-86	472-502	NAP		g1730714	220	86	1.00E-16	37	66	hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] (U94183) unknown [Glomerella cingulata] (Z28283) ORF YKR057w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18559	ENU02353	ANI61C4912	50-70	473-495	NAP		g2707187	301	116	1.00E-25	67	96	hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] (U94183) unknown [Glomerella cingulata] (Z28283) ORF YKR057w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18560	ENU02354	ANI61C9554	23-46	450-469	NAP		g2131127	277	102	2.00E-21	71	57	hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] (U94183) unknown [Glomerella cingulata] (Z28283) ORF YKR057w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18561	ENU02355	ANI61C6119	25-46	450-471	NAP		g586387	199	87	8.00E-17	46	31	hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] (U94183) unknown [Glomerella cingulata] (Z28283) ORF YKR057w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]
18562	ENU02356	ANI61C1090	35-54	463-482	NAP		g2673951	1172	247	3.00E-65	89	10	hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] (U94183) unknown [Glomerella cingulata] (Z28283) ORF YKR057w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRP137-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein I [Aspergillus fumigatus] ; (U62934) multidrug resistance protein I [Aspergillus fumigatus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18563	ENU02357	ANI50C1_11	66-86	484-514	NAP		g2493561	117	2.00E-33				Cytosine deaminase (cytosine aminohydrolase); hypothetical protein YPR062w - yeast (Saccharomyces cerevisiae); (Z49219) unknown [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae]; (U5193) cytosine deaminase [Saccharomyces cerevisiae]; (AF005261) cytosine deaminase [Saccharomyces cerevisiae]
18564	ENU02358	ANI61C2752:	40-59	469-488	NAP		g2493540	965	314	3.00E-85	99	22	catalase B; (U80672) catalase [Emmericella nidulans]
18565	ENU02359	ANI61C6673:	27-49	447-476	NAP		g731886	189	88	3.00E-17	32	83	"hypothetical 22.0 KD protein in FOX3-UBP7 intergenic region; probable membrane protein YIL157c - yeast (Saccharomyces cerevisiae); (Z38059) orf, len 197, CAL: 0.19 [Saccharomyces cerevisiae]"
18566	ENU02360	ANI61C1188:	42-63	471-491	NAP		g729839	985	240	4.00E-79	89	41	ketol -acid reductoisomerase precursor (acetohydroxy -acid reductoisomerase) (alpha -keto -beta -hydroxyacyl reductoisomerase); alpha -keto -beta -hydroxyacyl reductoisomerase - Neurospora crassa; (M84189) alpha -keto -beta -hydroxyacyl reductoisomerase [Neurospora crassa] (AF035619) pyridoxine biosynthesis protein [Cercospora nicotianae] (AL031540) short chain dehydrogenase [Schizosaccharomyces pombe]
18567	ENU02361	ANI61C9579:	45-65	473-494	NAP		g2979688	923	169	1.00E-41	73	46	Probable nicotinate phosphoribosyltransferase (NAPRTASE); probable nicotinate phosphoribosyltransferase (EC 2.4.2.11) - yeast (Saccharomyces cerevisiae); (Z75117) ORF YOR209c [Saccharomyces cerevisiae]
18568	ENU02362	ANI61C6739:	37-56	467-486	NAP		g3581884	362	58	3.00E-17	46	50	Coatomer beta subunit (beta -coat protein) (beta -COP); beta -COP protein - rat; (X57228) beta COP [Rattus norvegicus]
18569	ENU02363	ANI61C8503:	71-90	500-520	NAP		g2507262	786	64	4.00E-21	42	33	
18570	ENU02364	ANI61C5428:	23-42	446-474	NAP		g116923	715	222	9.00E-58	62	17	



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18579	ENU02373	ANI61C5863:	29-51	466-485	NAP		g1169869	267	50	0.00001			"eukaryotic translation initiation factor 3 gamma subunit (EIF-3 gamma) (EIF3 P62) (translation initiation factor EIF3, P62 subunit) (GCD10 protein); GCD10 protein - yeast (Saccharomyces cerevisiae) ; (X83511) Gcd10p [Saccharomyces cerevisiae] ; (Z71338) ORF YNL062c [Saccharomyces cerevisiae] ; (U12141) Gcd10p [Saccharomyces cerevisiae]"
18580	ENU02374	ANI61C3397:	27-47	453-483	NAP		g4206286	1929	173	5.00E-43	52	16	(AF043332) plasma membrane H(+)-ATPase [Emmericella nidulans] (AL022103) hypothetical protein [Schizosaccharomyces pombe]
18581	ENU02375	ANI61C1097	24-52	461-480	NAP		g2956778	409	80	2.00E-28	51	32	cyclin-dependent kinases regulatory subunit (cell division control protein CKS1) ; protein kinase CDC28 complex subunit CKS1 - yeast (Saccharomyces cerevisiae) ; (M26033) protein kinase [Saccharomyces cerevisiae] ; (X75891) CKS1 [Saccharomyces cerevisiae] ; (Z36004) ORF YBR135w [Saccharomyces cerevisiae] ; CKS1 gene [Saccharomyces cerevisiae]
18582	ENU02376	ANI61C3024:	67-86	503-523	NAP		g116484	296	87	8.00E-26			Isoleucyl-TRNA synthetase (isoleucine--TRNA ligase) (ILERS) ; (D90907) isoleucyl-tRNA synthetase [Synecocystis sp.]
18583	ENU02377	ANI61C1300:	23-44	459-480	NAP		g2501011	453	77	9.00E-14	28	16	hypothetical 30.5 KD protein C30A5.3 in chromosome III ; C30A5 protein - Caenorhabditis elegans ; (L10990) putative [Caenorhabditis elegans] (AL023794) putative proline oxidase precursor [Schizosaccharomyces pombe]
18584	ENU02378	ANI61C6297:	58-77	497-516	NAP		g465677	196	109	1.00E-23	37	60	
18585	ENU02379	ANI61C298:	65-85	504-523	NAP		g3192023	220	79	2.00E-14	32	33	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18586	ENU02380	ANI61C462:6	39-58	478-497	NAP		g4504799	837	127	2.00E-34	63	32	isovaleryl Coenzyme A dehydrogenase ; isovaleryl-CoA dehydrogenase precursor (IVD) ; isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human ; (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens]
18587	ENU02381	ANI61C9323:38-59	477-497		NAP		g1077341	137	50	0.000000	40	88	"hypothetical protein YLR281c - yeast (Saccharomyces cerevisiae) ; (U17243) This gene is in the -2 reading frame. There are also overlapping ORFs in the -3 reading frame, and in the +1 reading (on the other strand). The longest ORF was arbitrarily chosen as L8003.11 [Saccharomyces cerevisiae]" (U89492) arylsulfatase [Neurospora crassa]
18588	ENU02382	ANI61C1396:52-74	492-511		NAP		g2873363	212	108	4.00E-23	37	23	Anthranilate synthase component I ; anthranilate synthase (EC 4.1.3.27) component I - yeast (Saccharomyces cerevisiae) ; (X68327) anthranilate synthase (component 1) [Saccharomyces cerevisiae] ; (U18839) Trp2p: anthranilate synthase component I [Saccharomyces cerevisiae]
18589	ENU02383	ANI61C9179:56-75	494-515		NAP		g731012	1431	217	5.00E-56	74	31	Anthranilate synthase component I ; anthranilate synthase (EC 4.1.3.27) component I - yeast (Saccharomyces cerevisiae) ; (X68327) anthranilate synthase (component 1) [Saccharomyces cerevisiae] ; (U18839) Trp2p: anthranilate synthase component I [Saccharomyces cerevisiae]
18590	ENU02384	ANI61C6172:70-89	511-530		NAP		g3169083	279	81	6.00E-15	36	49	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18591	ENU02385	ANI61C3386:65-86	506-525		NAP		g2495634	69	3.00E-11				hypothetical 43.3 KD protein in EVGS-GLK intergenic region ; (AE000325) putative enzyme [Escherichia coli]
18592	ENU02386	ANI61C6376:46-65	486-506		NAP		g3219935	546	215	6.00E-56	70	92	probable peptidyl-prolyl cis-trans isomerase C57A10.03 ; (Z94864) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]

# Sequence Annotation

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18593	ENU02387	ANI61C2093:	42-62	484-503	NAP			g1711596	231	91	5.00E-18	40	16	putative sulfate transporter YPR003C ; probable membrane protein YPR003c-yeast (Saccharomyces cerevisiae) ; (Z48951) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz3p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] "mitochondrial 60S ribosomal protein L30 precursor (YML30) ; ribosomal protein Yml30 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X96722) ORF N0864 [Saccharomyces cerevisiae] ; (Z71528) ORF YNL252c [Saccharomyces cerevisiae] "
18594	ENU02388	ANI61C2410:	22-43	462-484	NAP			g1710602	192	73	9.00E-13	30	57	hypothetical 47.3 K.D protein C17G8.13C in chromosome I ; (Z69795) unknown [Schizosaccharomyces pombe] alpha-glucosidase (EC 3.2.1.20) MAL62 - yeast (Candida albicans) ; (M94674) alpha-glucosidase [Candida albicans] (AL023777) ma binding protein [Schizosaccharomyces pombe] 40S ribosomal protein S17 ; (M13933) ribosomal protein S17 [Cricketus griseus] ; (D25213) ribosomal protein S17 [Mus musculus] sorbitol dehydrogenase (L-iditol 2-dehydrogenase) ; L-iditol 2-dehydrogenase (EC 1.1.1.14) precursor - mouse ; (U27014) sorbitol dehydrogenase precursor [Mus musculus domesticus] hypothetical 45.7 K.D protein in RPS3-PSD1 intergenic region ; hypothetical protein YNL175c - yeast (Saccharomyces cerevisiae) ; (Z71451) ORF YNL175c [Saccharomyces cerevisiae]
18595	ENU02389	ANI61C6738:	27-55	458-489	NAP			g1723485	364	152	2.00E-36	43	41	
18596	ENU02390	ANI61C8016:	59-78	488-522	NAP			g323015	1408	118	3.00E-26	37	29	
18597	ENU02391	ANI61C7458:	22-45	462-485	NAP			g3184100	327	145	2.00E-34	43	61	
18598	ENU02392	ANI61C1126:	66-89	511-530	NAP			g133820	334	92	1.00E-31	62	91	
18599	ENU02393	ANI61C4302:	34-63	477-498	NAP			g2492773	574	96	1.00E-19	37	41	
18600	ENU02394	ANI61C879:	5 46-68	491-510	NAP			g1730806	196	87	6.00E-17	31	36	



Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18601	ENU02395	ANI61C631:1	53-73	489-517	NAP		g2497216	123	62	0.000000	28	22	003	hypothetical 83.4 KD protein in DSK2-CAT8 intergenic region ; hypothetical protein YMR277w - yeast
18602	ENU02396	ANI61C8419: 34-54	470-498	NAP		g1002864	555	198	2.00E-50	53	85		unknown [Saccharomyces cerevisiae] (U34346) unknown [Paracoccus denitrificans]	
18603	ENU02397	ANI61C2838: 45-64	488-510	NAP		g1850766	614	144	1.00E-56	86	86		(AB001288) ribosomal protein S23 homolog [Schizosaccharomyces pombe]	
18604	ENU02398	ANI61C4555: 47-79	491-512	NAP		g4589686	210	100	1.00E-20	33	16		(AB023225) KIAA1018 protein [Homo sapiens]	
18605	ENU02399	ANI61C7287: 45-66	492-511	NAP		g1176711	137	59	0.000000	22	89		hypothetical 21.6 KD protein F37A4.2 in chromosome III ; F37A4.2 protein - Caenorhabditis elegans ; (U00032) F37A4.2 gene product [Caenorhabditis elegans]	
18606	ENU02400	ANI50C1_10 35:32..540	480-506	NAP		g131056		237	4.00E-62	69	60		Aspergillopepsin II precursor (acid protease A) (protease A) ; aspergillopepsin II (EC 3.4.23.19) precursor - Aspergillus niger (var. macrosporus) ; (M68871) acid proteinase A [Aspergillus niger] ; acid protease A [Aspergillus niger macrosporus]	
18607	ENU02401	ANI61C5560: 53-73	501-520	NAP		g1353046	190	45	0.0003	37	22		hypothetical 65.3 KD protein in pre3-SAG1 intergenic region ; hypothetical protein YJR001w - yeast	
18608	ENU02402	ANI61C9150: 26-50	464-493	NAP		g1911486	388	90	4.00E-34	51	52		(Saccharomyces cerevisiae) ; (X87611) ORF YJR83.4 [Saccharomyces cerevisiae] ; (Z49501) ORF YJR001w [Saccharomyces cerevisiae] "(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18609	ENU02403	ANI61C8849:	72-93	520-539	NAP		g2497193	499	152	2.00E-36	44	33	hypothetical 56.2 KD protein in ERG8-UBP8 intergenic region ; probable membrane protein YMR221c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae]
		225..734											
18610	ENU02404	ANI61C6707:	62-81	508-530	NAP		g3451464	370	111	1.00E-35	59	88	(AL031349) N-acetyltransferase [Schizosaccharomyces pombe]
		985..475											
18611	ENU02405	ANI61C5252:	65-90	505-533	NAP		g3549891	562	102	2.00E-21	46	28	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi]
		1706..1196											
18612	ENU02406	ANI61C4094:	22-47	472-491	NAP		g1711561	283	110	6.00E-24	34	29	sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
		160..671											
18613	ENU02407	ANI61C3490:	22-45	472-491	NAP		g3851164	163	62	0.000000	23	32	(AF097181) tuffelin-interacting protein 10 [Mus musculus]
		1606..1095								003			
18614	ENU02408	ANI61C7357:	70-96	521-540	NAP		g4204901	215	71	7.00E-12	38	66	(U57100) orf256; putative triose phosphate isomerase [Brucella abortus]
		61..573											
18615	ENU02409	ANI61C5347:	46-65	495-516	NAP		g3929399		96	1.00E-19			proline-specific permease (proline transport protein) ; (X79797) proline permease [Emmericella nidulans]
		1544..1984											
18616	ENU02410	ANI61C6339:	34-54	480-506	NAP		g1352881	180	66	2.00E-10	37	94	hypothetical 15.7 KD protein in NUP85-SSC1 intergenic region ; probable membrane protein YJR044c - yeast (Saccharomyces cerevisiae) ; (Z49544) ORF YJR044c [Saccharomyces cerevisiae] ; (L36344) ORF; putative [Saccharomyces cerevisiae]
		2091..1577											
18617	ENU02411	ANI61C6057:	60-79	512-533	NAP		g4150918	288	113	7.00E-28	50	70	(Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
		1094..579											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18618	ENU02412	ANI61C3771:	22-41	470-496	NAP		g417274	407	181	3.00E-45			mitochondrial import inner membrane translocase subunit TIM23
		875..359											(mitochondrial protein import protein 3) (mitochondrial protein import protein MAS6) (membrane import machinery protein MIM23);
													mitochondrial inner membrane protein MIM23 - yeast (Saccharomyces cerevisiae); (X71633) MAS6
													[Saccharomyces cerevisiae]; (X74161) MIM23 [Saccharomyces cerevisiae]; (Z71632) ORF YNR017w
													[Saccharomyces cerevisiae] (AF048992) ribonuclease H1
													[Schizosaccharomyces pombe] (AL031535) transcription initiation factor ttfid 60 kd subu nit
													[Schizosaccharomyces pombe] (X96943)
18621	ENU02415	ANI61C1050	36-55	491-512	NAP		g1524045	459	132	1.00E-30	42	38	Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi]
		5:5005..5523											(AL033391) hypothetical membrane protein [Candida albicans]
18622	ENU02416	ANI61C3996:	23-44	480-499	NAP		g3850125	542	115	2.00E-25	41	32	(Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi]
		6129..5611											hypothetical 63.0 KD protein in PYC2-PDB1 intergenic region ; probable
18623	ENU02417	ANI61C8551:	32-54	489-508	NAP		g3549879	436	88	1.00E-22	40	28	membrane protein YBR220c - yeast (Saccharomyces cerevisiae); (Z36088) ORF YBR220c [Saccharomyces cerevisiae]
		3297..2779											(AL033396) putative alcohol phosphatidyl transferase [Candida albicans]
		9:3385..3906											"Cleavage and polyadenylation specificity factor, 160 KD subunit (CPSF 160 KD subunit); (U37012) cleavage and polyadenylation specificity factor [Homo sapiens] "
18624	ENU02418	ANI61C1086	60-79	520-539	NAP		g586338	913	126	9.00E-29	43	26	
18625	ENU02419	ANI61C4950:	27-58	486-506	NAP		g3850144	198	75	1.00E-17	36	60	
		575..54											
18626	ENU02420	ANI61C9832:	22-57	483-502	NAP		g1706102	133	77	7.00E-14	32	11	
		82..604											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18627	ENU02421	ANI61C6709:	23-46	472-503	NAP		g2500360	157	64	6.00E-15	38	60	60S ribosomal protein L14; ribosomal protein L14 - rat; (X94242) ribosomal protein L14 [Rattus norvegicus] hypothetical 55.1 KD protein in TRX1-RTA1 intergenic region; hypothetical protein YGR211w - yeast (Saccharomyces cerevisiae); (Z72996) ORF YGR211w [Saccharomyces cerevisiae]; (AF019769) zinc finger protein [Saccharomyces cerevisiae] (U81509) urease [Coccidioides immitis] (U68040) polyketide synthase [Cochliobolus heterostrophus] (U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (X96943) Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi] "(AE000952) methylmalonyl-CoA decarboxylase, biotin carboxyl carrier subunit (mmdC) [Archaeoglobus fulgidus]" (AE000855) endonuclease III [Methanobacterium thermoautotrophicum] "CAT5 protein (ubiquinone biosynthesis protein COQ7); CAT5 protein - yeast (Saccharomyces cerevisiae); (X82930) CAT5 [Saccharomyces cerevisiae]; (X90518) putative [Saccharomyces cerevisiae]; (X94335) YOR3284c [Saccharomyces cerevisiae]; (Z75033) ORF YOR125c [Saccharomyces cerevisiae]; (S81938) COQ7 [Saccharomyces cerevisiae, Peptide, 272 aa] [Saccharomyces cerevisiae]" (AE000352) putative transport protein [Escherichia coli]
18628	ENU02422	ANI61C5035:	40-60	499-521	NAP		g1723738	548	164	4.00E-40	43	34	
18629	ENU02423	ANI61C1400:	36-55	497-517	NAP		g2580518	3042	136	5.00E-39	66	15	
18630	ENU02424	ANI61C1002	29-48	489-510	NAP		g1546072	1185	68	5.00E-11	29	6	
18631	ENU02425	ANI61C1767:	53-74	510-534	NAP		g1438947	697	272	1.00E-72	67	35	
18632	ENU02426	ANI61C1570:	22-53	484-503	NAP		g1524045	385	66	8.00E-17	42	33	
18633	ENU02427	ANI61C2430:	22-53	474-504	NAP		g2648307	127	59	0.000000	32	99	
18634	ENU02428	ANI61C8832:	54-73	516-536	NAP		g2621854	84	52	0.000002	29	52	
18635	ENU02429	ANI61C303:9	28-48	491-510	NAP		g1168783	381	118	1.00E-34			
18636	ENU02430	ANI61C3361:	34-53	498-517	NAP		g1789036	257	61	0.000000	33	56	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18637	ENJU02431	ANI61C9483:	32-51	484-515	NAP		g133887	234	94	8.00E-19	54	96	"mitochondrial ribosomal protein S24 ; ribosomal protein S16, mitochondrial - Neurospora crassa ; (X06360) cyt-21 [Neurospora crassa] ; (J03533) ribosomal protein S-24 [Neurospora crassa]"
18638	ENJU02432	ANI61C2362:	48-67	510-531	NAP		g699196	316	104	4.00E-22			(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]
18639	ENJU02433	ANI61C9152:	63-82	525-546	NAP		g133336	145	53	1.00E-12			DNA-directed RNA polymerase II 32 KD polypeptide (B32) ; DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB4 - yeast (Saccharomyces cerevisiae) ; (X58099) RPB4 [Saccharomyces cerevisiae] ; (M27253) RNA polymerase II subunit RPB4 [Saccharomyces cerevisiae] ; (X87371) RNA polymerase II subunit 4 [Saccharomyces cerevisiae] ; (Z49415) ORF YJL140w [Saccharomyces cerevisiae]
18640	ENJU02434	ANI61C2487:	61-82	525-544	NAP		g2983039	285	132	2.00E-30	41	30	(AE000686) proline-tRNA synthetase [Aquifex aeolicus]
18641	ENJU02435	ANI50C3497	28-47	492-512	NAP		g462739		109	2.00E-23	38	26	NPL4 protein ; NPL4 protein - yeast (Saccharomyces cerevisiae) ; (X72224) NPL4 [Saccharomyces cerevisiae] ; (X74437) open reading frame YBR12.31 [Saccharomyces cerevisiae] ; (Z36039) ORF YBR170c [Saccharomyces cerevisiae]
18642	ENJU02436	ANI61C383:5	61-80	526-545	NAP		g399112	199	91	6.00E-18	33	16	beta-galactosidase (lactase) ; beta-galactosidase (EC 3.2.1.23) - yeast (Kluyveromyces marxianus var. lactis) ; (M84410) beta-D-galactosidase [Kluyveromyces lactis]
18643	ENJU02437	ANI61C6528:	28-49	488-513	NAP		g3880440	190	69	2.00E-11	32	96	(Z82062) cDNA EST yk415c12.5 comes from this gene [Caenorhabditis elegans]

# Sequence Database

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18644	ENU02438	ANI61C6109:	23-43	482-509	NAP		g3123100	351	99	6.00E-33	50	99	"hypothetical 15.9 KD protein C4A8.02C in chromosome I ; (Z98762) SPAC4A8.02c, unknown, len:142aa, similar eg. to YJBQ_ECOLI, P32698, hypothetical 15.7 kd protein, (138aa), fast a scores, opt:403, E0: 2.4e-32, (41.0% identity in 134 aa overlap) [Schizosaccharomyces pombe]"
		1824..1296											
18645	ENU02439	ANI61C5925:	38-57	504-524	NAP		g543649	245	86	2.00E-21	53	91	Rhodococcus erythropolis (fragment) ; (D14454) P47K protein [Rhodococcus erythropolis] ; ORF P47K [Rhodococcus erythropolis]
		1611..1083											
18646	ENU02440	ANI61C7364:	22-50	490-509	NAP		g585656	249	86	2.00E-16			Pyridoxamine 5'-phosphate oxidase (PNP/PMF oxidase) ; pyridoxamine-phosphate oxidase (EC 1.4.3.5) - yeast (Saccharomyces cerevisiae) ; (X76992) pyridoxamine-phosphate oxidase [Saccharomyces cerevisiae] ; (X76078) YBR0321 [Saccharomyces cerevisiae] ; (Z35904) ORF YBR035c [Saccharomyces cerevisiae] ; ORF YBR0321 [Saccharomyces cerevisiae] (AL023554) zinc finger protein [Schizosaccharomyces pombe] (AF034090) MAPKK kinase [Neurospora crassa]
		2988..3517											
18647	ENU02441	ANI61C137:	1 22-42	484-510	NAP		g3133097	114	48	0.00005	30	35	SAP1 protein ; hypothetical protein YER047c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer047cp [Saccharomyces cerevisiae] (AJ000084) putative acetyl transferase [Proteus mirabilis]
		940..1410											
18648	ENU02442	ANI61C1321:	23-47	490-511	NAP		g2654103	751	250	4.00E-66	67	25	sterigmatocystin 7-O-methyltransferase precursor ; (L25836) O-methyltransferase [Aspergillus flavus]
		82..612											
18649	ENU02443	ANI61C7991:	27-55	496-516	NAP		g731461	793	138	4.00E-41	57	19	hypothetical 59.3 KD protein C17C9.16C in chromosome I ; (Z73099) hypothetical protein [Schizosaccharomyces pombe]
		555..23											
18650	ENU02444	ANI61C8177:	61-81	531-550	NAP		g3395518	124	60	0.000000	28	88	
		4238..3705											
18651	ENU02445	ANI61C3627:	56-77	525-546	NAP		g2498701	127	63	0.000000	33	37	
		3038..3570											
18652	ENU02446	ANI61C8243:	41-62	507-531	NAP		g1723574	549	74	8.00E-13	33	33	
		920..388											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18653	ENU02447	ANI61C8767:	28-48	501-520	NAP		g3334833	66		2.00E-10			(AJ007932) ketoreductase [Streptomyces argillaceus]
18654	ENU02448	ANI61C4182:	35-54	497-528	NAP		g2330829	826	182	2.00E-45	52	11	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
18655	ENU02449	ANI61C7614:	28-47	502-521	NAP		g118066	259	104	5.00E-22	35	32	cyclohexanone monooxygenase ; (M19029) cyclohexanone monooxygenase [Acinetobacter sp.]
18656	ENU02450	ANI61C6208:	32-51	503-525	NAP		g1350839	257	114	5.00E-25	52	60	RIBOSE 5-phosphate isomerase (phosphoRIBOisomerase) ; (L35034) ribose 5-phosphate isomerase [Mus musculus]
18657	ENU02451	ANI61C8852:	60-79	530-554	NAP		g2832629		60	0.000000			(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]
18658	ENU02452	ANI61C1084:	39-60	513-534	NAP		g2131743	361	129	1.00E-29	52	85	hypothetical protein YLR009w - yeast (Saccharomyces cerevisiae) ; (Z73181) ORF YLR009w [Saccharomyces cerevisiae]
18659	ENU02453	ANI61C1271:	44-63	517-539	NAP		g1729996	667	228	2.00E-59	62	60	TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
18660	ENU02454	ANI61C1190:	25-44	502-522	NAP		g999873	616	106	9.00E-23	49	51	Lipase (E.C.3.1.1.3) [Triacylglycerol Acylhydrolase]
18661	ENU02455	ANI61C1070:	29-49	506-526	NAP		g1351617	728	138	4.00E-32	45	31	hypothetical 62.6 KD protein C29E6.02 in chromosome I ; (Z66525) unknown [Schizosaccharomyces pombe]
18662	ENU02456	ANI61C2194:	46-72	524-543	NAP		g1705519	153	68	3.00E-12	31	31	Benzaldehyde lyase (benzoin aldolase) (BL) (BZL) ; (U04048) benzaldehyde lyase [Pseudomonas fluorescens]
18663	ENU02457	ANI61C3754:	24-47	496-521	NAP		g2498971	574	110	8.00E-24	32	36	putative sterigmatoctylin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans]
18664	ENU02458	ANI61C9710:	22-44	487-520	NAP		g3192040	147	48	0.00004	28	98	(AL023796) hypothetical protein [Schizosaccharomyces pombe]

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18665	ENU02459	ANI61C7140:	29-48	505-527	NAP		g4505495	239	104	6.00E-22			8-oxoguanine DNA glycosylase ; (Y11731) DNA glycosylase/AP lyase [Homo sapiens] ; (Y11838) 8-oxoguanine DNA glycosylase homolog 1 [Homo sapiens] ; (AB000410) hOGG1 [Homo sapiens] ; (AF003595) 8-oxoguanine DNA glycosylase 1 [Homo sapiens] ; (U88527) 8-hydroxyguanine glycosylase [Homo sapiens]
18666	ENU02460	ANI61C3964:	40-59	515-538	NAP		g2492754	582	76	1.00E-18	42	57	sorbitol utilization protein SOU1 ; (AF002134) Sou1p [Candida albicans]
18667	ENU02461	ANI61C2208:	61-80	540-559	NAP		g1730712	372	78	4.00E-14	29	35	hypothetical 56.2 KD protein in UME3-HDA1 intergenic region ; hypothetical protein YNL022c - yeast (Saccharomyces cerevisiae) ; (Z71298) ORF YNL022c [Saccharomyces cerevisiae]
18668	ENU02462	ANI61C6637:	36-57	512-535	NAP		g1722203	276	101	5.00E-21	41	17	(M29688) DNA mismatch repair protein [Saccharomyces cerevisiae]
18669	ENU02463	ANI61C9213:	48-71	523-547	NAP		g3642873	690	257	3.00E-68	66	85	(AF026523) manganese superoxide dismutase; Mn-SOD [Penicillium chrysogenum] ; (AF026790) manganese superoxide dismutase [Penicillium chrysogenum] (U62028) negative acting factor [Fusarium solani f. sp. pisi]
18670	ENU02464	ANI61C8484:	52-71	532-551	NAP		g1470090	92	50	0.00001	27	38	



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18671	ENU02465	ANI61C1889:	41-61	516-540	NAP		g1346554	42	0.000000	1			probable myosin regulatory light chain ; (Z46793) similar to myosin regulatory light chain 2; cDNA EST EMBL:T01273 comes from this gene; cDNA EST EMBL:C09382 comes from this gene; cDNA EST EMBL:C07858 comes from this gene; cDNA EST yk404h1.3 comes from this gene; cDN...; (Z34801) similar to myosin regulatory light chain 2; cDNA EST EMBL:T01273 comes from this gene; cDNA EST EMBL:C09382 comes from this gene; cDNA EST EMBL:C07858 comes from this gene; cDNA EST yk404h1.3 comes from this gene; cDN...
18672	ENU02466	ANI61C7908:	50-69	526-550	NAP		g3929362	397	97	3.00E-24	41	29	Pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI]
18673	ENU02467	ANI61C2918:	49-68	526-550	NAP		g118572	180	59	0.000000	007		Granaticin polyketide synthase putative ketoacyl reductase 2 (ORF6) ; granaticin-producing polyketide synthase chain 6 - Streptomyces violaceoruber ; (X16144) ketoacyl reductase (AA 1-289) [Streptomyces violaceoruber] ; (X16300) ORF 6 (AA 1-249) [Streptomyces violaceoruber] ; (AJ011500) gra-orf6 [Streptomyces violaceoruber]
18674	ENU02468	ANI61C6924:	34-53	516-535	NAP		g4503609	375	50	3.00E-19			"electron-transfer-flavoprotein, beta polypeptide ; electron transfer flavoprotein beta-subunit (beta-ETF) ; electron transfer flavoprotein beta chain - human ; Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution ; (X71129) electron transfer flavoprotein beta subunit [Homo sapiens]"

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18675	ENU02469	ANI61C1036	37-56	521-540	NAP		g3560474	209	80	2.00E-19	32	51	(U81312) S-adenosyl-methionine-sterol-C- methyltransferase [Nicotiana tabacum]
		7:900..1447											
18676	ENU02470	ANI61C1112	72-93	556-575	NAP		g450864	536	198	2.00E-50	54	32	(L27993) alkaline phosphatase [Neurospora crassa]
		2:63..608											"hypothetical oxidoreductase in LYS1-HYR1 intergenic region ; probable
18677	ENU02471	ANI61C4008	32-56	512-535	NAP		g731922	414	130	8.00E-30	43	64	membrane protein YIR035c - yeast (Saccharomyces cerevisiae) ; (Z38061) orf, len 254, CAl: 0.24, 52.1% similar to orf complement(33925..34716), similar to DH11 human P28845 corticosteroid 11-beta-dehydrogenase [Saccharomyces cerevisiae] "
		89..634											"ADP,ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT) ; (Z49974) adenine nucleotide carrier
18678	ENU02472	ANI61C2566	53-77	533-557	NAP		g2497980	772	203	6.00E-75	83	51	[Schizosaccharomyces pombe] ; (AL023634) adp/atp translocase [Schizosaccharomyces pombe] "
		547..1											hypothetical 17.2 KD protein C3H1.03 in chromosome I ; (Z68144) hypothetical protein
18679	ENU02473	ANI61C3960	23-51	503-529	NAP		g1351687	108	49	0.00002	28	98	[Schizosaccharomyces pombe] alpha-glucosidase precursor (malase) ; (D45356) alpha-glucosidase [Aspergillus niger]
		1663..2211											(AL022002) hypothetical protein Rv1672c [Mycobacterium tuberculosis] eukaryotic translation initiation factor 2 beta subunit (EIF-2-beta) ; translation initiation factor eIF-2 beta chain - yeast (Saccharomyces cerevisiae) ; (M21813) translation initiation factor eIF2 beta-subunit [Saccharomyces cerevisiae] ; (Z67751) SUI3 [Saccharomyces cerevisiae] ; (Z73594) ORF YPL237w [Saccharomyces cerevisiae]
18680	ENU02474	ANI61C8321	50-76	536-556	NAP		g3023267	658	212	6.00E-65	66	18	(AL022071) fructosyl amine [Schizosaccharomyces pombe]
		87..635											
18681	ENU02475	ANI61C6620	43-64	531-551	NAP		g2916970	194	33	1.3			
		826..1376											
18682	ENU02476	ANI61C3952	72-91	560-580	NAP		g124205	193	62	0.000000			
		556..331											
18683	ENU02477	ANI61C5937	31-53	520-539	NAP		g2950465	215	76	3.00E-18	38	39	
		1283..733											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18684	ENU02478	ANI61C8339:	25-44	512-533	NAP		g1730644	243	100	1.00E-20	28	27	hypothetical 73.4 KD protein in ERG24-MET2 intergenic region ; probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae) ; (Z71555) ORF YNL279w [Saccharomyces cerevisiae] (AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
		1637..1087											"beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]" (AL035064) queuine tRNA-ribosyltransferase
18685	ENU02479	ANI61C1708:	22-51	509-530	NAP		g3810866	60	0.000000	01			[Schizosaccharomyces pombe]
		2796..3346											[Schizosaccharomyces pombe]
18686	ENU02480	ANI61C1532:	39-58	518-548	NAP		g461623	823	146	1.00E-34	53	17	"beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]" (AL035064) queuine tRNA-ribosyltransferase
		364..915											[Schizosaccharomyces pombe]
18687	ENU02481	ANI61C9801:	23-45	513-532	NAP		g4106673	413	153	6.00E-37	54	38	[Schizosaccharomyces pombe]
		99..650											Rodlet protein precursor ; Rodletless protein - Emeritella nidulans ; (M61113) rodlet peptide [Emeritella nidulans]
18688	ENU02482	ANI61C1130:	65-84	555-574	NAP		g133264	313	66	4.00E-14	59	81	(AL023590) amino acid permease [Schizosaccharomyces pombe]
		220..771											[Schizosaccharomyces pombe]
18689	ENU02483	ANI61C1027	69-88	560-579	NAP		g3136040	706	142	2.00E-33	39	34	hypothetical 61.8 KD peptide in MPR1-GCN20 intergenic region ; probable membrane protein YFR006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR006W [Saccharomyces cerevisiae]
		1:1045..1597											(X76302) nucleic acid binding protein [Homo sapiens]
18690	ENU02484	ANI61C9766:	47-66	535-557	NAP		g1175977	465	136	1.00E-31	37	34	(AF029913) unknown [Cochliobolus heterostrophus] ; (AF027687) unknown [Cochliobolus heterostrophus]
		32..584											hypothetical 27.3 KD protein in REF2-CBS2 intergenic region ; hypothetical protein YDR196c - yeast (Saccharomyces cerevisiae) ; (Z48784) unknown [Saccharomyces cerevisiae]
18691	ENU02485	ANI61C8436:	37-64	519-547	NAP		g431953	194	39	0.023	36	80	
		110..662											
18692	ENU02486	ANI61C6527:	24-53	516-535	NAP		g2583216	389	152	1.00E-36	47	82	
		3954..3401											
18693	ENU02487	ANI61C1190:	47-66	540-559	NAP		g2833198	332	128	3.00E-29	52	67	
		915..361											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18694	ENU02488	AN161C3516: 1458..2012	29-48	522-541	NAP		g3687456	303	127	8.00E-30	44	97	(AL031798) hypothetical protein [Schizosaccharomyces pombe]
18695	ENU02489	AN150C392_2:841..394	22-50	515-535	NAP		g2144770	209	1.00E-53	65	59	"acidic ribosomal protein P0.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (M37326) ribosomal protein L10e [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (U19028) Rpl10ep [Saccharomyces cerevisiae] "	
18696	ENU02490	AN161C7084: 230..785	24-43	518-537	NAP		g2414606	252	104	6.00E-22	46	94	(Z99295) hypothetical protein [Schizosaccharomyces pombe]
18697	ENU02491	AN161C7236: 3666..4222	27-48	522-541	NAP		g548420	373	84	6.00E-31	54	90	mitochondrial import receptor subunit TOM20 (mitochondrial 20 KD outer membrane protein) (MOM19 protein) (translocase of outer membrane 20 KD subunit) ; (M80528) mitochondrial outer membrane protein 19 [Neurospora crassa]
18698	ENU02492	AN161C7717: 2362..2919	68-87	550-583	NAP		g4456822	352	141	5.00E-33	42	100	(AL035548) hypothetical oligoribonuclease [Schizosaccharomyces pombe]
18699	ENU02493	AN161C4632: 1025..468	68-87	564-583	NAP		g2351250	325	89	3.00E-17	43	25	(U23425) ropy-2 [Neurospora crassa]
18700	ENU02494	AN161C1096: 4:3004..2446	71-97	554-587	NAP		g2498530	198	100	9.00E-21	40	56	mitochondrial inheritance component MDM12 ; (U64674) mitochondrial inheritance component Mdm12p [Schizosaccharomyces pombe]
18701	ENU02495	AN161C1484: 714..154	50-83	546-567	NAP		g2708305	766	154	2.00E-43	47	35	(AF016369) U4/U6 small nuclear ribonucleoprotein hPrp4 [Homo sapiens]
18702	ENU02496	AN161C3181: 1268..1827	42-65	537-559	NAP		g1054845	1435	159	2.00E-57	62	39	(X92680) allelic to VPS4 [Saccharomyces cerevisiae]
18703	ENU02497	AN161C9072: 149..708	72-94	569-589	NAP		g1764098	178	31	0.000003	37	20	(U81794) putative permease [Uromyces fabae]
18704	ENU02498	AN161C2133: 927..1487	66-88	562-584	NAP		g1877327	60	0.000000	01			(Z92771) hypothetical protein Rv3272 [Mycobacterium tuberculosis]

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18705	ENU02499	ANI61C884:7	29-49	528-547	NAP		g2500493	324	98	3.00E-27	66	97	putative 40S ribosomal protein in SNF2-CPA1 intergenic region ; ribosomal protein S10.e.A - yeast (Saccharomyces cerevisiae) ; (Z75201) ORF YOR293w [Saccharomyces cerevisiae]
18706	ENU02500	ANI61C8267: 774..213	45-66	543-564	NAP		g481285	342	130	9.00E-30	38	26	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger ; (Z26938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger] ; NADPH cytochrome P450 reductase [Aspergillus niger] (AJ223998) PCZA361.9 [Amycolatopsis orientalis] (AL023592) putative phosphatidylinositol- glycan-class c protein [Schizosaccharomyces pombe] myoSIN-2 isoform ; myosin myo2 - yeast (Saccharomyces cerevisiae) ; (M35532) myosin I isoform (myo2) [Saccharomyces cerevisiae] ; (Z75234) ORF YOR326w [Saccharomyces cerevisiae]
18707	ENU02501	ANI61C8414: 2231..2792	48-67	548-567	NAP		g2894160	229	71	4.00E-18	38	59	Deoxyribose-phosphate aldolase (phosphodeoxyribaldolase) (deoxyribaldolase) ; deoxyribose aldolase (deoC) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32791) deoxyribose-phosphate aldolase (deoC) [Haemophilus influenzae Rd]
18708	ENU02502	ANI61C9773: 22-44	22-44	523-542	NAP		g3136049	270	129	2.00E-29	40	56	hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae) ; (U55021) O3615p [Saccharomyces cerevisiae] ; (Z75078) ORF YOR171c [Saccharomyces cerevisiae] (AF027979) carnitine acetyl transferase [Magnaporthe grisea] (Z97210) hypothetical protein [Schizosaccharomyces pombe]
18709	ENU02503	ANI61C8325: 3431..2869	54-75	553-574	NAP		g127736	322	62	4.00E-18	43	9	
18710	ENU02504	ANI61C3214: 2968..2406	56-76	557-576	NAP		g1169268	326	108	2.00E-23	43	81	
18711	ENU02505	ANI61C1078 7:2457..1894	44-65	546-565	NAP		g2132075	519	117	5.00E-26	30	30	
18712	ENU02506	ANI61C8080: 10..573	31-59	533-552	NAP		g2688966	991	259	1.00E-68	64	30	
18713	ENU02507	ANI61C1189: 9840..9276	41-60	539-563	NAP		g2239219	194	46	0.000000	34	79	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18714	ENU02508	AN161C6833: 2401..1837	52-71	553-574	NAP		g3041696	845	214	4.00E-55	63	60	"Acetolactate synthase small subunit precursor (AHAS) (acetohydroxy-acid synthase small subunit) (ALS) ; (X59720) YCL009c, len:309 [Saccharomyces cerevisiae]"
18715	ENU02509	AN161C7768: 51..615	72-91	575-594	NAP		g3130049	632	142	4.00E-51	69	52	(AL023518) Tall p transaldolase [Schizosaccharomyces pombe]
18716	ENU02510	AN161C5105: 1804..1239	70-91	573-593	NAP		g1762781	477	198	2.00E-50	51	18	(U65685) phosphoinositide-specific phospholipase C [Botryotinia fuckeliana]
18717	ENU02511	AN161C6332: 6021..5456	69-96	573-592	NAP		g1175934	861	61	3.00E-14	34	15	hypothetical 117.8 KD protein in STE2-FRS2 intergenic region ; probable membrane protein YFL025c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL025C [Saccharomyces cerevisiae]
18718	ENU02512	AN161C9824: 3254..3820	65-90	570-589	NAP		g2370595	1364	167	6.00E-41	60	19	(AJ001414) GTPase activating protein [Yarrowia lipolytica]
18719	ENU02513	AN161C1043: 5:2496..3062	47-67	552-571	NAP		g2492633	987	207	4.00E-53	56	44	probable glutaryl-CoA dehydrogenase precursor (GCD) ; (Z66513) similar to acyl-CoA dehydrogenase; cDNA EST EMBL:D70283 comes from this gene; cDNA EST EMBL:D66714 comes from this gene; cDNA EST EMBL:D70641 comes from this gene; cDNA EST EMBL:D70573 comes from this gene; cDNA EST EM...
18720	ENU02514	AN161C4425: 625..1191	27-47	532-551	NAP		g3868940	433	84	6.00E-25	42	40	(AB015054) Alg2 [Rhizomucor pusillus] ; (AB015055) Alg2 [Rhizomucor pusillus]

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18721	ENU02515	AN161C1211	35-65	541-560	NAP		g4506439	556	129	4.00E-47			retinoblastoma-binding protein 7 ; histone acetyltransferase type B subunit 2 (retinoblastoma binding protein P46) (retinoblastoma-binding protein 7) ; retinoblastoma-binding protein RbAp46 - human ; (X72841) IEF 7442 [Homo sapiens] ; (U35143) retinoblastoma-binding protein RbAp46 [Homo sapiens] ; (AF090306) retinoblastoma binding protein [Rattus norvegicus] ; retinoblastoma-binding protein [Homo sapiens]
18722	ENU02516	AN161C4036	50-69	559-576	NAP		g729327	166	41	0.0006	25	47	glucose 1-dehydrogenase IV (GLCDH-IV) ; glucose 1-dehydrogenase (EC 1.1.1.47) - Bacillus megaterium ; (D10626) glucose dehydrogenase [Bacillus megaterium]
18723	ENU02517	AN161C3865	60-81	566-586	NAP		g4587575	251	109	1.00E-23	39	59	"(AC006550) Belongs to PF01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gb AA585719, gb AA728503 and gb T22272 come from this gene. [Arabidopsis thaliana]" (U81827) 8 kDa cytoplasmic dynein light chain [Emeticella nidulans] (D85924) myosin [Mus musculus]
18724	ENU02518	AN161C6288	48-68	551-574	NAP		g4099025	316	62	2.00E-16	84	97	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
18725	ENU02519	AN161C7365	46-65	549-572	NAP		g1945080	48	0.00005				[Schizosaccharomyces pombe]
18726	ENU02520	AN161C1062	30-51	538-558	NAP		g2842503	301	80	5.00E-27	43	75	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
18727	ENU02521	AN161C6548	44-63	553-572	NAP		g729712	1373	225	2.00E-58			casein kinase I homolog HHP1 ; hhp1 protein - fission yeast (Schizosaccharomyces pombe) ; casein kinase-I homolog hhp1 - Yeast (Schizosaccharomyces pombe) ; (X78871) Hhp1 protein kinase [Schizosaccharomyces pombe] ; (U10863) casein kinase-I [Schizosaccharomyces pombe] ; (AL031261) casein kinase I homologue [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18728	ENU02522	AN161C1038	43-68	553-572	NAP		g2842501		81	7.00E-15			(AL021748) putative quinine oxidoreductase [Schizosaccharomyces pombe]
18729	ENU02523	AN161C7455: 9	23-42	533-552	NAP		g4506235	165	69	2.00E-11	36	73	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 ; 26S proteasome regulatory subunit P27 ; (AB003177) proteasome subunit p27 [Homo sapiens]"
18730	ENU02524	AN161C1020	61-80	561-591	NAP		g3929392	633	201	4.00E-62	82	57	vacuolar ATP synthase subunit D (V-ATPase D subunit) ; (AF053230) vacuolar ATPase subunit D [Neurospora crassa]
18731	ENU02525	AN150C1_10	26-46	538-557	NAP		g416837		84	6.00E-16	34	40	cytochrome P450-TERP (cytochrome P450 108) ; cytochrome P450terp - Pseudomonas sp ; (M91440) P450terp [Pseudomonas sp.]
18732	ENU02526	AN161C8486: 319..894	42-64	554-574	NAP		g3560214	806	207	5.00E-53	67	30	(AL031536) tma splicing protein [Schizosaccharomyces pombe]
18733	ENU02527	AN161C9210: 378..952	62-83	572-594	NAP		g126192	739	106	2.00E-22			2-isopropylmalate synthase (alpha-isopropylmalate synthase) (alpha-IPM synthetase) ; 2-isopropylmalate synthase (EC 4.1.3.12) - yeast (Saccharomyces cerevisiae) ; (M12893) alpha-isopropylmalate synthase (EC 4.1.3.12) long form [Saccharomyces cerevisiae] ; (Z50161) 2-isopropylmalate Synthase [Saccharomyces cerevisiae] ; (Z71380) ORF YNL104c [Saccharomyces cerevisiae]
18734	ENU02528	AN161C6322: 2524..1949	55-73	569-588	NAP		g3873823	169	59	0.000000	39	72	(Z73422) predicted using Genefinder [Caenorhabditis elegans]
18735	ENU02529	AN161C5608: 1306..731	71-91	581-604	NAP		g1173624	114	65	3.00E-10	27	36	(U34744) cytochrome P-450 [Phlaenopsis sp. "hybrid SM9108"]
18736	ENU02530	AN161C8209: 1438..2014	43-62	557-577	NAP		g3114281	437	186	9.00E-47	46	84	"Chain M, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain 1, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution"



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18737	ENU02531	AN161C1107	22-44	536-556	NAP		g1730718	297	140	8.00E-33	43	31	probable mannosyltransferase KTR5 ; probable membrane protein YNL029c - yeast (Saccharomyces cerevisiae) ; (Z71305) ORF YNL029c [Saccharomyces cerevisiae]
18738	ENU02532	AN161C1137	56-75	563-591	NAP		g731738	596	122	3.00E-27	37	12	DNA replication helicase DNA2 ; probable purine nucleotide-binding protein YHR164c - yeast (Saccharomyces cerevisiae) ; (U00027) Dna2p: DNA replication helicase [Saccharomyces cerevisiae]
18739	ENU02533	AN161C2857	24-59	533-559	NAP		g2130462	205	100	7.00E-21	36	30	poly A polymerase (EC 2.7.7.-) - fission yeast (Schizosaccharomyces pombe) ; (X79705) polymerase [Schizosaccharomyces pombe] ; (AL035216) poly A polymerase [Schizosaccharomyces pombe]
18740	ENU02534	AN161C3020	34-54	543-569	NAP		g133341	289	91	6.00E-18	51	96	DNA-directed RNA polymerase II 14.2 KD polypeptide (B12.6) ; DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB9 - yeast (Saccharomyces cerevisiae) ; (M73060) RNA polymerase II subunit RPB9 [Saccharomyces cerevisiae] ; (Z72592) ORF YGL070c [Saccharomyces cerevisiae]
18741	ENU02535	AN161C2411	53-72	570-589	NAP		g1351662	660	205	2.00E-52	48	30	hypothetical 74.4 KD protein C30D11.09 in chromosome I ; hypothetical protein SPAC30D11.09 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe]
18742	ENU02536	AN161C9242	36-57	553-573	NAP		g2633748	305	94	6.00E-19	38	76	(Z99111) similar to glucose 1-dehydrogenase [Bacillus subtilis] (AF008220) yteR [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18743	ENU02537	AN161C8858	23-45	536-560	NAP		g2293194	303	99	3.00E-20			

# Gene Ontology

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18744	ENU02538	ANI61C508:2	28-56	545-565	NAP		g1077558	33	0.005				hypothetical protein YDR063w - yeast (Saccharomyces cerevisiae) ; (X84162) unknown [Saccharomyces cerevisiae] ; (Z49209) unknown [Saccharomyces cerevisiae] ; (Z74359) ORF YDR063w [Saccharomyces cerevisiae] (Z99753) hypothetical protein [Schizosaccharomyces pombe]
18745	ENU02539	ANI61C7498: 22-52		540-559	NAP		g2465148	135	75	4.00E-13	32	45	[Schizosaccharomyces pombe]
18746	ENU02540	ANI61C464:7	45-73	556-582	NAP		g1708006	215	105	2.00E-22	37	95	probable glucokinase (gluconate kinase) ; (Z69727) probable glucokinase [Schizosaccharomyces pombe]
18747	ENU02541	ANI61C1052	23-49	534-561	NAP		g3873699	160	94	1.00E-18	44	85	(Z73102) predicted using Genefinder; Similarity to viral non-structural proteins (SW:POLN_EEVV3); cDNA EST EMBL:D65747 comes from this gene; cDNA EST EMBL:D69295 comes from this gene; cDNA EST EMBL:C10380 comes from this gene;
18748	ENU02542	ANI61C7840: 38-57		557-577	NAP		g1705999	291	123	1.00E-27	33	37	Coatomer delta subunit (delta-coat protein) (delta-COP) ; (X94265) coat protein delta-cop [Bos primigenius] (Z99168) putative heat shock transcription factor [Schizosaccharomyces pombe]
18749	ENU02543	ANI61C2563: 65-85		584-604	NAP		g3327019	230	89	1.00E-18	41	28	"fructose-bisphosphate aldolase ; (Y11135) fructose-1,6-bisphosphate aldolase type II [Bacillus stearothermophilus]" probable calcium-binding protein ALG-2 (PMP41) (ALG-257) ; (U49112) ALG-2 [Mus musculus] sterigmatocystin biosynthesis regulatory protein ; sterigmatocystin synthesis transcriptional regulator aflR - Emmericella nidulans ; (U34740) pathway specific transcription factor [Emmericella nidulans] (L07492) sugar transport protein [Saccharomyces cerevisiae]
18750	ENU02544	ANI61C9392: 47-66		555-586	NAP		g4033506	206	86	2.00E-16	35	60	
18751	ENU02545	ANI61C9841: 37-56		544-576	NAP		g2506252	340	145	2.00E-34	39	97	
18752	ENU02546	ANI61C9701: 66-87		586-605	NAP		g1703202	228	67	1.00E-10	35	44	
18753	ENU02547	ANI61C537:8	36-55	543-575	NAP		g409547	138	45	0.0006	38	24	

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18754	ENU02548	ANI61C9833: 27-46	27-46	545-567	NAP		g3877351	308	75	9.00E-18			(Z66520) similar to ERG-3 like protein [Caenorhabditis elegans]
18755	ENU02549	ANI61C215:8 22-41	22-41	543-562	NAP		g3881138	159	85	5.00E-16	38	96	(AL023846) Y52B11C.1 [Caenorhabditis elegans]
18756	ENU02550	ANI61C1039 72-92	72-92	596-615	NAP		g2804470		64	0.000000			(AF043701) contains similarity to ankyrin repeats and protein kinases [Caenorhabditis elegans]
18757	ENU02551	ANI61C3473: 42-61	42-61	556-585	NAP		g465713	216	71	9.00E-18	32	67	hypothetical 30.3 KD protein in APE1/LAP4-CWP1 intergenic region ; hypothetical protein YKL099c - yeast (Saccharomyces cerevisiae) ; (X71133) YKL449 [Saccharomyces cerevisiae] ; (Z28099) ORF YKL099c [Saccharomyces cerevisiae]
18758	ENU02552	ANI61C1071 27-47	27-47	551-570	NAP		g4506617	391	102	1.00E-27	59	67	ribosomal protein L17 ; 60S ribosomal protein L17 (L23) ; ribosomal protein L17 - human ; (X53777) putative ribosomal protein (AA 1-184) [Homo sapiens]
18759	ENU02553	ANI61C8712: 58-77	58-77	577-602	NAP		g2498702	79	48	0.00007	34	38	sternmatocystin 7-O-methyltransferase precursor ; (L25835) O-methyltransferase [Aspergillus flavus] ; (L25834) O-methyltransferase [Aspergillus parasiticus] ; (L22091) O-methyltransferase [Aspergillus parasiticus]
18760	ENU02554	ANI61C2827: 31-60	31-60	556-575	NAP		g114988	1001	363	e-100	98	16	Kinesin-like protein BIMC ; kinesin-related protein bimC - Emericella nidulans ; (M32075) kinesin-like protein (bimC) [Emericella nidulans]
18761	ENU02555	ANI61C9570: 44-63	44-63	568-589	NAP		g1084581	396	118	4.00E-36	50	89	hypothetical protein YER007c-a - yeast (Saccharomyces cerevisiae) ; (U18778) Yel007c-ap [Saccharomyces cerevisiae]
18762	ENU02556	ANI61C7729: 31-50	31-50	557-576	NAP		g2231082	1314	100	8.00E-21	37	19	(Y07891) dynamin-related protein [Schizosaccharomyces pombe]
18763	ENU02557	ANI61C4165: 69-95	69-95	591-614	NAP		g3264834	1030	187	4.00E-47	50	55	(AF072541) xyliol dehydrogenase; XDH [Galactocandida mastotermis]

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18764	ENU02558	ANI61C8730:	71-90	594-616	NAP		g130879	580	131	1.00E-48			Proteasome component PUP1 precursor (macropain subunit PUP1) (proteinase YSCE subunit PUP1) (multicatalytic endopeptidase complex subunit PUP1) ; probable multicatalytic endopeptidase complex (EC 3.4.99.46) chain PUP1 - yeast (Saccharomyces cerevisiae) ; (X61189) PUP1 [Saccharomyces cerevisiae] ; (U55020) Pup1p [Saccharomyces cerevisiae] ; (Z75065) ORF YOR157c [Saccharomyces cerevisiae]
18765	ENU02559	ANI61C1935:	52-71	576-598	NAP		g2117760	802	92	1.00E-25	50	33	"aspartate transaminase (EC 2.6.1.1), cytosolic - yeast (Saccharomyces cerevisiae) ; (Z73199) ORF YLR027c [Saccharomyces cerevisiae]" (AL023780) zinc finger protein [Schizosaccharomyces pombe] (L48797) toxin pump [Cochliobolus carbonum]
18766	ENU02560	ANI61C6513:	22-47	545-568	NAP		g3184113	116	66	2.00E-10	35	30	Autophagy serine/threonine-protein kinase APCI1 ; probable membrane protein YGL180w - yeast (Saccharomyces cerevisiae) ; (X91489) putative ser/thr protein kinase [Saccharomyces cerevisiae] ; (Z72702) ORF YGL180w [Saccharomyces cerevisiae] ; (D29991) Apg1p [Saccharomyces cerevisiae]
18767	ENU02561	ANI61C886:	1 40-59	565-587	NAP		g1063421	252	84	6.00E-16	28	34	nuclear protein SNF7 ; SNF7 protein - yeast (Saccharomyces cerevisiae) ; (Z73197) ORF YLR025w [Saccharomyces cerevisiae]
18768	ENU02562	ANI61C5484:	72-92	590-619	NAP		g1730043	222	77	2.00E-17	39	19	[Saccharomyces cerevisiae] (AF100925) mating type protein MAT-1-3 [Gibberella fujikuroi] SPT10 protein ; regulatory protein SPT10 - yeast (Saccharomyces cerevisiae) ; (L24435) SPT10 [Saccharomyces cerevisiae] ; (Z49402) ORF YJL127c [Saccharomyces cerevisiae]
18769	ENU02563	ANI61C4438:	68-86	594-615	NAP		g730759	197	49	0.000000	33	71	
18770	ENU02564	ANI61C7200:	48-70	571-596	NAP		g3834684	121	66	2.00E-10	30	86	
18771	ENU02565	ANI61C1125	59-78	584-607	NAP		g464786	235	94	1.00E-26	34	28	

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18772	ENU02566	AN161C8336:	59-88	589-608	NAP		g3722	816	258	2.00E-68	63	32	(X52633) GAP1 protein (AA 1-601) [Saccharomyces cerevisiae]
18773	ENU02567	834..243 AN161C7975:	36-55	566-585	NAP		g4056551	666	154	9.00E-57	62	33	(AL034583) putative elongation initiation factor subunit [Schizosaccharomyces pombe]
18774	ENU02568	44..636 AN161C1803:	65-100	582-615	NAP		g1805251	273	101	4.00E-21	35	34	(U58946) transposase [Aspergillus awamori]
18775	ENU02569	6:7336..6744 AN161C1115	53-73	584-603	NAP		g1723280	354	106	1.00E-22	43	52	hypothetical 34.8 KD protein C4H3.04C in chromosome I ; (Z69380) unknown [Schizosaccharomyces pombe]
18776	ENU02570	1066..1659 AN161C8494:	59-80	589-610	NAP		g3913497	637	84	3.00E-33	54	58	putative carboxymethylcarnitine dienehydrolase (DHLH) ; hypothetical protein YDL086w - yeast (Saccharomyces cerevisiae) ; (Z74134) ORF YDL086w [Saccharomyces cerevisiae]
18777	ENU02571	114..708 AN161C6927:	47-66	568-599	NAP		g729230	652	191	1.00E-64	82	12	chromosome segregation protein CUT3 ; cut3 protein - fission yeast (Schizosaccharomyces pombe) ; (D30788) cut3 protein [Schizosaccharomyces pombe]
18778	ENU02572	960..366 AN161C4306:	37-57	558-589	NAP		g2132076	302	64	2.00E-18	33	44	hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae) ; (U55021) O3625p [Saccharomyces cerevisiae] ; (Z75081) ORF YOR173w [Saccharomyces cerevisiae]
18779	ENU02573	7640..8235 AN161C6203:	62-81	582-615	NAP		g4322563	441	103	3.00E-40	60	91	(AF089838) phosphatidylglycerol/phosphatidylinositol transfer protein [Aspergillus oryzae]
18780	ENU02574	1:2151..1556 AN161C1145	71-94	605-624	NAP		g2257524	619	127	2.00E-41	56	62	(AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe]
18781	ENU02575	7..692 AN161C941:	28-46	560-581	NAP		g539079	440	147	2.00E-37	54	14	peroxisomal assembly protein 5 - yeast (Pichia pastoris)

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18782	ENU02576	AN161C3194:	23-43	547-577	NAP		g1333371	207	74	7.00E-18			DNA-directed RNA polymerases I and III 16 KD polypeptide (AC19) ; DNA-directed RNA polymerase (EC 2.7.7.6) I/III chain AC19 - yeast
		726..130											(Saccharomyces cerevisiae) ; (M64991) AC19 RNA polymerase subunit [Saccharomyces cerevisiae] ; (Z69382) Subunit of RNA polymerase I and III [Saccharomyces cerevisiae] ; (Z71390) ORF YNL113w [Saccharomyces cerevisiae]
18783	ENU02577	AN161C8284:	40-59	573-595	NAP		g461540	796	171	7.00E-57			"phospho-2-dehydro-3-deoxyheptanate aldolase, tyrosine-inhibited (phospho-2-keto-3-deoxyheptanate aldolase) (DAHPh synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) ; 2-dehydro-3-deoxyphosphoheptanate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae) ; (L20296) homology with DAHP-synthase (ARO4) gene [Saccharomyces cerevisiae] ; (X61107) phospho-2-dehydro-3-deoxyheptanate aldolase [Saccharomyces cerevisiae] ; (Z36118) ORF YBR249c [Saccharomyces cerevisiae] "
		197..794											
18784	ENU02578	AN161C1878:	45-65	572-601	NAP		g4176538	316	67	1.00E-10	37	51	(AL035260) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]
		1258..660											
18785	ENU02579	AN161C3975:	66-86	587-622	NAP		g1351702	337	76	2.00E-13	31	36	hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
		1819..2417											
18786	ENU02580	AN161C9713:	63-86	594-619	NAP		g2995375	924	212	4.00E-59	66	46	(AL022245) ser/thr protein kinase [Schizosaccharomyces pombe] ; (AL031603) protein kinase. [Schizosaccharomyces pombe]
		1295..697											
18787	ENU02581	AN161C3218:	70-89	606-626	NAP		g3184080	394	68	4.00E-11	60	85	(AL023781) hypothetical protein [Schizosaccharomyces pombe]
		1079..1677											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18788	ENU02582	ANI61C1056	46-65	578-602	NAP		g1722905	157	66	3.00E-14	34	26	"endo-1,4-beta-xyylanase D precursor (xyylanase D) (XYLD) ; endo-1,4-beta-xyylanase (EC 3.2.1.8) D - Cellulomonas fimi ; (X76729) endo-1,4-beta-xyylanase [Cellulomonas fimi]"
18789	ENU02583	ANI61C1120	72-91	610-629	NAP		g3184056		56	0.000000			(AL023776) hypothetical protein [Schizosaccharomyces pombe]
18790	ENU02584	ANI61C8956: 131..730	25-46	555-582	NAP		g2598037	257	60	3.00E-17	31	43	(AJ01272) manganese resistance 1 protein [Saccharomyces cerevisiae]
18791	ENU02585	ANI61C7700: 916..316	22-55	561-580	NAP		g133264	341	73	7.00E-21	52	96	Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans]
18792	ENU02586	ANI61C5260: 2894..2294	44-63	581-602	NAP		g1710503	609	161	3.00E-46	69	85	"probable 60S ribosomal protein L18 (RP28) ; ribosomal protein L18-e, cytosolic - fission yeast [Schizosaccharomyces pombe] ; (AL031528) 60s ribosomal protein 118 [Schizosaccharomyces pombe]"
18793	ENU02587	ANI61C3974: 733..1334	48-79	588-607	NAP		g120609	630	199	4.00E-53			Uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTASE) ; uracil phosphoribosyltransferase (EC 2.4.2.9) chain FUR1 - yeast (Saccharomyces cerevisiae) ; (M36485) uracil phosphoribosyltransferase (FUR1) [Saccharomyces cerevisiae] ; (U10398) Fur1p: Uracil phosphoribosyltransferase [Saccharomyces cerevisiae] ; (X79811) FUR1 [Saccharomyces cerevisiae] hypothetical protein YPL225w - yeast (Saccharomyces cerevisiae) ; (Z73581) ORF YPL225w [Saccharomyces cerevisiae]
18794	ENU02588	ANI61C1048 3:6359..6960	27-46	564-586	NAP		g2132237	287	112	2.00E-24	48	93	(AL034433) hypothetical protein [Schizosaccharomyces pombe] (X78082) NADH:ubiquinone oxidoreductase (complex I) [Neurospora crassa]
18795	ENU02589	ANI61C7255: 750..1351	30-49	565-589	NAP		g4007771	210	100	1.00E-20	29	30	(AL034433) hypothetical protein [Schizosaccharomyces pombe]
18796	ENU02590	ANI61C8977: 603..2	33-54	570-592	NAP		g577597	347	138	3.00E-32	49	79	(X78082) NADH:ubiquinone oxidoreductase (complex I) [Neurospora crassa]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18797	ENU02591	ANI61C7354:	69-88	610-629	NAP		g586551	490	87	8.00E-17	35	53	hypothetical 33.5 KD protein in MRPS9-YSW1 intergenic region ; probable membrane protein YBR147w - yeast (Saccharomyces cerevisiae) ; (Z36016) ORF YBR147w [Saccharomyces cerevisiae]
18798	ENU02592	ANI61C8993:	22-53	564-582	NAP		g1170922	293	101	1.00E-30	39	37	Ammonium transporter MEP2 ; ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae) ; (X83608) ammonium transporter [Saccharomyces cerevisiae] ; (Z46843) NH3 permease [Saccharomyces cerevisiae] ; (Z71418) ORF YNL142w [Saccharomyces cerevisiae] (X60381) ORF2 [Saccharomyces cerevisiae]
18799	ENU02593	ANI61C8845:	22-49	563-582	NAP		g388249	198	106	2.00E-22	39	60	hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YJL055w - yeast (Saccharomyces cerevisiae) ; (Z49330) ORF YJL055w [Saccharomyces cerevisiae]
18800	ENU02594	ANI61C3564:	39-58	578-600	NAP		g1352984	365	114	6.00E-25	42	68	hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YJL055w - yeast (Saccharomyces cerevisiae) ; (Z49330) ORF YJL055w [Saccharomyces cerevisiae]
18801	ENU02595	ANI61C3979:	43-62	585-604	NAP		g1352982		52	0.000004			hypothetical protein in DFR1 3'region
18802	ENU02596	ANI61C1076:	32-51	574-593	NAP		g1361982	354	167	5.00E-41	44	34	4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis thaliana ; (U18675) 4-coumarate--coenzyme A ligase [Arabidopsis thaliana]
18803	ENU02597	ANI61C3755:	34-53	577-596	NAP		g3135990	322	97	1.00E-25	45	30	(AL023589) membrane transporter [Schizosaccharomyces pombe]
18804	ENU02598	ANI61C5967:	35-55	576-597	NAP		g2499919	494	134	3.00E-31	45	20	hypothetical zinc metalloproteinase T16A9.4
18805	ENU02599	ANI61C4286:	23-50	559-587	NAP		g1083278	163	87	1.00E-16	33	27	cytochrome P450 3A13 - mouse ; (X63023) cytochrome P-450I1A [Mus musculus] ; cytochrome P450 Cyp3a-13 [Mus musculus]



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18806	ENU02600	ANI61C197:6	25-46	566-589	NAP		g1911486	466	102	2.00E-21	49	61	"(S80872) putative TcI-nariner class transposase/IS630-TcI homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"
18807	ENU02601	ANI61C9009: 45-64		589-609	NAP		g2619026	435	155	3.00E-37	43	46	(AF027868) Yoan [Bacillus subtilis]; (Z99114) similar to hypothetical proteins [Bacillus subtilis]
18808	ENU02602	ANI61C6045: 34-53		570-598	NAP		g1749484	203	76	1.00E-13	41	47	"(D89138) similar to Saccharomyces cerevisiae ORF YGL208W, EMBL Accession Number Z72730 [Schizosaccharomyces pombe]"
18809	ENU02603	ANI61C1111 28-49		570-593	NAP		g2498970	485	157	6.00E-38	40	73	putative sterigmatocystin biosynthesis protein STCQ; (U34740) similar to A. parasiticus putative aflatoxin biosynthesis protein [Emmericella nidulans]
18810	ENU02604	ANI61C1209: 55-78		600-621	NAP		g2132284	367	91	1.00E-36	39	89	hypothetical protein YPR107c - yeast (Saccharomyces cerevisiae); (U32445) P8283.17 gene product [Saccharomyces cerevisiae]
18811	ENU02605	ANI61C4438: 68-86		612-634	NAP		g730759	197	49	0.000000	35	74	nuclear protein SNF7; SNF7 protein - yeast (Saccharomyces cerevisiae); (Z73197) ORF YLR025w [Saccharomyces cerevisiae]
18812	ENU02606	ANI61C5883: 29-48		564-595	NAP		g731875	437	148	3.00E-35	39	65	"mitochondrial FAD carrier protein FLX1; carrier protein FLX1, inner membrane - yeast (Saccharomyces cerevisiae); (Z38059) orf, len: 311, CAI: 0.12, similar to peroxisomal membrane protein and mitochondrial carrier proteins [Saccharomyces cerevisiae]; (L41168) inner membrane carrier protein [Saccharomyces cerevisiae]"
18813	ENU02607	ANI61C7524: 66-86		614-633	NAP		g128337	1671	324	2.00E-88	98	29	G2-specific protein kinase NIMA (never in mitosis); probable protein kinase nimA (EC 2.7.1.-) - Emmericella nidulans; (M20249) never in mitosis protein [Emmericella nidulans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18814	ENU02608	ANI61C1107	24-42	565-591	NAP		g2879805	600	131	3.00E-30	37	12	(AL021813) hypothetical protein [Schizosaccharomyces pombe]
18815	ENU02609	ANI61C8051	36-55	585-604	NAP		g1706087	910	173	7.00E-43	50	37	cytochrome P450-DIT2 (cytochrome P450 56) ; cytochrome P450 56 - yeast (Saccharomyces cerevisiae) ; (U32274) Dit2p: cytochrome P450; CAL: 0.13 [Saccharomyces cerevisiae]
18816	ENU02610	ANI61C757:1	22-46	571-590	NAP		g126597	577	203	8.00E-59	58	87	"N,O-diacetylmutamidase (lysozyme CH) ; lysozyme (EC 3.2.1.17) - fungus (Chalara sp.) "
18817	ENU02611	ANI61C8231: 1762..1152	61-81	594-629	NAP		g130117	813	110	9.00E-24	49	27	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]
18818	ENU02612	ANI61C3107: 769..1380	43-62	591-612	NAP		g730334	405	108	3.00E-23	32	35	putative polypeptide biosynthesis protein PKSJ ; (U11039) unknown [Bacillus subtilis] ; (Z99112) pksJ [Bacillus subtilis] ; (Z99113) pksJ [Bacillus subtilis]
18819	ENU02613	ANI61C7361: 452..1063	63-82	613-632	NAP		g3687462	370	100	5.00E-29	45	91	(AL031798) coatomer zeta subunit [Schizosaccharomyces pombe]
18820	ENU02614	ANI61C9833: 2306..2917	42-61	592-611	NAP		g1723488	87	61	0.000000	42	8	hypothetical 104.0 KD protein C32A11.03C in chromosome I ; (Z69796) unknown [Schizosaccharomyces pombe]
18821	ENU02615	ANI61C8431: 242..853	72-92	611-641	NAP		g2914565	413	141	1.00E-36	48	70	"Chain A, Yeast Chorismate Mutase, T226s Mutant, Complex With Trp "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18822	ENU02616	ANI61C3868:	22-45	572-593	NAP		g417817	409	176	1.00E-43			protein-S isoprenylcysteine O-methyltransferase (isoprenylcysteine carboxylmethyltransferase) ; farnesyl cysteine carboxyl-methyltransferase - yeast (Saccharomyces cerevisiae) ; (L07952) farnesyl cysteine carboxyl-methyltransferase [Saccharomyces cerevisiae] ; (L15442) isoprenylcysteine carboxyl methyltransferase [Saccharomyces cerevisiae] ; (U33007) Ste14p: farnesyl cysteine carboxyl-methyltransferase; YDR410C; CAL: 0.12 [Saccharomyces cerevisiae]
18823	ENU02617	ANI61C3365:	53-72	592-624	NAP		g3116144	110	54	0.000001	27	64	(AL023290) hypothetical protein [Schizosaccharomyces pombe]
18824	ENU02618	ANI61C502:6	49-72	596-621	NAP		g482219	290	113	8.00E-25	38	20	hypothetical protein ZK757.3 - Caenorhabditis elegans
18825	ENU02619	ANI61C1027	72-93	620-644	NAP		g2494676	1242	123	7.00E-28	38	36	EPD1 protein precursor ; (AB005130) EPD1 [Candida maltosa]
18826	ENU02620	ANI61C1166:	44-67	597-616	NAP		g4530327	890	205	2.00E-80	79	30	(AF110494) mitochondrial precursor protein import receptor tom70 [Neurospora crassa]
18827	ENU02621	ANI61C8770:	70-89	623-642	NAP		g1710055	788	148	2.00E-35	44	44	RDS1 protein ; rds1 protein - fission yeast (Schizosaccharomyces pombe) ; (X77328) rds1 [Schizosaccharomyces pombe]
18828	ENU02622	ANI61C293:2	30-50	583-602	NAP		g1929333	120	61	0.000000	26	97	(Z93767) ywrF [Bacillus subtilis] ; (Z99122) ywrF [Bacillus subtilis]
18829	ENU02623	ANI61C5354:	65-83	619-638	NAP		g464725	689	249	2.00E-65	69	91	"40S ribosomal protein S8 (S14) (Y59) (RP19) ; ribosomal protein S8.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z26879) ribosomal protein S8 [Saccharomyces cerevisiae] ; (Z35833) ORF YBL072c [Saccharomyces cerevisiae] ; (U18839) Rps8bp: Ribosome protein, small subunit [Saccharomyces cerevisiae] " (U13050) pectate lyase D [Fusarium solani f. sp. pisi]
18830	ENU02624	ANI61C3563:	58-77	611-631	NAP		g1526987	450	183	7.00E-46	54	77	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18831	ENU02625	AN161C8909:	30-49	582-603	NAP		g2773042	750	105	3.00E-22	41	17	(AF038440) phospholipase D2 [Homo sapiens]
18832	ENU02626	2964..3579 AN161C1583:	22-45	571-596	NAP		g1723912	78	50	0.00002	33	11	hypothetical 73.5 KD protein in SCS3-SUP44 intergenic region ; hypothetical protein YGL124c - yeast (Saccharomyces cerevisiae) ; (Z72646) ORF YGL124c [Saccharomyces cerevisiae] ; (X94106) G2889 [Saccharomyces cerevisiae]
18833	ENU02627	AN161C1141	71-97	626-645	NAP		g83699	1733	264	5.00E-70	98	57	dehydroshikimate dehydratase (EC 4.2.1.-) - Emeritella nidulans ; (M77665) dehydroshikimate dehydratase [Emeritella nidulans]
18834	ENU02628	AN161C915:2	43-62	591-617	NAP		g799150	179	98	7.00E-20	40	14	"(U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici]"
18835	ENU02629	AN161C5294:	22-45	576-598	NAP		g730717	400	117	1.00E-31	50	90	"signal sequence processing protein SEC11 ; signal peptidase (EC 3.4.99.-) SEC11 - yeast (Saccharomyces cerevisiae) ; (Z38061) sec11, len: 167, CAl: 0.17 SCI1_yeast P15367 signal sequence processing protein [Saccharomyces cerevisiae]"
18836	ENU02630	AN161C4039:	60-79	610-636	NAP		g132172	699	154	5.00E-37	38	38	PIM1 protein ; pim1 hypothetical protein - fission yeast (Schizosaccharomyces pombe)
18837	ENU02631	AN161C3092:	22-53	580-599	NAP		g3219941	318	77	5.00E-25	34	94	hypothetical 24.7 KD protein C3A12.04C in chromosome I ; (Z95395) conserved hypothetical protein [Schizosaccharomyces pombe]
18838	ENU02632	AN161C6403:	52-82	609-629	NAP		g586394	356	134	4.00E-31			hypothetical 98.1 KD TRP-ASP repeats containing protein in PAF1-MRPL27 intergenic region ; hypothetical protein YBR281c - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2018-ORF [Saccharomyces cerevisiae] ; (Z36150) ORF YBR281c [Saccharomyces cerevisiae] ; ORF YBR2018 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18839	ENU02633	ANI61C8982: 6024..5404	52-71	610-630	NAP		g3170178	71	5.00E-12				(AF039689) antigen NY-CO-7 [Homo sapiens]
18840	ENU02634	ANI61C3314: 1350..1971	48-67	605-627	NAP		g3004934	801	189	2.00E-47	46	43	(AF036871) annexin XIV [Neurospora crassa]
18841	ENU02635	ANI61C748:1 7..638	38-58	582-617	NAP		g2132293	228	75	3.00E-21	38	53	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325)
18842	ENU02636	ANI61C7556: 2814..3435	41-62	601-620	NAP		g2624417	384	126	1.00E-28	53	88	[Saccharomyces cerevisiae] (AJ002959) Ubiquitin carrier protein [Zea mays]
18843	ENU02637	ANI61C9743: 949..327	23-42	581-603	NAP		g2492754	518	127	5.00E-29	44	63	sorbitol utilization protein SOU1; (AF002134) Sou1p [Candida albicans]
18844	ENU02638	ANI61C8297: 1068..446	70-89	630-650	NAP		g3327876	189	87	8.00E-17	35	47	(AB016218) unknown: similar to human GA17 protein
18845	ENU02639	ANI61C7885: 124..746	22-53	575-602	NAP		g3738142	459	80	1.00E-45	57	99	[Schizosaccharomyces pombe] (AL031852) u-snmp-associated cyclophilin [Schizosaccharomyces pombe]
18846	ENU02640	ANI61C8732: 3940..4562	22-50	573-602	NAP		g459002	392	118	2.00E-32	42	78	(U00036) R151.6 gene product [Caenorhabditis elegans]
18847	ENU02641	ANI61C1042 3:907..1529	68-87	630-649	NAP		g1730032	250	52	2.00E-14	35	66	2-deoxy-D-glucuronate 3-dehydrogenase (2-keto-3-deoxyglucuronate oxidoreductase); (U29581) ORF_f253 [Escherichia coli]; (AE000368) 2-deoxy-D-glucuronate 3-dehydrogenase [Escherichia coli]
18848	ENU02642	ANI61C5330: 798..174	68-87	631-650	NAP		g2924501	390	43	0.001	30	23	(AL022019) conserved hypothetical protein [Schizosaccharomyces pombe]
18849	ENU02643	ANI61C172:3 1..656	47-71	610-630	NAP		g113701	203	50	4.00E-14	42	27	Acetamidase; amds protein - Emericella nidulans; (M16371) acetamidase enzyme [Emericella nidulans]

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18850	ENU02644	ANI61C9290:	49-68	611-633	NAP		g549626	261	102	2.00E-21	36	92	hypothetical 22.0 KD protein in LAS1-CCPI intergenic region ; hypothetical protein YKR065c - yeast (Saccharomyces cerevisiae) ; (Z28290) ORF YKR065c [Saccharomyces cerevisiae]
18851	ENU02645	ANI61C5915:	33-53	598-617	NAP		g586521	369	153	9.00E-37	43	26	hypothetical 86.4 KD protein in PHO5-VPS15 intergenic region ; hypothetical protein YBR094w - yeast (Saccharomyces cerevisiae) ; (X78993) hyp. protein [Saccharomyces cerevisiae] ; (Z35963) ORF YBR094w [Saccharomyces cerevisiae] (AL035216) nucleolar protein involved in pre-rRNA processing [Schizosaccharomyces pombe]
18852	ENU02646	ANI61C1650:	23-42	588-607	NAP		g4160346	1532	218	3.00E-56	65	38	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMG-CoA reductase) ; (X94307) HMG-CoA reductase [Gibberella fujikuroi] quinate permease (quinate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
18853	ENU02647	ANI61C995:8	56-75	621-640	NAP		g2495263	743	248	3.00E-65	56	21	7alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) - Eubacterium sp. (strain VPI 12708) ; (M58473) 7-alpha-hydroxysteroid dehydrogenase [Eubacterium sp. VPI 12708]
18854	ENU02648	ANI61C3926:	55-74	621-640	NAP		g131761	220	112	3.00E-24	30	38	"hypothetical 42.5 KD protein in TSM1-ARE1 intergenic region ; probable membrane protein YCR044c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR044c, len:357 [Saccharomyces cerevisiae]"
18855	ENU02649	ANI61C5699:	46-69	611-631	NAP		g98747	248	116	2.00E-25	30	78	hypothetical protein YDR140w - yeast (Saccharomyces cerevisiae) ; (Z48179) unknown [Saccharomyces cerevisiae] (AF010138) transcription factor [Mus musculus]
18856	ENU02650	ANI61C2043:	34-53	600-620	NAP		g140496	284	136	2.00E-31	36	55	
18857	ENU02651	ANI61C7025:	28-50	596-615	NAP		g1077536	260	109	2.00E-23	40	77	
18858	ENU02652	ANI61C2654:	40-59	608-627	NAP		g2281697	434	57	0.000000	28	17	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18859	ENU02653	ANI61C6471: 22-55		590-610	NAP		g4538667	391	126	8.00E-29	65	85	(AL049474) clathrin coat assembly protein [Schizosaccharomyces pombe]
18860	ENU02654	ANI61C2906: 22-53		583-610	NAP		g762850	299	76	2.00E-13	40	100	(L41166) p21 protein [Schizosaccharomyces pombe]; (Z99262) p21 protein; cell cycle regulatory protein; interacts with cdc2 in the control of the M-G1 transition [Schizosaccharomyces pombe]
18861	ENU02655	ANI61C7933: 37-56		606-625	NAP		g1077514	302	114	5.00E-25	46	76	hypothetical protein YDR013w - yeast (Saccharomyces cerevisiae) ; (Z48008) unknown [Saccharomyces cerevisiae] ; (X95966) orf:PZA208 [Saccharomyces cerevisiae] ; (Z74309) ORF YDR013w [Saccharomyces cerevisiae]
18862	ENU02656	ANI61C9492: 46-65		616-635	NAP		g1723848	277	89	4.00E-17	46	85	"putative mitochondrial 60S ribosomal protein L7/L12 precursor ; probable ribosomal protein L12, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z72591) ORF YGL068w [Saccharomyces cerevisiae]"
18863	ENU02657	ANI61C6172: 38-57		608-627	NAP		g3169083	279	111	6.00E-24	37	61	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18864	ENU02658	ANI61C6638: 28-52		598-617	NAP		g3915558	169	92	3.00E-18	29	62	hypothetical 36.5 KD protein in GBSA-TLPB intergenic region ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18865	ENU02659	ANI61C1015: 56-77		625-645	NAP		g2131385	270	87	1.00E-16	40	33	hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae) ; (Z50046) unknown [Saccharomyces cerevisiae]
18866	ENU02660	ANI61C1039: 44-63		613-634	NAP		g2104422	323	113	1.00E-24	42	26	(Z95395) putative membrane transport protein [Schizosaccharomyces pombe]
18867	ENU02661	ANI61C7015: 22-42		591-613	NAP		g1078629	1199	309	1.00E-83	97	31	DNA binding protein - Emericella nidulans ; (Z47081) DNA binding protein [Emericella nidulans]
18868	ENU02662	ANI61C3159: 25-44		585-616	NAP		g1749831	731	165	2.00E-40	45	26	(Z56279) beta-xyl-o-glucosidase [Thermoanaerobacter brockii]
18869	ENU02663	ANI50C7416: 23-42		596-615	NAP		g1781180	47	0.0001	32	29	(Z83859) hypothetical protein Rv1867 [Mycobacterium tuberculosis]	

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18870	ENU02664	AN161C3242:	42-61	604-634	NAP		g1173168	299	139	2.00E-32	40	75	Hypothetical 31.5 KD protein; (U05664) homologous to Swiss-Prot Accession Number P20435: Saccharomyces cerevisiae RNA polymerase subunit RPO26 [Sulfolobus acidocaldarius]
		178..812											(U48234) spU2AF23
18871	ENU02665	AN161C4376:	45-66	620-639	NAP		g2347143	660	224	4.00E-58	55	89	[Schizosaccharomyces pombe]
		881..1482											choline transport protein; choline transport protein - yeast
18872	ENU02666	AN161C9847:	71-96	646-666	NAP		g117619	704	131	4.00E-30	36	34	(Saccharomyces cerevisiae); (J05603) choline transport protein
		8262..7625											[Saccharomyces cerevisiae]; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
18873	ENU02667	AN161C6047:	22-45	598-617	NAP		g729998	505	174	6.00E-43	45	49	"MRNA capping enzyme (MRNA guanylyltransferase) (GTP--RNA guanylyltransferase); (U16143) GTP:RNA guanylyltransferase [Schizosaccharomyces pombe]; (U18811) GTP--RNA guanylyltransferase
		138..775											[Schizosaccharomyces pombe]; (Z97211) mma capping enzyme, mma guanylyltransferase
18874	ENU02668	AN161C1029	60-86	633-655	NAP		g1708418	1571	354	2.00E-97	86	54	[Schizosaccharomyces pombe]"
		4:6013..6650											eukaryotic initiation factor 4A (EIF-4A); (X80796) translation initiation factor eIF-4A [Schizosaccharomyces pombe]; (U40627) cell cycle control protein eIF-4A [Schizosaccharomyces pombe]
18875	ENU02669	AN161C8590:	22-41	593-617	NAP		g3879236		36	0.25			(Z66499) T01B7.8 [Caenorhabditis elegans]
		5557..4920											hypothetical protein YOL071w - yeast
18876	ENU02670	AN161C352:9	52-75	628-648	NAP		g2132007	181	79	2.00E-14	40	89	(Saccharomyces cerevisiae); (Z74813) ORF YOL071w [Saccharomyces cerevisiae]
		224..9862											



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18877	ENU02671	AN161C1805: 2409..2293	40-64	618-637	NAP		g728904	335	95	5.00E-19	41	15	calcium-transporting ATPase 2 (vacuolar CA2+-ATPase); Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae); (U03060) calcium ATPase [Saccharomyces cerevisiae]; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
18878	ENU02672	AN161C9127: 1359..1998	44-63	622-641	NAP		g2959364	326	146	1.00E-34	39	78	(AL022117) putative o-methyltransferase [Schizosaccharomyces pombe]
18879	ENU02673	AN161C3023: 1260..621	40-63	617-637	NAP		g1083278	114	55	4.00E-11	32	35	cytochrome P450 3A13 - mouse; (X63023) cytochrome P-450IIIA [Mus musculus]; cytochrome P450 Cyp3a-13 [Mus musculus]
18880	ENU02674	AN161C3023: 1260..621	40-63	617-637	NAP		g1083278	114	55	4.00E-11	32	35	cytochrome P450 3A13 - mouse; (X63023) cytochrome P-450IIIA [Mus musculus]; cytochrome P450 Cyp3a-13 [Mus musculus]
18881	ENU02675	AN161C8458: 2393..1754	63-85	641-660	NAP		g3885836		51	5.00E-14			(AF091042) putative cercosporin transporter [Cercospora kikuchii]
18882	ENU02676	AN161C8439: 103..745	68-103	649-668	NAP		g2133270	576	100	5.00E-53	91	78	HAP3 protein - Emericella nidulans; (U35341) HapC [Emericella nidulans]
18883	ENU02677	AN161C9069: 831..188	27-46	609-628	NAP		g1617552	2322	229	4.00E-78	97	38	(U70043) NsdD [Emericella nidulans]; (U70044) DNA binding protein NsdD [Emericella nidulans]
18884	ENU02678	AN161C2652: 1432..789	66-87	634-667	NAP		g2956779	556	194	4.00E-49	53	38	(AL022103) histidyl-trna synthetase [Schizosaccharomyces pombe]
18885	ENU02679	AN161C2281: 3007..2364	22-41	604-623	NAP		g127297	124	53	0.000001			MPV17 protein; mpv17 protein - mouse; (M36411) Mpv17 [Mus musculus]
18886	ENU02680	AN161C1422: 79..722	22-52	604-623	NAP		g1870230	1304	436	e-122	99	81	(AC000133) ORF [Emericella nidulans]
18887	ENU02681	AN161C1079: 4:2116..1472	62-83	642-664	NAP		g4033573	239	85	5.00E-23	43	88	(Z99262) hypothetical protein [Schizosaccharomyces pombe]
18888	ENU02682	AN161C843:7 34..90	22-52	603-624	NAP		g4106666	421	171	5.00E-42	44	71	(AL035064) putative ubiquinone biosynthesis protein
18889	ENU02683	AN161C66:29 64..2320	36-56	611-638	NAP		g2842509	416	101	9.00E-41	44	38	[Schizosaccharomyces pombe] (AL021748) hypothetical protein [Schizosaccharomyces pombe]

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18890	ENU02684	AN161C2870:	64-84	648-667	NAP		g1723479	377	164	4.00E-40	43	89	hypothetical 24.9 KD protein C17G8.07 in chromosome I ; (Z69795) unknown [Schizosaccharomyces pombe]
18891	ENU02685	AN161C7394:	68-87	650-673	NAP		g1723879	252	95	5.00E-19	37	73	hypothetical 32.1 KD protein in MAD1-SCY1 intergenic region ; probable membrane protein YGL085w - yeast (Saccharomyces cerevisiae) ; (Z72607) ORF YGL085w [Saccharomyces cerevisiae]
18892	ENU02686	AN161C7972:	55-75	628-660	NAP		g1351612	274	113	7.00E-28	40	61	hypothetical oxidoreductase C23D3.11 in chromosome I ; hypothetical protein SPAC23D3.11 - fission yeast (Schizosaccharomyces pombe) probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr284cp [Saccharomyces cerevisiae]
18893	ENU02687	AN161C1056	22-47	601-627	NAP		g2132491	274	75	1.00E-25	40	61	Uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTASE) ; uracil phosphoribosyltransferase - Bacillus subtilis ; (Z38002) uracil phosphoribosyltransferase [Bacillus subtilis] ; (Z99122) uracil phosphoribosyltransferase [Bacillus subtilis] ; uracil phosphoribosyltransferase [Bacillus subtilis]
18894	ENU02688	AN161C5718:	51-74	637-657	NAP		g731073	251	48	0.00006			ubiquitin-like protein 9 - Arabidopsis thaliana (AL049559) riboflavin synthase alpha chain [Schizosaccharomyces pombe] (AE000314) putative racemase [Escherichia coli] ; (D90856) similar to [SwissProt Accession Number P31458] [Escherichia coli]
18895	ENU02689	AN161C3229:	24-52	611-630	NAP		g1362010	267	117	3.00E-28	70	30	(AB010901) ribosomal protein L21 homolog [Schizosaccharomyces pombe]
18896	ENU02690	AN161C1148	69-88	652-676	NAP		g4581523	425	178	3.00E-44	53	87	
18897	ENU02691	AN161C8540:	71-90	653-679	NAP		g1788580	657	146	9.00E-35	40	52	
18898	ENU02692	AN161C7170:	42-62	632-651	NAP		g2865171	478	118	3.00E-38	69	90	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18899	ENU02693	AN150C6324	71-95	661-680	NAP		g465873	63	0.000000	002	25	33	hypothetical 59.1 KD protein F22B7.6 in chromosome III ; (F22b7.6 protein - Caenorhabditis elegans ; (L12018) putative [Caenorhabditis elegans] hypothetical 98.3 KD protein C9G1.06C in chromosome I ; (Z98763) hypothetical src homology domain containing protein [Schizosaccharomyces pombe] (AC005757) R32611_2 [Homo sapiens] (AL031534) putative asparagine synthase [Schizosaccharomyces pombe]
18900	ENU02694	AN161C5149:	48-67	639-658	NAP		g3183389	540	153	8.00E-37	39	23	PSI protein ; DNAJ-like protein homolog - fission yeast (Schizosaccharomyces pombe) ; (L37753) Psi protein [Schizosaccharomyces pombe] ; Dnal-like protein [Schizosaccharomyces pombe]
18901	ENU02695	AN161C8056:	50-69	641-660	NAP		g3688090	189	59	2.00E-13	43	86	"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus]" (AL023634) hypothetical protein [Schizosaccharomyces pombe]
18902	ENU02696	AN161C5061:	23-42	603-634	NAP		g3560144	370	145	3.00E-34	41	38	probable membrane protein YPL264c - yeast (Saccharomyces cerevisiae) ; (Z73620) ORF YPL264c [Saccharomyces cerevisiae] hypothetical 29.3 KD protein C3F10.08C in chromosome I ; (Z69369) hypothetical protein [Schizosaccharomyces pombe]
18903	ENU02697	AN161C5317:	29-48	619-642	NAP		g1346878	585	141	3.00E-33	39	51	
18904	ENU02698	AN161C2530:	45-64	637-658	NAP		g2492825	298	89	3.00E-17	29	52	
18905	ENU02699	AN161C3258:	38-57	633-652	NAP		g3150262	564	146	1.00E-34	38	61	
18906	ENU02700	AN161C1430:	65-84	660-679	NAP		g2133013	401	93	1.00E-18	34	51	
18907	ENU02701	AN161C6665:	45-67	634-660	NAP		g1723253	130	61	0.000000		01	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18908	ENU02702	AN161C6366:	25-56	619-640	NAP		g1352984	390	132	1.00E-39	46	81	hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YJL055w - yeast (Saccharomyces cerevisiae) ; (Z49330) ORF YJL055w [Saccharomyces cerevisiae]
18909	ENU02703	AN161C718:4	33-55	618-648	NAP		g3150116	754	191	4.00E-48	45	39	(AL023595) amino acid permease [Schizosaccharomyces pombe]
18910	ENU02704	AN161C5178:	40-60	636-655	NAP		g1730641	299	79	3.00E-14	29	30	hypothetical 65.0 KD protein in MET2-SEC2 intergenic region ; probable membrane protein YNL275w - yeast (Saccharomyces cerevisiae) ; (Z71551) ORF YNL275w [Saccharomyces cerevisiae]
18911	ENU02705	AN161C6874:	49-69	643-664	NAP		g3043428	670	174	1.00E-66	68	97	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
18912	ENU02706	AN161C1298:	66-86	663-682	NAP		g2492997	438	98	2.00E-33	62	68	probable succinyl-COA:3-ketoacid-COenzyme A transferase subunit B (succinyl COA:3-OXoacid COA-transferase) (OXCT B) ; (Z95556) scob [Mycobacterium tuberculosis]
18913	ENU02707	AN161C3599:	22-44	620-639	NAP		g522301	535	160	8.00E-39	41	46	(L35053) homolog of retroviral gag genes; putative [Magnaporthe grisea]
18914	ENU02708	AN161C1083	72-92	670-689	NAP		g4150918	302	113	1.00E-24	40	81	(Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
18915	ENU02709	AN161C8998:	31-51	627-648	NAP		g1170551	183	88	7.00E-17	37	96	"mitochondrial inner membrane protease subunit 2 ; proteinase 2 precursor, mitochondrial inner membrane - yeast (Saccharomyces cerevisiae) ; (Z49213) Imp2p [Saccharomyces cerevisiae] "
18916	ENU02710	AN161C6525:	53-72	651-670	NAP		g3850129	585	166	2.00E-40	56	85	(AL033391) conserved hypothetical protein [Candida albicans]
18917	ENU02711	AN161C7950:	70-89	668-687	NAP		g130117	1210	96	1.00E-54	58	30	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18918	ENU02712	ANI61C3150:	59-80	658-677	NAP		g2492777	537	155	7.00E-39	55	52	hypothetical ZINC-type alcohol dehydrogenase-like protein in pre-FET4 intergenic region ; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae) ; (Z54141) unknown [Saccharomyces cerevisiae] (AB012725) zinc finger protein [Mus musculus]
		993..1653											
18919	ENU02713	ANI61C1022	33-53	629-651	NAP		g3298472		38	0.088			hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product [Saccharomyces cerevisiae]
		0:15..675											
18920	ENU02714	ANI61C8624:	23-50	619-642	NAP		g731611	247	110	1.00E-23	35	89	hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product [Saccharomyces cerevisiae]
		2360..1699											
18921	ENU02715	ANI61C8624:	23-50	619-642	NAP		g731611	247	110	1.00E-23	35	89	hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product [Saccharomyces cerevisiae]
		2360..1699											
18922	ENU02716	ANI61C8082:	57-76	659-678	NAP		g2144564	606	151	9.00E-61	61	61	phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6) - yeast (Saccharomyces cerevisiae) ; (M67445) phosphoribosyl-amino-imidazolesuccinocarboxamide synthetase [Saccharomyces cerevisiae] ; (L22015) Adel p: phosphoribosyl amino imidazolesuccinocarboxamide synthetase [Saccharomyces cerevisiae] ORM1 protein ; probable membrane protein YGR038w - yeast (Saccharomyces cerevisiae) ; (Z72823) ORF YGR038w [Saccharomyces cerevisiae]
		2923..2260											
18923	ENU02717	ANI61C9181:	28-47	622-649	NAP		g1723661	472	169	1.00E-49	59	76	
		6564..5901											

# Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18924	ENU02718	ANI61C2491:	23-49	624-645	NAP		g130880	799	167	6.00E-41			"Proteasome component Y7 (macropain subunit Y7) (proteinase YSCE subunit 7) (multicatalytic endopeptidase complex subunit Y7); multicatalytic endopeptidase complex (EC 3.4.99.46) chain Y7 - yeast (Saccharomyces cerevisiae) ; Chain B, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain P, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; (X56731) proteasome Y7 subunit [Saccharomyces cerevisiae] ; (Z46660) proteasome component Y gene, len: 250, CAI:0.15, PRCX_ yeast P23639 [Saccharomyces cerevisiae]"
18925	ENU02719	ANI50C3665	47-66	649-669	NAP		g2995341		121	5.00E-27	41	39	(AL022244) hypothetical protein [Schizosaccharomyces pombe]
18926	ENU02720	ANI61C3667:	33-56	632-656	NAP		g120593	319	74	8.00E-13			L-fucose permease ; fucose permease - Escherichia coli ; (X15025) fucP ORF (AA 1-438) [Escherichia coli] ; (U29581) L-fucose permease [Escherichia coli] ; (AE000364) fucose permease [Escherichia coli] (Z98601) mitochondrial 40s ribosomal protein mtp4. [Schizosaccharomyces pombe]
18927	ENU02721	ANI61C1677:	22-49	626-645	NAP		g4038620	521	186	1.00E-46	51	83	Elongation factor 2 (EF-2) ; (D83975) elongation factor 2 [Schizosaccharomyces pombe] ; (D83976) elongation factor 2 [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans]
18928	ENU02722	ANI61C5936:	72-92	677-696	NAP		g3122054	1121	364	e-100	77	26	(AL035065) protein translation factor sui1. [Schizosaccharomyces pombe]
18929	ENU02723	ANI61C5502:	27-47	617-652	NAP		g1870209	961	265	e-104	86	40	
18930	ENU02724	ANI61C6250:	54-74	655-679	NAP		g4106682	245	59	7.00E-11	59	82	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18931	ENU02725	ANI61C9933:	61-80	666-687	NAP		g1175363	535	198	3.00E-50	44	70	hypothetical protein H11014 ; hypothetical protein H11014 - Haemophilus influenzae (strain Rd KW20) ; (U32782) conserved hypothetical protein [Haemophilus influenzae Rd]
		144..812											
18932	ENU02726	ANI61C8405:	22-43	623-649	NAP		g3925782	333	146	1.00E-34	48	91	(AL034353) putative 60s ribosomal protein [Schizosaccharomyces pombe]
		2151..1485											
18933	ENU02727	ANI61C205:1	45-66	653-672	NAP		g4581877	144	92	3.00E-18	30	40	(AF120278) proline dehydrogenase; PRODH [Homo sapiens]
		473..2142											
18934	ENU02728	ANI61C3750:	33-54	640-660	NAP		g2367392	873	118	4.00E-26	34	30	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]
		1137..468											
18935	ENU02729	ANI61C1118	32-52	641-660	NAP		g488189	367	87	7.00E-22	29	51	(U00063) weakly similar to R. rickettsii protein P34 [Caenorhabditis elegans]
		4:5694..5023											
18936	ENU02730	ANI61C4356:	23-42	632-651	NAP		g1020413	319	145	4.00E-34	34	41	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
		86..756											
18937	ENU02731	ANI61C8178:	66-85	676-695	NAP		g1173334	401	157	9.00E-38	52	82	RAS-like GTP-binding protein RYL2 ; (L06970) ras-like protein [Yarrowia lipolytica]
		1686..1015											
18938	ENU02732	ANI61C9465:	22-52	631-651	NAP		g2226413	148	41	0.00002	43	65	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
		4908..4237											
18939	ENU02733	ANI61C1088	57-77	667-687	NAP		g1706202	656	152	1.00E-61	70	87	Cutinase precursor (L1) ; (D38311) Cutinase [Aspergillus oryzae]
		5:1706..2378											
18940	ENU02734	ANI61C9472:	44-64	646-674	NAP		g464287	410	145	2.00E-34	56	82	"NADH-ubiquinone oxidoreductase 21 KD subunit (complex 1-21KD) (Cl- 21KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 20.9K chain - Neurospora crassa ; (X60829) NADH dehydrogenase, 21 kDa subunit [Neurospora crassa]"
		810..138											
18941	ENU02735	ANI61C4807:	25-47	631-655	NAP		g418596	431	91	3.00E-19	56	93	putative 40S ribosomal protein YHR148W ; hypothetical protein YHR148w - yeast (Saccharomyces cerevisiae) ; (X69480) uORF1 [Saccharomyces cerevisiae] ; (U10397) Yhr148wp [Saccharomyces cerevisiae] (AE000955) 2-nitropropane dioxygenase (necd2) [Archaeoglobus fulgidus]
		3495..2823											
18942	ENU02736	ANI61C11:25	22-53	632-652	NAP		g2648355	318	73	3.00E-17	34	72	
		73..3245											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18943	ENU02737	ANI61C5118:	71-91	675-702	NAP		g2492756	213	47	0.0001			putative stigmastocystin biosynthesis ketoreductase STCE ; (U34740)
		756..83											putative ketoreductase [Emericella nidulans]
18944	ENU02738	ANI61C1354:	23-53	635-654	NAP		g729965	467	124	9.00E-39	66	44	"saccharopine dehydrogenase [NAD+, L-lysine forming] (lysine--2-oxoglutarate reductase) (SDH) ; saccharopine dehydrogenase (NAD+, L-lysine-forming) - yeast (Yarrowia lipolytica) (strain W29) ; (M34929)
		82..755											saccharopine dehydrogenase [Yarrowia lipolytica] "
18945	ENU02739	ANI61C3530:	26-45	638-657	NAP		g3420982	502	112	2.00E-24	57	52	(Z97628) Similarity to Brugia peptidylprolyl isomerase (TR:G984562) [Caenorhabditis elegans] ; (Z81080) Similarity to Brugia peptidylprolyl isomerase (TR:G984562) [Caenorhabditis elegans]
		5..678											(AL034382) putative ras-related GTP-binding protein [Schizosaccharomyces pombe]
18946	ENU02740	ANI61C5321:	57-76	663-689	NAP		g3947880	533	120	4.00E-49	62	98	hypothetical protein YDR071c - yeast (Saccharomyces cerevisiae) ; (Z46796) unknown [Saccharomyces cerevisiae] ; (Z74367) ORF YDR071c
		303..977											[Saccharomyces cerevisiae]
18947	ENU02741	ANI61C566:1	22-40	629-654	NAP		g1077519	163	85	4.00E-16	36	98	hypothetical protein YDR071c - yeast (Saccharomyces cerevisiae) ; (Z46796) unknown [Saccharomyces cerevisiae] ; (Z74367) ORF YDR071c
		660..986											[Saccharomyces cerevisiae]
18948	ENU02742	ANI61C7088:	22-57	636-655	NAP		g626443	140	68	5.00E-11	32	96	hypothetical protein YLR193c - yeast (Saccharomyces cerevisiae) ; (U14913) Ylr193cp [Saccharomyces cerevisiae]
		2908..3583											(Z69637) predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI)
18949	ENU02743	ANI61C1134	54-73	668-687	NAP		g3876766	272	104	2.00E-23	45	86	YCAC (SW:YCAC_ECOLI)
		4:2479..1804											[Caenorhabditis elegans]
18950	ENU02744	ANI61C1253:	25-44	637-659	NAP		g2995384	706	242	2.00E-71	83	82	(A1004810) cytochrome P450 monooxygenase [Zea mays]
		7105..6501											(AL034463) hypothetical protein [Schizosaccharomyces pombe]
18951	ENU02745	ANI61C7538:	22-56	638-657	NAP		g4007800	323	61	3.00E-15	43	92	[Schizosaccharomyces pombe]
		242..920											(K01609) gall [Saccharomyces carlsbergensis]
18952	ENU02746	ANI61C9073:	30-49	634-665	NAP		g171567	338	131	7.00E-34	35	42	
		3923..3246											



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18953	ENU02747	AN161C7240:	70-92	686-705	NAP		g3006178	279	89	3.00E-17	32	32	(AL022304) putative mma transport regulator [Schizosaccharomyces pombe]
18954	ENU02748	AN161C3687:	61-80	670-697	NAP		g3169083	261	108	4.00E-23	36	66	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18955	ENU02749	AN161C1049	31-51	648-667	NAP		g3041738	1512	81	2.00E-51	61	35	"T-complex protein 1, ETA subunit (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF interacting protein); (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]"
18956	ENU02750	AN161C5629:	40-59	643-676	NAP		g100489	133	72	3.00E-12			transposase Tam3 - garden snapdragon transposon Tam3; (X55078) Tam3-transposase [Antirrhinum majus]; (AB013982) transposase [Antirrhinum majus]; (AB013983) transposase [Antirrhinum majus]; (AB013984) transposase [Antirrhinum majus]; (AB013986) transposase [Antirrhinum majus]; (AB013990) transposase [Antirrhinum majus]; (AB013991) transposase [Antirrhinum majus]; (AB013995) transposase [Antirrhinum majus]; (AB013997) transposase [Antirrhinum majus]
18957	ENU02751	AN161C7852:	57-88	664-693	NAP		g3650378	1057	154	5.00E-37	51	10	(AL031740) putative rRNA biogenesis protein; trp5 homolog; multiple S1 ma binding domain protein [Schizosaccharomyces pombe]
18958	ENU02752	AN161C5415:	49-70	668-687	NAP		g2414668	256	86	3.00E-16	39	85	(Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe]
18959	ENU02753	AN161C7921:	69-88	678-708	NAP		g2501555	296	100	3.00E-24	38	62	possible apospory-associated protein C; (U13148) possible apospory-associated protein [Pennisetum ciliare] (A131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga menziesii]
18960	ENU02754	AN161C7147:	33-53	639-673	NAP		g4090259	218	83	2.00E-15	37	85	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18961	ENU02755	AN161C7273:	22-47	642-662	NAP		g1723256	227	84	2.00E-19	34	93	"hypothetical 23.0 KD protein C3F10.12C in chromosome I; (Z69369) SPAC3F10.12c, unknown, 201, similar to transcription factors and SW:CBF1_yeast P17106 centromere-binding protei n 1 (39.8% identity in 113 aa overlap), contains PS00038 Myc-type, 'helix-loop-helix' dimerization dom..."
18962	ENU02756	AN161C7786:	25-47	647-666	NAP		g1363314	213	53	2.00E-11	36	19	probable cell division control protein p55CDC - rat; (U05341) p55CDC [Rattus norvegicus]
18963	ENU02757	AN161C1129	54-75	674-695	NAP		g549750	253	67	1.00E-10	39	71	hypothetical 29.4 KD protein in STE6-LOS1 intergenic region; hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae); (Z28207) ORF YKL207w [Saccharomyces cerevisiae]
18964	ENU02758	AN161C566:5	22-50	645-664	NAP		g1679882	1002	279	2.00E-74	61	31	(L35484) acetylglutamate synthase [Neurospora crassa]
18965	ENU02759	AN161C6119:	23-44	647-666	NAP		g3123033	365	90	3.00E-31	37	86	vacuolar protein sorting-associated protein VPS28; hypothetical protein YPL065w - yeast (Saccharomyces cerevisiae); (U39205) Lpe5p [Saccharomyces cerevisiae]; (U50630) Vps28p [Saccharomyces cerevisiae]
18966	ENU02760	AN161C8915:	46-79	664-690	NAP		g1633466	111	56	0.000000	27	79	"Crystal Structure Of Bacteriorhodopsin In Purple Membrane ; Structure Of Bacteriorhodopsin At 3.0 Angstrom Determined By Electron Crystallography ; Chain A, X-Ray Structure Of The Bacteriorhodopsin Trimerlipid Complex ; Bacteriorhodopsinlipid complex " (AL031743) phosphatidylethanolamine methyltransferase. [Schizosaccharomyces pombe]
18967	ENU02761	AN161C6486:	22-51	638-666	NAP		g3650386	1486	102	3.00E-21	38	20	putative oxidoreductase precursor BLI-4 ; (X89499) bli-4 protein [Neurospora crassa]
18968	ENU02762	AN161C6019:	35-59	662-682	NAP		g3023397	320	160	8.00E-39	41	54	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18969	ENU02763	ANI61C1042	32-51	660-679	NAP		g1730832	258	111	6.00E-24	37	61	hypothetical 31.6 KD protein in SIN4-URE2 intergenic region ; hypothetical protein YNL232w - yeast (Saccharomyces cerevisiae) ; (Z69381) N1154 [Saccharomyces cerevisiae] ; (Z71508) ORF YNL232w [Saccharomyces cerevisiae] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous] ubiquitin carboxyl-terminal hydrolase 5 (ubiquitin thiolesterase 5) (ubiquitin-specific processing protease 5) (DEubiquitinating enzyme 5) ; ubiquitin-specific proteinase UBP5 (EC 3.4.-.-) - yeast (Saccharomyces cerevisiae) ; (U10082) ubiquitin-specific protease [Saccharomyces cerevisiae] ; (U18917) Ubp5p: ubiquitin-specific protease [Saccharomyces cerevisiae] (AE000848) ribonuclease PH [Methanobacterium thermoautotrophicum] (Z99165) dehydrogenase [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] "Phenylalanyl-TRNA synthetase beta chain cytoplasmic (phenylalanine--TRNA ligase beta chain) ; phenylalanine--TRNA ligase (EC 6.1.1.20) beta chain, cytosolic - yeast (Saccharomyces cerevisiae) ; (D50617) cytoplasmic phenylalanyl-TRNA synthetase beta chain [Saccharomyces cerevisiae] "
		7:1698..2387											
18970	ENU02764	ANI61C191:1	22-52	647-670	NAP		g2804298	89	68	5.00E-11	26	40	
		251..561											
18971	ENU02765	ANI61C8095:	72-92	702-721	NAP		g731042	398	118	1.00E-32			
		52..743											
18972	ENU02766	ANI61C6486:	55-74	675-704	NAP		g2621768	73	40	0.0003	31	72	
		5121..5812											
18973	ENU02767	ANI61C9140:	22-55	651-672	NAP		g2408060	306	133	1.00E-30	44	66	
		81..773											
18974	ENU02768	ANI61C1828:	56-76	687-706	NAP		g2635242	347	102	3.00E-21	28	65	
		2180..1488											
18975	ENU02769	ANI61C8024:	58-77	680-708	NAP		g1174509	898	315	2.00E-85	71	41	
		152..844											

# Database Overview

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18976	ENU02770	ANI61C4361:	67-86	696-718	NAP		g586321		47	0.000002			hypothetical 25.3 KD protein in RIM2-MS11 intergenic region ; hypothetical protein YBR193c - yeast (Saccharomyces cerevisiae) ; (Z21487) unknown product [Saccharomyces cerevisiae] ; (Z36062) ORF YBR193c [Saccharomyces cerevisiae] Potential proteasome component C5 (multicatalytic endopeptidase complex subunit C5) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain PRS3 - yeast (Saccharomyces cerevisiae) ; (M34777) proteasome subunit [Saccharomyces cerevisiae] ; (D00845) proteasome subunit [Saccharomyces cerevisiae] ; (X78214) PRS3 [Saccharomyces cerevisiae] ; (Z35802) ORF YBL041w [Saccharomyces cerevisiae] (Y15013) copalyl diphosphate synthase [Gibberella fujikuroi] (AB024617) isochloroderm C-15 hydroxylase [Gibberella zeae] (Z81110) predicted using Genefinder; cDNA EST EMBL.D76086 comes from this gene; cDNA EST EMBL.T00045 comes from this gene; cDNA EST EMBL.D73101 comes from this gene; cDNA EST EMBL.C077... (AF063095) SELIL [Mus musculus]
18977	ENU02771	ANI61C3960:	23-58	646-675	NAP		g130882	593	259	2.00E-68			
18978	ENU02772	ANI61C7782:	60-79	690-712	NAP		g3549899	1287	146	1.00E-34	32	23	
18979	ENU02773	ANI61C548:	69-88	698-721	NAP		g4589927	232	52	3.00E-13	32	39	
18980	ENU02774	ANI61C5279:	28-47	662-681	NAP		g3879255	261	117	7.00E-26	34	56	
18981	ENU02775	ANI61C6626:	69-88	704-723	NAP		g4159995	577	93	2.00E-18			
18982	ENU02776	ANI61C4759:	46-65	680-700	NAP		g3135013	808	323	1.00E-87	66	25	
18983	ENU02777	ANI61C322:	52-71	688-707	NAP		g586554	160	56	0.000000	32	92	
											3		(AJ005963) 100 kDa protein [Ajellomyces capsulatus] "hypothetical 21.1 KD protein in FUS1-AGP1 intergenic region ; hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae) ; (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18984	ENU02778	ANI61C8274:	72-93	708-727	NAP		g1171666	303	70	3.00E-16	51	87	NADH-ubiquinone oxidoreductase 14.8 KD subunit (complex I-14.8KD) (CI-14.8KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) - Neurospora crassa ; (X76344) NADH dehydrogenase (ubiquinone) [Neurospora crassa]
18985	ENU02779	ANI61C7893:	43-62	679-701	NAP		g1708501	245	73	8.00E-22	36	11	Integrin alpha chain-like protein (alpha-INT1) ; (U35070) integrin-like protein alpha Int1p [Candida albicans]
18986	ENU02780	ANI61C301:5	24-43	650-684	NAP		g1064798	256	83	6.00E-20	40	47	(D78193) homologous to gp:PSEFD_1 (formaldehyde dehydrogenase) [Bacillus subtilis] ; (Z99124) similar to formaldehyde dehydrogenase [Bacillus subtilis]
18987	ENU02781	ANI61C1078	57-82	697-717	NAP		g3152652	365	155	4.00E-37	38	49	"(AF064870) endo-1,3(4)-beta-glucanase [Xanthophyllomyces dendrorhous]"
18988	ENU02782	ANI61C3321:	57-77	698-717	NAP		g1723660	211	76	6.00E-20	33	89	hypothetical 27.6 KD protein in RPL26B-ACB1 intergenic region ; probable membrane protein YGR036c - yeast (Saccharomyces cerevisiae) ; (Z72821) ORF YGR036c [Saccharomyces cerevisiae]
18989	ENU02783	ANI61C301:5	24-43	650-684	NAP		g1064798	256	83	6.00E-20	40	47	(D78193) homologous to gp:PSEFD_1 (formaldehyde dehydrogenase) [Bacillus subtilis] ; (Z99124) similar to formaldehyde dehydrogenase [Bacillus subtilis]
18990	ENU02784	ANI61C3956:	42-74	677-703	NAP		g3702646	401	66	3.00E-10			(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
18991	ENU02785	ANI61C6073:	23-42	659-684	NAP		g2132916	448	136	2.00E-31	43	32	probable membrane protein YOR206w - yeast (Saccharomyces cerevisiae) ; (Z75114) ORF YOR206w [Saccharomyces cerevisiae]
18992	ENU02786	ANI61C2284:	70-90	707-731	NAP		g3766371	328	152	2.00E-36	40	90	(AL031907) hypothetical protein [Schizosaccharomyces pombe]
18993	ENU02787	ANI61C7986:	63-82	705-724	NAP		g3006189	646	81	4.00E-32	63	62	(AL022304) 60s ribosomal protein 17-c. [Schizosaccharomyces pombe]

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18994	ENU02788	ANI61C7899	40-59	680-702	NAP			g417305	788	113	2.00E-30	42	35	"mannosyl-oligosaccharide alpha-1,2-mannosidase (MAN(9)-alpha-mannosidase) ; alpha-mannosidase MNS1 (EC 3.2.1.-) - yeast (Saccharomyces cerevisiae) ; (M63598) alpha-mannosidase [Saccharomyces cerevisiae] ; (Z49631) ORF YJR131w [Saccharomyces cerevisiae] "
		4999..4295												probable membrane protein YLR130c - yeast (Saccharomyces cerevisiae) ; (X91258) L3120 [Saccharomyces cerevisiae] ; (U53881) Ylr130cp [Saccharomyces cerevisiae] ; (Z73302) ORF YLR130c [Saccharomyces cerevisiae]
18995	ENU02789	ANI61C6615	72-96	715-734	NAP			g1363710	345	90	2.00E-17	27	54	(D84656) ORF N118 [Schizosaccharomyces pombe]
		2346..1642												general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
18996	ENU02790	ANI61C8963	62-81	706-725	NAP			g1507666	100	38	0.073			(AF104986) calmodulin [Magnaporthe grisea]
		3632..4337												choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
18997	ENU02791	ANI61C7925	59-82	699-723	NAP			g1703215	374	77	2.00E-16	31	37	hypothetical 24.0 KD protein in EMP47-SEC53 intergenic region ; probable membrane protein YFL046w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL046W [Saccharomyces cerevisiae]
		1866..2573												(AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]
18998	ENU02792	ANI61C1046	24-46	662-688	NAP			g4028590	625	144	3.00E-54	89	99	
		1:848..1554												
18999	ENU02793	ANI61C1518	34-63	668-698	NAP			g117619		80	2.00E-17			
		2666..1960												
19000	ENU02794	ANI61C7112	66-85	710-730	NAP			g1175951	328	114	1.00E-25	40	91	
		2765..3471												
19001	ENU02795	ANI61C9541	61-92	700-726	NAP			g4160573	199	86	3.00E-16	33	24	
		60..767												

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19002	ENU02796	ANI61C7325:	24-43	670-689	NAP		g3417433	411	117	9.00E-26	46	57	(AL031262) putative transcription factor [Schizosaccharomyces pombe]
19003	ENU02797	3090..2383 ANI61C3136:	22-52	668-687	NAP		g3914054	783	256	1.00E-67	53	30	MUTS protein homolog 1 : (Z98559) dna mismatch repair muts family [Schizosaccharomyces pombe]
19004	ENU02798	1862..1155 ANI61C7329:	22-53	663-687	NAP		g4160343	482	102	8.00E-28	37	69	(AL035216) similar to rat synaptic glycoprotein sc2 [Schizosaccharomyces pombe]
19005	ENU02799	1958..1251 ANI61C7521:	40-59	687-706	NAP		g117093	285	69	4.00E-13	50	86	cytochrome C oxidase polypeptide VI precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain VI precursor - yeast (Saccharomyces cerevisiae) ; (M10138) cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] ; (U00062) Cox6p: cytochrome c oxidase subunit VI [Saccharomyces cerevisiae]
19006	ENU02800	898..187 ANI61C1008	34-53	680-700	NAP		g1764155	252	134	5.00E-31	42	39	(U16782) chlorophenol monooxygenase [Ralstonia eutropha]
19007	ENU02801	8:14..556 ANI61C4037:	67-87	701-736	NAP		g992654	72	46	9.00E-10	45	8	(U33115) high copy suppressor of polymerase alpha mutations [Saccharomyces cerevisiae]
19008	ENU02802	1171..1882 ANI61C8195:	22-39	668-691	NAP		g126652	315	144	9.00E-35	38	71	"lysozyme M1 precursor (1,4-beta-N-acetylmuramidase M1) ; lysozyme (EC 3.2.1.17) M1 precursor - Streptomyces globisporus ; (M30645) N-acetylmuramidase M1 precursor [Streptomyces globisporus]" (U85498) glutamate-cysteine ligase catalytic subunit [Mus musculus]
19009	ENU02803	82..793 ANI61C2626:	23-45	670-692	NAP		g1945070	727	223	9.00E-58	51	34	hypothetical protein YOR252w - yeast (Saccharomyces cerevisiae) ; (Z75160) ORF YOR252w [Saccharomyces cerevisiae]
19010	ENU02804	2735..2631 ANI61C3329:	71-91	714-741	NAP		g2132100		75	4.00E-13	30	87	mitochondrial uncoupling protein homolog YKL120w - yeast (Saccharomyces cerevisiae) ; (L04948) mitochondrial transporter protein [Saccharomyces cerevisiae] ; (Z28120) ORF YKL120w [Saccharomyces cerevisiae]
19011	ENU02805	108..820 ANI61C8183:	34-53	684-704	NAP		g417500	568	127	6.00E-44	55	62	mitochondrial carrier protein PMT ; mitochondrial uncoupling protein homolog YKL120w - yeast (Saccharomyces cerevisiae) ; (L04948) mitochondrial transporter protein [Saccharomyces cerevisiae] ; (Z28120) ORF YKL120w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19012	ENU02806	AN161C1120	55-78	704-725	NAP		g2833337	103	73	2.00E-12	30	36	Dihydrofolate reductase / thymidylate synthase (DHFR-TS) ; (U20781)
		5:6686..5974											dihydrofolate reductase-thymidylate synthase [Trypanosoma brucei] (AJ009973) hexokinase [Aspergillus niger]
19013	ENU02807	AN161C2275:	65-86	716-735	NAP		g4140255	2000	401	e-111	83	48	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
		1667..955											choline transport protein [Saccharomyces cerevisiae] ; (Z772599)
19014	ENU02808	AN161C559:8	22-49	664-693	NAP		g117619		37	0.17			ORF YGL077c [Saccharomyces cerevisiae]
		37..124											(AF022892) orotidine monophosphate pyrophosphorylase [Coccidioides immitis]
19015	ENU02809	AN161C7117:	27-46	676-698	NAP		g4249578	892	355	2.00E-97	75	97	"(S76267) Sng2 homolog=brf1 [Schizosaccharomyces pombe=fission yeast, Peptide, 1530 aa]
		1674..961											[Schizosaccharomyces pombe] "
19016	ENU02810	AN161C414:1	26-51	675-698	NAP		g913016	332	124	3.00E-32	37	14	[Schizosaccharomyces pombe] "
		4..724											(U41625) coded for by C. elegans cDNA yk52e10.5; coded for by C. elegans cDNA yk50f4.3; coded for by C. elegans cDNA yk50f4.5; Similar to acetyl-coenzyme A synthetase. [Caenorhabditis elegans] (AF036871) annexin XIV [Neurospora crassa]
19017	ENU02811	AN161C1124:	22-45	667-694	NAP		g1118129	524	88	4.00E-27	41	25	hypothetical protein YOL135c - yeast (Saccharomyces cerevisiae) ; (Z74877)
		887..1601											ORF YOL135c [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae]
19018	ENU02812	AN161C2113:	71-90	725-744	NAP		g3004934	490	144	6.00E-34	35	49	acid proteinase capC precursor - chesnut blight fungus ; (X83997) acid proteinase [Cryphonectria parasitica]
		847..132											
19019	ENU02813	AN161C8918:	54-74	697-727	NAP		g2132018	288	96	2.00E-25	36	94	
		643..1358											
19020	ENU02814	AN161C8241:	30-49	673-704	NAP		g2133287	421	189	2.00E-47	43	85	
		1541..2257											



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19021	ENU02815	ANI61C952:1	34-68	683-709	NAP		g130582	173	92	4.00E-18	28	17	Retrovirus-related pol polyprotein from transposon TNT 1-94 [contains: protease; reverse transcriptase; endonuclease]; hypothetical protein - common tobacco; (X13777) ORF [Nicotiana tabacum]
		569..852											
19022	ENU02816	ANI61C9559: 23-58		678-698	NAP		g3913768	102	61	0.000000	28	98	phosphoglycolate phosphatase (PGP); (AE000735) phosphoglycolate phosphatase [Aquifex aeolicus]
		713..1430								009			
19023	ENU02817	ANI61C6527: 66-84		722-741	NAP		g3122361	271	116	2.00E-25	42	86	putative lipote-protein ligase B (lipote biosynthesis protein B); (Z98980) hypothetical protein [Schizosaccharomyces pombe]
		2787..2619											
19024	ENU02818	ANI50C2369 01_1:30..748	22-43	672-698	NAP		g118126		59	0.000000	36	90	regulatory protein CYS-3; regulatory protein cys-3 - Neurospora crassa; (M26008) cys-3 [Neurospora crassa]
									05				
19025	ENU02819	ANI61C1250: 36-55		693-712	NAP		g2499588	1079	248	e-100	98	62	cell division control protein 2 (cyclin-dependent protein kinase); (U07169) protein kinase functional homolog of cdc2 [Emmentella nidulans]
		3498..2780											
19026	ENU02820	ANI61C1099 9:1170..1888	44-65	689-720	NAP		g2804298	372	85	4.00E-16	32	28	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
19027	ENU02821	ANI61C1040 27-47		684-703	NAP		g2132880	284	83	8.00E-23	27	89	probable membrane protein YOR087w - yeast (Saccharomyces cerevisiae); (Z74995) ORF YOR087w [Saccharomyces cerevisiae]
		9:1373..655											
19028	ENU02822	ANI61C5788: 22-49		678-698	NAP		g131031	328	113	1.00E-29	41	96	putative PRT1 protein; probable PRT1 protein - yeast (Hansenula polymorpha); (X15111) put. PRT1 protein (AA 1-221) (1 is 1st base in codon) [Pichia angusta]
		5396..6114											
19029	ENU02823	ANI61C1758: 72-92		729-748	NAP		g2497056	214	86	3.00E-16	36	47	putative dioxigenase YLL057C; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
		10004..9286											
19030	ENU02824	ANI61C1211: 22-41		680-699	NAP		g3183014	706	150	3.00E-65	65	85	GTP cyclohydrolase I (GTP-CH-I); (Z98849) gtp cyclohydrolase I [Schizosaccharomyces pombe]
		821..102											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19031	ENU02825	AN161C8770:	47-67	698-724	NAP		g2981719	776	91	1.00E-30	44	30	Crystal Structures Of The Copper-Containing Amine Oxidase From <i>Arthrobacter Globiformis</i> In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone ; Crystal Structures Of The Copper-Containing Amine Oxidase From <i>Arthrobacter Globiformis</i> In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone
19032	ENU02826	AN161C6467:	22-47	681-700	NAP		g461926	228	69	5.00E-22	33	95	Haloacetate dehalogenase H-2 ; haloacetate dehalogenase (EC 3.8.1.3) H-2 - <i>Moraxella</i> sp. plasmid pUO1 ; (D90423) haloacetate dehalogenase H-2 [ <i>Moraxella</i> sp.]
19033	ENU02827	AN161C9085:	57-76	716-735	NAP		g2506921	158	45	0.0006	37	55	"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613) dioxygenase [ <i>Escherichia coli</i> ] ; (U73857) dioxygenase [ <i>Escherichia coli</i> ] ; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [ <i>Escherichia coli</i> ] "
19034	ENU02828	AN161C3566:	44-65	697-723	NAP		g731439	132	54	0.000001	28	91	hypothetical 25.6 KD protein in NTF2-SRP1 intergenic region ; hypothetical protein YER010c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U18778) Yer010cp [ <i>Saccharomyces cerevisiae</i> ] (AF051914) C-4 methyl sterol oxidase [ <i>Candida albicans</i> ] (AL035521) hypothetical protein [ <i>Arabidopsis thaliana</i> ] (Z98056) putative glyoxylate pathway regulator [ <i>Schizosaccharomyces pombe</i> ] (Z98600) hypothetical atp-dependent transporter [ <i>Schizosaccharomyces pombe</i> ]
19035	ENU02829	AN161C353:	27-56	688-706	NAP		g2970627	908	304	4.00E-82	60	71	
19036	ENU02830	AN161C8203:	23-44	682-702	NAP		g4455171	303	146	1.00E-34	33	27	
19037	ENU02831	AN161C7700:	57-76	717-736	NAP		g2281979	362	131	5.00E-30	46	64	
19038	ENU02832	AN161C9556:	26-45	687-706	NAP		g2330757	649	259	4.00E-68	61	86	

# Database Selection

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19039	ENU02833	AN161C1110	42-66	703-722	NAP		g585896	267	130	1.00E-29	38	94	"probable mitochondrial 60S ribosomal protein L16 precursor ; ribosomal protein L16 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X78214) L16 ribosomal protein [Saccharomyces cerevisiae] ; (Z35799) ORF YBL038w [Saccharomyces cerevisiae]"
19040	ENU02834	AN161C590:8	45-65	707-726	NAP		g549607	409	125	2.00E-36	38	35	hypothetical 74.7 KD TRP-ASP repeats containing protein in DAL80-GAP1 intergenic region ; hypothetical protein YKR036c - yeast (Saccharomyces cerevisiae) ; (Z28261) ORF YKR036c [Saccharomyces cerevisiae] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] (AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana] hypothetical monooxygenase Y4FC ; (AE000072) Y4fC [Rhizobium sp. NGR234] (AL031852) short-chain dehydrogenase [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans] ALP11 protein ; (Z69727) homolog of co-factor B [Schizosaccharomyces pombe] ; (AB008750) Alp11 [Schizosaccharomyces pombe] "hypothetical 29.0 KD protein in PWP2-SUP61 intergenic region ; probable membrane protein YCR059c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR059c, len:258 [Saccharomyces cerevisiae]" probable glutamate 5-kinase (gamma-glutamyl kinase) (GK) ; (Z98597) hypothetical glutamate 5-kinase [Schizosaccharomyces pombe]
19041	ENU02835	AN161C6543: 27-52	3639..2915	690-709	NAP		g2414650	346	93	2.00E-31	69	93	
19042	ENU02836	AN161C7500: 22-51	2405..1681	684-704	NAP		g3426048	540	167	6.00E-52	51	50	
19043	ENU02837	AN161C4138: 57-76	622..1346	719-739	NAP		g2496621	310	118	3.00E-26	50	64	
19044	ENU02838	AN161C1289: 23-48	12..737	685-706	NAP		g3738145	147	90	1.00E-17	31	64	
19045	ENU02839	AN161C5187: 60-80	2678..1953	721-743	NAP		g1870209	857	132	4.00E-34	38	42	
19046	ENU02840	AN161C3158: 50-69	1742..2468	715-734	NAP		g1723421	318	87	1.00E-16	34	78	
19047	ENU02841	AN161C6895: 23-43	1106..1832	688-707	NAP		g140519	120	74	9.00E-13	29	72	
19048	ENU02842	AN161C5862: 25-49	104..830	684-709	NAP		g3183130	554	200	1.00E-50	52	52	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19049	ENNU02843	AN161C3285:	33-52	700-718	NAP		g3850101	378	137	7.00E-32	47	93	(AL033388) putative ma-binding protein [Schizosaccharomyces pombe]
19050	ENNU02844	2094..1367 AN161C459:7	60-79	726-745	NAP		g3135988	652	69	3.00E-19	46	37	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19051	ENNU02845	441..6714 AN161C5557:	56-77	723-742	NAP		g2501603	311	123	9.00E-28	38	31	hypothetical 77.0 KD protein in HES1-SEC63 intergenic region ; hypothetical protein YOR243c - yeast (Saccharomyces cerevisiae) ; (Z75151) ORF YOR243c [Saccharomyces cerevisiae]
19052	ENNU02846	AN161C1617:	23-41	688-709	NAP		g1806234		63	1.00E-16			(Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis]
19053	ENNU02847	47..774 AN161C7616:	64-83	731-750	NAP		g2697132	287	87	3.00E-22	36	84	(AF036580) necrosis and ethylene inducing peptide [Fusarium oxysporum f. sp. erythroxyli]
19054	ENNU02848	1734..1006 AN161C990:2	69-88	735-755	NAP		g1491795	486	201	6.00E-51	38	26	"(U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus]"
19055	ENNU02849	444..1716 AN161C3212:	34-53	699-720	NAP		g585695	232	120	1.00E-26	32	41	Pisatin demethylase (cytochrome P450 57A2) ; pisatin demethylase - fungus (Nectria haematococca) ; (X73145) pisatin demethylase [Nectria haematococca]
19056	ENNU02850	AN161C1640:	34-53	699-720	NAP		g3006187	283	134	5.00E-31	35	74	(AL022304) hypothetical protein [Schizosaccharomyces pombe]
19057	ENNU02851	1744..1016 AN161C3047:	56-77	723-742	NAP		g1723441	353	95	6.00E-19	40	51	hypothetical 36.3 KD protein C56F8.09 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe]
19058	ENNU02852	4114..3386 AN161C3602:	47-66	707-733	NAP		g731385	269	63	3.00E-17	39	73	[Schizosaccharomyces pombe] hypothetical 33.7 KD protein in ISC10 3'region ; hypothetical protein YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae]
19059	ENNU02853	6005..6734 AN161C2954:	48-67	714-735	NAP		g2258125	164	64	0.000000	29	39	(Z83828) AmMst-1 [Armatia muscaria]
19060	ENNU02854	27..756 AN161C8514:	67-87	722-755	NAP		g3287949	418	147	3.00E-39	41	30	hypothetical 79.5 KD protein C17A5.12 in chromosome I ; (Z98849) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19061	ENU02855	AN161C943:1	33-52	700-721	NAP			g140459	61	0.000000	01			"hypothetical 30.7 KD protein in RVS161-ADP1 intergenic region ; hypothetical protein YCR010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR010c, len:283 [Saccharomyces cerevisiae]"
19062	ENU02856	AN161C7480:1	70-88	735-759	NAP			g3915154	245	102	3.00E-21	33	39	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichoides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichoides] "probable ATP-dependent permease precursor ; ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae) ; (X59720) YCR011c, len:1049 [Saccharomyces cerevisiae]"
19063	ENU02857	AN161C6213:1	69-100	740-758	NAP			g113449	552	152	2.00E-36	47	21	hypothetical 34.9 KD protein in RPL44-DCD1 intergenic region ; hypothetical protein YHR142w - yeast (Saccharomyces cerevisiae) ; (U10397) Yhr142wp [Saccharomyces cerevisiae] (AB013443) cytochrome P450 [Coprinus cinereus] putative mitochondrial carrier protein [Candida albicans] putative para-hydroxybenzoate—polyprenyltransferase precursor (PHB:polyprenyltransferase) ; (Z69728) unknown [Schizosaccharomyces pombe]
19064	ENU02858	AN161C9775:1	55-75	724-744	NAP			g731723	589	178	5.00E-44	46	68	Tryptophan synthase ; tryptophan synthase (EC 4.2.1.20) - Neurospora crassa ; (J04594) tryptophan synthetase [Neurospora crassa] acetyl-hydrolyase ; (M64783) acetyl-hydrolyase [Streptomyces hygroscopicus] (AL049522) putative phosphatase component [Schizosaccharomyces pombe]
19065	ENU02859	AN161C1733:1	72-99	742-762	NAP			g3721844	296	73	5.00E-25	36	40	
19066	ENU02860	AN161C7086:1	22-41	693-712	NAP			g3859687	527	150	8.00E-36	53	77	
19067	ENU02861	AN161C920:1	46-65	717-737	NAP			g1706003	76	3.00E-13				
19068	ENU02862	AN161C2401:1	40-59	711-731	NAP			g136372	2405	310	e-109	80	34	
19069	ENU02863	AN161C5992:1	69-87	728-760	NAP			g1352065	69	2.00E-11				
19070	ENU02864	AN161C933:1	25-54	695-717	NAP			g4539598	322	76	9.00E-15	33	62	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19071	ENU02865	AN161C7676:	68-87	728-760	NAP		g3123232	643	152	1.00E-58	53	78	Description general stress protein 39 (GSP39) ; (AB001488) belongs to the insect-type alcohol dehydrogenase / ribitol dehydrogenase family. [Bacillus subtilis] ; (Z99106) similar to alcohol dehydrogenase [Bacillus subtilis] "Chain N, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain 2, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution "
19072	ENU02866	AN161C8467:	23-48	694-716	NAP		g3114282	484	163	1.00E-39	47	93	
19073	ENU02867	AN161C9642:	40-59	706-735	NAP		g1175965	388	171	5.00E-42	41	99	hypothetical 25.2 KD protein in TH15 5'region and in TH112 5'region ; hypothetical protein YFL061w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL061W [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae] ; (Z71611) ORF YNL335w [Saccharomyces cerevisiae] (Y11113) endoglucanase IV [Hypocrea jecorina] (AL034583) hypothetical protein [Schizosaccharomyces pombe] (D85230) hypothetical protein [Plectonema boryanum] hypothetical 69.8 KD protein in BDF1-SFP1 intergenic region ; hypothetical protein YLR401c - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr401cp [Saccharomyces cerevisiae] (U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (Z99759) hypothetical protein [Schizosaccharomyces pombe] glutamate synthase (NADH) precursor (NADH-GOGAT) ; glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa ; (L01660) NADH-glutamate synthase [Medicago sativa]
19074	ENU02868	AN161C6810:	22-41	692-717	NAP		g2315274	731	297	5.00E-80	56	70	
19075	ENU02869	AN161C7686:	54-73	730-749	NAP		g4056557	266	107	8.00E-23			
19076	ENU02870	AN161C4371:	33-53	712-731	NAP		g1339949	174	73	2.00E-12	26	91	
19077	ENU02871	AN161C1115	24-44	702-722	NAP		g2833203	515	189	1.00E-47	50	35	
19078	ENU02872	AN161C1748:	64-86	739-762	NAP		g1438947	932	269	2.00E-94	68	46	
19079	ENU02873	AN161C7911	42-71	721-740	NAP		g2467272	867	356	9.00E-98	72	31	
19080	ENU02874	AN161C1719:	40-60	720-739	NAP		g417073	754	302	1.00E-81	58	11	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19081	ENJU02875	ANI61C7336:	72-92	753-772	NAP		g2808725		57	0.000000			(AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis]
19082	ENJU02876	6318..7060 ANI61C280:2	25-45	706-725	NAP		g113589	814	201	4.00E-51	48	65	Allantoinase ; allantoinase (EC 3.5.3.4) - Neurospora crassa ; (J02927)
19083	ENJU02877	148..1406 ANI61C5029:	33-53	709-734	NAP		g3183342	248	102	3.00E-21	36	57	allantoinase [Neurospora crassa] hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596)
19084	ENJU02878	93..836 ANI61C5155:	43-62	717-744	NAP		g2132846		79	4.00E-14			hypothetical protein [Schizosaccharomyces pombe] probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]
19085	ENJU02879	104..847 ANI61C6256:	27-47	709-728	NAP		g731773	599	105	2.00E-44	59	69	hypothetical 31.9 KD protein in BET1-PAN1 intergenic region ; probable membrane protein YIL003w - yeast (Saccharomyces cerevisiae)
19086	ENJU02880	67..809 ANI61C4645:	30-61	713-732	NAP		g2132214	233	98	7.00E-20			hypothetical protein YPL164c - yeast (Saccharomyces cerevisiae) ; (Z73520) ORF YPL164c [Saccharomyces cerevisiae] ; (X96770) P2550 protein [Saccharomyces cerevisiae] (Z83864) hypothetical protein Rv3854c [Mycobacterium tuberculosis]
19087	ENJU02881	19..763 ANI61C6841:	72-96	741-774	NAP		g1781102	552	185	4.00E-46	38	50	hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae) ; (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae] "
19088	ENJU02882	208..952 ANI61C1062	54-74	735-756	NAP		g585554	137	54	0.000001	29	92	(AL022071) fructosyl amine [Schizosaccharomyces pombe] (AL035655) 60s ribosomal protein 136 [Schizosaccharomyces pombe]
19089	ENJU02883	2:1192..448 ANI61C1146	54-73	737-756	NAP		g2950465	544	144	8.00E-34	37	52	
19090	ENJU02884	6:1707..963 ANI61C7987:	46-74	725-748	NAP		g4490679	180	82	6.00E-15	56	43	
		325..1069											

# Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19091	ENU02885	ANI61C1043	44-64	728-747	NAP		g231710	779	256	1.00E-67	86	89	cell division control protein 42 homolog (CDC42SP) ; cell division control protein CDC42 - fission yeast (Schizosaccharomyces pombe) ; (M83650) CDC42sp [Schizosaccharomyces pombe] ; (L25677) Cdc42p [Schizosaccharomyces pombe] hypothetical 22.4 KD protein C6G10.10C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] (AE000853) conserved protein [Methanobacterium thermoautotrophicum] acetyl-CoA hydrolase (acetyl-CoA deacylase) (acetyl-CoA acylase) (acetate utilization protein) ; acu-8 protein - Neurospora crassa ; (M31521) acetate permease (acu-8) [Neurospora crassa]
19092	ENU02886	ANI61C4663	22-41	705-725	NAP		g3219969	156	70	2.00E-11	29	96	"phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) ; 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae) ; (L20296) homology with DAHP-synthase (ARO4) gene [Saccharomyces cerevisiae] ; (X61107) phospho-2-dehydro-3-deoxyheptonate aldolase [Saccharomyces cerevisiae] ; (Z36118) ORF YBR249c [Saccharomyces cerevisiae] "
19093	ENU02887	ANI61C7186	30-52	715-734	NAP		g2621836	150	84	9.00E-16	32	92	(AL031853) putative zinc finger protein [Schizosaccharomyces pombe] (AB014595) KIAA0695 protein [Homo sapiens]
19094	ENU02888	ANI61C8897	60-81	741-764	NAP		g113310	1070	193	6.00E-99	79	47	
19095	ENU02889	ANI61C6534	22-45	707-726	NAP		g461540	883	336	9.00E-92			
19096	ENU02890	ANI61C3210	49-68	729-754	NAP		g3738206	215	46	0.0003			
19097	ENU02891	ANI61C4686	30-49	715-737	NAP		g3327204	609	125	8.00E-44	44	31	



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19098	ENNU02892	ANI61C8599:	47-66	736-755	NAP		g465105	644	174	1.00E-61	54	31	(U04841) lanosterol synthase [Saccharomyces cerevisiae]
19099	ENNU02893	2096..1347 ANI61C4266:	45-64	725-755	NAP		g731476	201	81	1.00E-14	42	55	hypothetical 14.4 KD protein in RNRI-ALD3 intergenic region ; hypothetical protein YER072w - yeast (Saccharomyces cerevisiae) ; (U18813) Yer072wp [Saccharomyces cerevisiae] (AF008220) yler [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis] (AF025475) Masc1 [Ascombolus immersus]
19100	ENNU02894	ANI61C1600:	43-67	732-753	NAP		g2293194	289	89	4.00E-23			(AE001036) L-carnitine dehydratase (catB-2) [Archaeoglobus fulgidus] (AL049558) putative phosphatidylinositol-kinase [Schizosaccharomyces pombe]
19101	ENNU02895	ANI61C9279:	34-53	722-744	NAP		g2558956	343	124	5.00E-34	40	43	(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]
19102	ENNU02896	ANI61C9067:	62-86	746-773	NAP		g2649608		60	4.00E-17			ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5) ; HUS5 protein - fission yeast (Schizosaccharomyces pombe) ; (X81846) hus5 [Schizosaccharomyces pombe] ; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe] ;
19103	ENNU02897	ANI61C8232:	62-82	752-774	NAP		g4581508	727	190	4.00E-69	63	11	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5) ; HUS5 protein - fission yeast (Schizosaccharomyces pombe) ; (X81846) hus5 [Schizosaccharomyces pombe] ; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe] ;
19104	ENNU02898	ANI61C8865:	33-52	726-745	NAP		g4160583	699	281	4.00E-75	53	80	[Schizosaccharomyces pombe] ;
19105	ENNU02899	ANI61C1147:	23-48	714-736	NAP		g731040	531	157	6.00E-38			ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5) ; HUS5 protein - fission yeast (Schizosaccharomyces pombe) ; (X81846) hus5 [Schizosaccharomyces pombe] ; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe] ;
19106	ENNU02900	ANI61C1073	60-80	754-773	NAP		g3024226	547	69	2.00E-23	35	53	[Schizosaccharomyces pombe] ;
19107	ENNU02901	6:1321..566 ANI61C352:7	26-46	719-739	NAP		g1730615	390	107	3.00E-36	48	90	ubiquitin-conjugating enzyme [Schizosaccharomyces pombe] NOT56-like protein ; (Y09022) Not56-like protein [Homo sapiens] ERV25 protein precursor ; probable membrane protein YML012w - yeast (Saccharomyces cerevisiae) ; (Z49810) unknown [Saccharomyces cerevisiae] (Z97336) carnitine racemase homolog [Arabidopsis thaliana] (AL034565) putative abhydrolase [Schizosaccharomyces pombe]
19108	ENNU02902	ANI61C7690:	65-84	751-780	NAP		g2244799	108	62	0.000000	32	69	
19109	ENNU02903	793..36 ANI61C1026:	22-49	709-737	NAP		g4049528	342	82	1.00E-25	39	70	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19110	ENU02904	ANI61C5273:	22-52	721-740	NAP		g731758	419	176	1.00E-43	44	37	hypothetical 67.8 KD protein in IK11-ERG9 intergenic region ; hypothetical protein YHR188c - yeast (Saccharomyces cerevisiae) ; (U00030) Yhr188cp [Saccharomyces cerevisiae] (D85777) cysteine dioxygenase [Homo sapiens]
19111	ENU02905	ANI61C2115:	63-87	750-782	NAP		g1747324	200	68	3.00E-18	47	76	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN50 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Yal061 wp [Saccharomyces cerevisiae]
19112	ENU02906	ANI61C9458:	48-72	740-767	NAP		g731294	532	108	3.00E-41	39	59	"putative ATP-dependent RNA helicase T26G10.1 in chromosome III ; ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans ; (Z29115) similar to RNA helicases, deleted exon 1397-1495 which introduced stop codon at 3' splice; 5' splice looks v. good; ?possible alternate final exon.; cDNA EST yk368a4.3 comes from this gene; cDNA EST yk368a4.5 comes fr..."
19113	ENU02907	ANI61C9311:	40-60	735-759	NAP		g465975	1254	314	4.00E-85			making-type switching protein SW110 ; SW110 protein - fission yeast (Schizosaccharomyces pombe) ; (X61926) SW110 [Schizosaccharomyces pombe] ; (AL031534) mating-type switching protein swi10. [Schizosaccharomyces pombe]
19114	ENU02908	ANI61C8348:	22-46	723-743	NAP		g549012	512	216	2.00E-55	44	98	(U89492) arylsulfatase [Neurospora crassa]
19115	ENU02909	ANI61C3366:	38-57	737-761	NAP		g2873363	346	95	8.00E-40	40	35	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19116	ENU02910	ANI61C3113:	68-99	772-791	NAP		g2507070	429	39	0.027	32	39	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19117	ENU02911	ANI61C8607: 2162..1397	65-84	768-788	NAP		g549705	61	0.000000	007			36.1 KD protein in BUD2-MIF2 intergenic region ; SEC14 protein homolog YKL091c - yeast (Saccharomyces cerevisiae) ; (Z28091) ORF YKL091c [Saccharomyces cerevisiae]
19118	ENU02912	ANI61C1114 0:928..162	53-72	754-777	NAP		g1175102	266	123	2.00E-27	32	85	hypothetical protein H10077 ; hypothetical protein H10077 - Haemophilus influenzae (strain Rd KW20) ; (U32693) H. influenzae predicted coding region H10077 [Haemophilus influenzae Rd] (Z99113) ymaE [Bacillus subtilis]
19119	ENU02913	ANI61C1138 0:1440..2206	40-61	742-764	NAP		g2634109	235	107	8.00E-23	36	93	(D89119) unnamed protein product [Schizosaccharomyces pombe]
19120	ENU02914	ANI61C4135: 42..808	63-82	767-787	NAP		g1749446	399	153	1.00E-36	53	50	(U04540) flavocytochrome b5 chimeric protein [synthetic construct] ; (L27087) cytochrome b5 [Artificial gene]
19121	ENU02915	ANI61C1442: 992..224	62-81	769-788	NAP		g488428	181	75	6.00E-13	33	33	pseudouridyate synthase 3 (pseudouridine synthase 3) (depressed growth-rate protein DEG1) ; depressed growth-rate protein DEG1 - yeast (Saccharomyces cerevisiae) ; (D50617) depressed growth-rate protein [Saccharomyces cerevisiae] ; (D44600) depressed growth-rate protein DEG1 [Saccharomyces cerevisiae]
19122	ENU02916	ANI61C9241: 2204..1435	45-68	749-772	NAP		g399356	561	171	5.00E-42	49	44	RTM1 protein ; RTM1 protein - yeast (Saccharomyces cerevisiae) ; (U02618) RTM1 gene product [Saccharomyces cerevisiae]
19123	ENU02917	ANI61C4650: 3141..3910	72-91	774-799	NAP		g730689	120	50	0.00001	30	64	quinate permease (quinate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa] (AF088907) clock-controlled gene-8 protein [Neurospora crassa]
19124	ENU02918	ANI61C3926: 848..78	55-74	759-783	NAP		g131761	220	112	3.00E-24	34	38	
19125	ENU02919	ANI61C5774: 818..48	24-43	729-752	NAP		g3746897	178	96	3.00E-19	29	85	

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19126	ENU02920	AN161C3373: 3533..2763	27-60	736-755	NAP		g2133034	475	135	3.00E-31	39	37	probable membrane protein YPR156c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (U28371) Similar to <i>S. cerevisiae</i> hypothetical protein Ybr008p (Swiss Prot. accession number P38124) [ <i>Saccharomyces cerevisiae</i> ]
19127	ENU02921	AN161C6835: 5945..6715	42-61	751-770	NAP		g3130039	414	154	7.00E-37	40	95	(AL023534) hypothetical protein [ <i>Schizosaccharomyces pombe</i> ]
19128	ENU02922	AN161C1057: 3:1358..2128	59-78	767-787	NAP		g1787246	178	64	9.00E-10	29	91	(AE000202) putative synthetase [ <i>Escherichia coli</i> ]
19129	ENU02923	AN161C5814: 411..1182	49-68	752-778	NAP		g3130041	640	229	2.00E-59	53	64	(AL023534) hypothetical protein [ <i>Schizosaccharomyces pombe</i> ] ; (AL031534) homology to longevity assurance protein.
19130	ENU02924	AN161C138:2 054..1283	25-45	732-754	NAP		g1175373	237	80	3.00E-18	31	31	[ <i>Schizosaccharomyces pombe</i> ] hypothetical 72.5 KD protein C2F7.10 in chromosome I ; hypothetical protein SPAC2F7.10 - fission yeast ( <i>Schizosaccharomyces pombe</i> ) ; (Z50142) unknown
19131	ENU02925	AN161C8631: 5833..5062	26-47	731-755	NAP		g2290382	1118	441	e-123	78	53	[ <i>Schizosaccharomyces pombe</i> ] (U89985) serine/threonine protein phosphatase PPT1 [ <i>Neurospora crassa</i> ] (AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [ <i>Schizosaccharomyces pombe</i> ] (AL031798) 40s ribosomal protein s20.
19132	ENU02926	AN161C2278: 2096..2868	44-63	755-774	NAP		g2257524	396	159	2.00E-38	41	92	[ <i>Schizosaccharomyces pombe</i> ] het-c4 protein - <i>Podospira anserina</i> ; (L36210) het-c [ <i>Podospira anserina</i> ] putative mitochondrial carrier
19133	ENU02927	AN161C8986: 4696..3924	43-62	752-773	NAP		g3687464	320	131	6.00E-30	62	65	YGR257C ; hypothetical protein YGR257c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z73042) ORF YGR257c [ <i>Saccharomyces cerevisiae</i> ] ; (X99228) mitochondrial carrier protein [ <i>Saccharomyces cerevisiae</i> ] (L78243) alternative splice (exon 17) [ <i>Homo sapiens</i> ]
19134	ENU02928	AN161C1011: 2918..2145	53-72	765-784	NAP		g2133323	588	163	1.00E-39	64	94	
19135	ENU02929	AN161C1071: 5:3566..2793	62-92	773-793	NAP		g1723767	361	137	1.00E-31	40	62	
19136	ENU02930	AN161C8371: 3..777	24-59	736-755	NAP		g1374920	227	86	2.00E-22	33	14	

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19137	ENU02931	AN161C9255: 4223..3449	23-51	735-755	NAP		g2764632	796	217	1.00E-67	71	99	(AJ001520) 19.3kD iron-sulfur subunit of mitochondrial complex I
19138	ENU02932	AN161C9182: 4568..5342	22-45	735-754	NAP		g2808634	860	192	2.00E-48	40	29	[Neurospora crassa] (AJ001909) transcriptional activator [Aspergillus niger]
19139	ENU02933	AN161C9243: 1724..2497	25-44	730-757	NAP		g2493049	303	59	5.00E-19	58	85	"ATP synthase delta chain, mitochondrial precursor ; (Z82020) ATP-synthase delta-subunit [Agaricus bisporus]"
19140	ENU02934	AN161C9220: 11..785	25-58	738-757	NAP		g4586458	113	85	7.00E-16	33	60	(AB025252) reverse transcriptase [Magnaporthe grisea]
19141	ENU02935	AN161C1049: 7:8419..7645	51-72	763-783	NAP		g133892	473	90	2.00E-22	80	82	40S ribosomal protein S26E (CRP5) (13.6 kD ribosomal protein) ; ribosomal protein S26.e - Neurospora crassa ; (X55637) ribosomal protein [Neurospora crassa]
19142	ENU02936	AN161C1059: 9:3190..2415	24-42	738-757	NAP		g1730831	543	214	5.00E-55	44	68	hypothetical 40.7 kD protein in SIN4-URE2 intergenic region ; hypothetical protein YNL231c - yeast (Saccharomyces cerevisiae) ; (Z69381) Similar to hypothetical yeast protein L3502 [Saccharomyces cerevisiae] ; (Z71507) ORF YNL231c [Saccharomyces cerevisiae]
19143	ENU02937	AN161C6671: 1311..2086	56-76	763-789	NAP		g2281983	809	252	3.00E-66	59	81	(Z98056) hypothetical protein [Schizosaccharomyces pombe]
19144	ENU02938	AN161C8852: 60..836	34-68	734-767	NAP		g2494268	252	64	1.00E-21	37	98	putative sterigmatocystin biosynthesis protein STCT ; (U34740) putative translation elongation factor 1 gamma [Emericella nidulans]
19145	ENU02939	AN161C7170: 3870..3094	22-43	737-756	NAP		g1710780	744	225	1.00E-70	84	99	40S ribosomal protein S9 (S7) ; (X96613) cytoplasmic ribosomal protein S7 [Podospira anserna]
19146	ENU02940	AN161C6870: 1542..2318	24-43	737-758	NAP		g2494700	514	161	6.00E-39	51	77	hypothetical 31.2 kD protein in CYSF-AMIA intergenic region ; (AE000330) putative regulator [Escherichia coli]
19147	ENU02941	AN161C4612: 1762..986	70-92	785-804	NAP		g3080524	1235	75	6.00E-13	38	34	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
19148	ENU02942	AN161C7417: 2566..1791	66-86	774-800	NAP		g2842510	211	115	5.00E-25	36	26	(AL021748) hypothetical protein [Schizosaccharomyces pombe]

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19149	ENNU02943	AN161C17:10	61-80	777-796	NAP		g1723966	355	152	2.00E-36	43	77	hypothetical 32.0 KD protein in GOG5-NIF3 intergenic region ; hypothetical protein YGL224c - yeast (Saccharomyces cerevisiae) ; (Z72746) ORF YGL224c [Saccharomyces cerevisiae]
19150	ENNU02944	AN161C9622: 1254..477	56-75	769-791	NAP		g2132860	366	107	2.00E-29	41	99	probable membrane protein YOL162w - yeast (Saccharomyces cerevisiae) ; (Z74904) ORF YOL162w [Saccharomyces cerevisiae]
19151	ENNU02945	AN161C8718: 2042..1265	22-44	737-757	NAP		g2654181	1289	195	1.00E-99	75	55	(AF034963) calmodulin-dependent protein kinase; CgCMK [Glomerella cingulata]
19152	ENNU02946	AN161C8415: 1102..1880	24-52	741-760	NAP		g2494268	342	123	2.00E-27	38	97	putative sterigmatocystin biosynthesis protein STCT ; (U34740) putative translation elongation factor 1 gamma [Emicella nidulans]
19153	ENNU02947	AN161C1835: 798..1578	56-75	772-794	NAP		g4140255	1017	153	2.00E-36	43	43	(AJ009973) hexokinase [Aspergillus niger]
19154	ENNU02948	AN161C9772: 3490..4270	24-53	741-762	NAP		g4586977	2840	272	3.00E-72	47	10	(AB018382) Mok13; Mok13 is homologous to Mok1 which is an alpha-glucan synthase [Schizosaccharomyces pombe]
19155	ENNU02949	AN161C1091 7:1624..2403	42-65	762-781	NAP		g1346290	1048	216	5.00E-63	49	47	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluveromyces lactis]
19156	ENNU02950	AN161C3316: 3446..2665	70-89	790-809	NAP		g4106687	480	178	4.00E-44	39	64	(AL035065) putative nadh-dependent flavin oxidoreductase [Schizosaccharomyces pombe]
19157	ENNU02951	AN161C6374: 5737..4955	22-55	741-762	NAP		g731752	432	178	3.00E-44	46	94	hypothetical 26.3 KD protein in OYE2-GND1 intergenic region ; hypothetical protein YHR181w - yeast (Saccharomyces cerevisiae) ; (U00028) Yhr181wp [Saccharomyces cerevisiae]
19158	ENNU02952	AN161C1159: 9524..10306	61-81	776-801	NAP		g929862	648	141	7.00E-33	35	51	(X83502) J0916 [Saccharomyces cerevisiae]
19159	ENNU02953	AN161C5218: 1501..720	47-66	768-787	NAP		g3650379	811	250	1.00E-65	77	95	(AL031740) 60s ribosomal protein 110a. [Schizosaccharomyces pombe]

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19160	ENU02954	ANI61C9551: 3908..4690	22-42	738-762	NAP		g730589	347	153	1.00E-36	41	99	"mitochondrial 60S ribosomal protein L6 precursor (YML6) ; ribosomal protein L6 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (U10397) MRPL6p: Mitochondrial ribosomal protein L6 [Saccharomyces cerevisiae]"
19161	ENU02955	ANI61C1209: 3642..4425	25-46	740-766	NAP		g1168402	689	273	7.00E-73	69	99	minor allergen ALT A 7 (ALT A VII) ; minor allergen - Alternaria alternata ; (X78225) minor allergen [Alternaria alternata]
19162	ENU02956	ANI61C1656: 210..993	42-61	764-783	NAP		g3929362	202	53	3.00E-20	34	35	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVII]
19163	ENU02957	ANI61C1095: 1452..668	61-80	781-803	NAP		g2828147	486	86	4.00E-34	54	88	(AF042384) BC-2 protein [Homo sapiens]
19164	ENU02958	ANI50C6268: _1:785..6	55-76	762-797	NAP		g586551		76	3.00E-13	27	73	hypothetical 33.5 KD protein in MRPS9-YSW1 intergenic region ; probable membrane protein YBR147w - yeast (Saccharomyces cerevisiae) ; (Z36016) ORF YBR147w [Saccharomyces cerevisiae]
19165	ENU02959	ANI61C1064: 9:1676..891	22-51	745-765	NAP		g1429204	568	208	3.00E-53	56	98	(X99215) leucine zipper [Aspergillus niger]
19166	ENU02960	ANI61C1050: 5:88..873	25-44	747-768	NAP		g114971	456	109	6.00E-45	50	23	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucosylhydrolase) ; beta-glucosidase (EC 3.2.1.21) precursor - yeast (Kluveromyces marxianus var. marxianus) ; (X05918) beta-glucosidase (AA 1 - 845) [Kluveromyces marxianus]
19167	ENU02961	ANI50C1_19: 01:889..103	26-46	751-770	NAP		g1706333		343	7.00E-94	61	45	pyruvate decarboxylase ; (U00967) pyruvate decarboxylase [Aspergillus parasiticus]

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19168	ENU02962	AN161C7922:	72-91	796-816	NAP		g1176153	290	131	6.00E-30	35	86	"hypothetical 27.4 KD protein in RNPB-SOHA intergenic region (ORF 1); (U18997) ORF_f256 [Escherichia coli]; (AE000394) orf, hypothetical protein [Escherichia coli]"
19169	ENU02963	AN161C1099	42-73	768-787	NAP		g1723499	448	171	7.00E-42	52	47	hypothetical 46.7 KD protein C19G10.05 in chromosome 1; (Z69909) putative proteasome regulatory subunit
19170	ENU02964	AN161C9746:	72-91	799-818	NAP		g3874345	51	0.00001				[Schizosaccharomyces pombe] (Z81035) predicted using GeneFinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes from...
19171	ENU02965	AN161C7857:	25-44	753-772	NAP		g3935151	377	133	9.00E-44	43	94	(AC005106) T25N20.15 [Arabidopsis thaliana]
19172	ENU02966	AN161C8794:	62-81	791-810	NAP		g1705884	725	98	1.00E-57	58	50	"probable citrate synthase, mitochondrial precursor"
19173	ENU02967	AN161C6439:	54-73	783-802	NAP		g2370322	173	55	2.00E-11	32	40	(Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis]
19174	ENU02968	AN161C1076	63-82	792-813	NAP		g1709170	263	112	3.00E-24	35	82	26S proteasome regulatory subunit MTS3; (X92682) 26S protease regulatory subunit
19175	ENU02969	AN161C4271:	32-55	762-782	NAP		g2132860	453	124	7.00E-30	46	93	[Schizosaccharomyces pombe]; 26S protease subunit [Schizosaccharomyces pombe]
19176	ENU02970	AN161C9024:	34-54	756-784	NAP		g1336011	548	180	1.00E-44	42	47	probable membrane protein YOL162w - yeast (Saccharomyces cerevisiae); (Z74904) ORF YOL162w [Saccharomyces cerevisiae] (U56245) kynurenine 3-monoxygenase [Drosophila melanogaster]



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19177	ENU02971	ANI61C8832:	25-44	745-776	NAP		g731651	1143	205	2.00E-52	41	38	hypothetical aldehyde-dehydrogenase like protein in PUT2-SRB2 intergenic region ; hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) ; (U00062) Yhr039cp [Saccharomyces cerevisiae]
19178	ENU02972	ANI61C9335:	23-44	756-776	NAP		g465506	334	162	3.00E-39	43	97	HTP reductase ; RIB7 protein - yeast (Saccharomyces cerevisiae) ; (X71329) YBR 12.03 [Saccharomyces cerevisiae] ; (Z36022) ORF YBR153w [Saccharomyces cerevisiae] ; (Z21622) HTP reductase [Saccharomyces cerevisiae]
19179	ENU02973	ANI61C8182:	47-67	774-800	NAP		g417454	823	309	1.00E-83	63	94	proliferating cell nuclear antigen (PCNA) ; proliferating cell nuclear antigen - fission yeast (Schizosaccharomyces pombe) ; (X54857) proliferating cell nuclear antigen [Schizosaccharomyces pombe] ; (AL035637) proliferating cell nuclear antigen [Schizosaccharomyces pombe] (AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]
19180	ENU02974	ANI61C3990:	72-91	802-825	NAP		g4007792	716	287	6.00E-77	60	20	"40S ribosomal protein S6 ; ribosomal protein S6.e, cytosolic - fission yeast (Schizosaccharomyces pombe) ; (M36382) ribosomal protein S6 (rps6) precursor [Schizosaccharomyces pombe] ; (Z54308) 40S ribosomal protein [Schizosaccharomyces pombe]
19181	ENU02975	ANI61C2420:	44-63	778-797	NAP		g133980	591	136	2.00E-31	75	64	"
19182	ENU02976	ANI61C5533:	64-88	788-818	NAP		g3901117	570	122	2.00E-27	37	30	(AJ012752) maltose permease [Saccharomyces cerevisiae]
19183	ENU02977	ANI61C3559:	24-47	751-779	NAP		g2258125	526	190	9.00E-51	49	47	(Z83828) ArmMst-1 [Amanita muscaria]

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19184	ENU02978	AN161C4093:	56-75	792-811	NAP		g3929361	758	167	2.00E-67	75	94	NADH-ubiquinone oxidoreductase 23 KD subunit precursor (complex I-23KD) (CI-23KD) ; (X95547)
		748..1548											ferredoxin-like iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]
19185	ENU02979	AN161C7409:	55-75	793-812	NAP		g1679597	207	37	0.15	32	91	(Z50095) mannosidase [Agaricus bisporus]
19186	ENU02980	AN161C3696:	54-73	793-812	NAP		g2996620	207	83	2.00E-15	32	91	(AF009224) beta-ketoadipate enol-lactone hydrolase [Acinetobacter sp. ADP I] ; beta-ketoadipate enol-lactone hydrolase [Acinetobacter calcoaceticus]
		1569..769											(U80063) lipase LipA [Streptomyces cinnamomeus]
19187	ENU02981	AN161C8073:	22-46	761-780	NAP		g2435400	162	71	9.00E-12	34	55	vacuolar ATP synthase 16 KD
		6666..5866											proteolipid subunit (V-ATPase C-subunit) ; (AF008924) V-ATPase C-subunit [Aedes aegypti]
19188	ENU02982	AN150C8867	50-69	787-808	NAP		g3334403	69	69	3.00E-11	53	99	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
		_3:902..102											mucin - rhesus macaque (fragment) ; (U00483) mucin [Macaca mulatta]
19189	ENU02983	AN161C8446:	47-68	783-806	NAP		g1654074	217	52	0.000005	35	53	GCN20 protein ; GCN20 protein - yeast (Saccharomyces cerevisiae) ; (U19971) Gcn20p [Saccharomyces cerevisiae] ; (D50617) YFR009W [Saccharomyces cerevisiae]
		6996..6195											"(AF069298) similar to ATPases associated with various cellular activities (Pfam: AAA_hmm, score: 230.91) [Arabidopsis thaliana]"
19190	ENU02984	AN161C4168:	53-76	793-812	NAP		g2134574	200	35	0.74	37	95	"cytochrome P450 52L9 (CYPLIA9) (alkane-inducible P450-ALK5-A) ; cytochrome P450 ALK5-A, alkane-inducible - yeast (Candida maltosa) ; (D12717) n-alkane inducible cytochrome P-450 [Candida maltosa]"
		1493..234											(AJ010475) RNA helicase [Arabidopsis thaliana]
19191	ENU02985	AN161C1026	56-79	796-816	NAP		g1169871	956	211	2.00E-81	65	33	
		3:1614..811											
19192	ENU02986	AN161C7203:	38-57	779-798	NAP		g3193292	520	116	1.00E-25	42	66	
		17..819											
19193	ENU02987	AN161C1049	37-58	778-798	NAP		g3913326	467	99	7.00E-22	41	42	
		1:851..48											
19194	ENU02988	AN161C6305:	23-42	766-784	NAP		g3776027	624	107	6.00E-38	45	31	
		82..885											

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19195	ENU02989	ANI61C8325:	23-45	766-785	NAP		g4455301	337	88	7.00E-22	45	87	(AL035528) putative protein [Arabidopsis thaliana]
19196	ENU02990	2398..1594 ANI61C2426:	22-41	765-784	NAP		g1723231	229	114	7.00E-25	36	92	hypothetical 27.1 KD protein CID4.09C in chromosome I ; (Z69239) unknown [Schizosaccharomyces pombe]
19197	ENU02991	ANI61C1087:	52-71	790-814	NAP		g1764133	346	115	4.00E-25	36	94	(U81790) PIG8 [Uromyces fabae]
19198	ENU02992	793..1597 ANI61C3686:	64-83	807-827	NAP		g126066	230	83	3.00E-15	35	52	L-lactate dehydrogenase (LDH) ; L-lactate dehydrogenase (EC 1.1.1.27) chain Ldh1 - maize ; (Z11754) lactate dehydrogenase [Zea mays]
19199	ENU02993	558..848 ANI61C9004:	56-75	798-820	NAP		g2507431	967	266	2.00E-70	48	55	"phenylalanyl-TRNA synthetase mitochondrial precursor (phenylalanine--TRNA ligase) (PHERS) ; phenylalanine--tRNA ligase (EC 6.1.1.20) alpha chain precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49219) MstIp [Saccharomyces cerevisiae] ; (Z71255) MstIp [Saccharomyces cerevisiae]" (AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda]"
19200	ENU02994	104..910 ANI61C9827:	37-57	766-801	NAP		g2245570	205	84	5.00E-16	36	23	(AL022117) hypothetical protein [Schizosaccharomyces pombe]
19201	ENU02995	686..1493 ANI61C8366:	63-87	808-828	NAP		g2959376	980	203	1.00E-51	56	68	(AC006069) similar to yeast ccc1 protein [Arabidopsis thaliana]
19202	ENU02996	1075..1883 ANI61C1234:	35-54	782-801	NAP		g4220472	301	73	2.00E-23	34	98	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19203	ENU02997	3091..2283 ANI61C5032:	49-68	786-815	NAP		g2497056	586	123	1.00E-27	41	56	"(U52064) Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus] ; (U75698) ORF 73; extensive acidic domains, potential leucine zipper; immediate early protein homolog [Kaposi's sarcoma-associated herpesvirus]"
19204	ENU02998	1371..2180	37-58	778-804	NAP		g1633572	115	47	0.0002			

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19205	ENU02999	ANI61C8256:	41-60	790-809	NAP		g2497179	145	57	0.000000	28	18	hypothetical 113.2 KD protein in SSO2-HSC82 intergenic region ; hypothetical protein YMR185w - yeast (Saccharomyces cerevisiae) ; (Z49808) unknown [Saccharomyces cerevisiae]
		855..45											
19206	ENU03000	ANI61C45:26	33-53	782-801	NAP		g125886	657	181	5.00E-45	41	67	lactate 2-monoxygenase (lactate oxidase) ; lactate 2-monoxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monoxygenase [Mycobacterium smegmatis]
		82..3492											
19207	ENU03001	ANI61C6754:	22-52	769-790	NAP		g1723578	652	266	2.00E-70	49	83	probable oxidoreductase C26F1.07 in chromosome I ; (Z73100) unknown [Schizosaccharomyces pombe]
		4137..4947											
19208	ENU03002	ANI61C6415:	58-77	809-828	NAP		g4376408	384	96	1.00E-30	36	64	[Chlamydia pneumoniae]
		841..1654											
19209	ENU03003	ANI61C1054	29-50	780-799	NAP		g2648302	290	108	4.00E-32	46	79	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpce-2) [Archaeoglobus fulgidus]"
		0:6432..6207											
19210	ENU03004	ANI61C6496:	24-57	776-795	NAP		g4557817	1234	250	7.00E-66	54	48	3-oxoacid CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor ; succinyl-CoA:3-ketoacid-coenzyme A transferase precursor (succinyl CoA:3-oxoacid CoA-transferase) (OXCCT) ; (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]
		9172..9986											
19211	ENU03005	ANI61C4798:	41-62	793-812	NAP		g2388907	606	50	0.00002			(Z98974) hypothetical protein [Schizosaccharomyces pombe]
		1015..1828											
19212	ENU03006	ANI61C9801:	59-78	812-831	NAP		g416589	445	207	7.00E-53	42	49	AFG1 protein ; AFG1 protein - yeast (Saccharomyces cerevisiae) ; (U18779) Afg1p [Saccharomyces cerevisiae]
		4737..3923											
19213	ENU03007	ANI61C9149:	42-65	794-814	NAP		g2253701	524	90	1.00E-45	53	89	(AF003835) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Rattus norvegicus]
		1260..2074											
19214	ENU03008	ANI61C7738:	65-91	810-837	NAP		g2146821	107	48	0.000000	29	32	alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae)
		2704..1890											
19215	ENU03009	ANI61C2364:	23-50	772-796	NAP		g4539279	867	259	2.00E-75	55	18	(AL049498) rho1 gdp-gtp exchange protein 1 [Schizosaccharomyces pombe]
		513..1328											

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19216	ENU03010	ANI61C1752:	55-74	809-828	NAP		g1723371	1081	406	e-113	63	51	hypothetical protein in CRTE 3'region (ORF2) ; (M87280) ORF2 [Erwinia herbicola]
		1711..896											(X92509) crg1 [Ustilago maydis]
19217	ENU03011	ANI61C3291:	25-55	778-799	NAP		g1514667	331	104	1.00E-26	36	63	"(AF068712) similar to cytochrome P450 (Pfam: p450.hmm, score: 265.98) [Caenorhabditis elegans]"
		621..1437											
19218	ENU03012	ANI61C6315:	46-75	801-820	NAP		g3168924		64	9.00E-10			microfibrillar-associated protein 1 ; microfibrillar protein MFAP1 - human
		1601..785											: (U04209) associated microfibrillar protein [Homo sapiens]
19219	ENU03013	ANI61C7472:	55-72	813-832	NAP		g1709012	253	59	0.000000	34	55	(U78597) kinesin light chain [Plectonema boryanum]
		146..965								04			GAR1 protein ; GAR1 protein - fission yeast (Schizosaccharomyces pombe) ; (Z19576) snoRNP protein GAR1 [Schizosaccharomyces pombe] ; (AB000537) snoRNP protein GAR1 [Schizosaccharomyces pombe] ; (Z95397) Gar1p [Schizosaccharomyces pombe] ; (AL021747) gar1 protein; small nucleolar rnp required for pre-mrna for pre-mrna processing [Schizosaccharomyces pombe]
19220	ENU03014	ANI61C9978:	40-59	794-818	NAP		g2645229	488	199	3.00E-50	40	55	"5-formyltetrahydrofolate cyclo-ligase (5,10-methenyl-tetrahydrofolate synthetase) (methenyl-THF synthetase) (MTHFS) ; indoleacetate-lysine synthetase (EC 6.3.2.20) - human ; (L38928) 5,10-methenyltetrahydrofolate synthetase [Homo sapiens]"
		1088..817											hypothetical 39.6 KD protein in MTD1-NUP133 intergenic region ; hypothetical protein YKR081c - yeast (Saccharomyces cerevisiae) ; (Z27116) ORF YKR401 [Saccharomyces cerevisiae] ; (Z28306) ORF YKR081c [Saccharomyces cerevisiae]
19221	ENU03015	ANI61C3973:	51-70	810-829	NAP		g544370	439	82	1.00E-30			
		2387..3207											
19222	ENU03016	ANI61C1000	22-41	777-800	NAP		g1706921	173	81	1.00E-14	36	99	
		4:4568..3748											
19223	ENU03017	ANI61C406:9	39-58	798-818	NAP		g549638	500	171	4.00E-42	38	77	
		57..136											

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19224	ENU03018	ANI61C8156:	67-86	826-846	NAP		g452120		64	2.00E-15			(L28112) complete cds [Rattus norvegicus]
19225	ENU03019	ANI61C6265:	25-46	785-805	NAP		g2326188	622	182	4.00E-49	43	79	(U81606) mixed-linked glucanase precursor [Cochliobolus carbonum]
19226	ENU03020	ANI61C8257:	40-59	799-820	NAP		g1175386	245	77	2.00E-13	30	78	hypothetical 37.7 KD protein C18B11.06 in chromosome 1; hypothetical protein SPAC18B11.06 - fission yeast (Schizosaccharomyces pombe) ; (Z50728) hypothetical protein [Schizosaccharomyces pombe]
19227	ENU03021	ANI61C8772:	43-62	796-823	NAP		g1208451	347	129	2.00E-29	32	67	(D64004) hypothetical protein [Synechocystis sp.]
19228	ENU03022	ANI61C7523:	22-41	784-803	NAP		g1078634	1309	281	e-130	98	36	sepB protein - Emeritella nidulans ; sepB protein - Emeritella nidulans ; (X86399) sepB [Emeritella nidulans] probable membrane protein YPR011c - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz11p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] (AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana] (X78712) glycerol kinase [Homo sapiens]
19229	ENU03023	ANI61C5260:	22-50	770-804	NAP		g1362406	531	131	8.00E-30	46	65	(AF020040) xylose reductase [Pichia guilliermondii] (Z93941) YuxA [Bacillus subtilis] ; (Z99120) alternate gene name: yvxA; similar to retinol dehydrogenase [Bacillus subtilis]
19230	ENU03024	ANI61C1027:	22-50	786-805	NAP		g3318617	537	140	3.00E-52	64	71	ribulose-phosphate 3-epimerase (pentose-5-phosphate 3-epimerase) (PPE) (RPE) ; POS18 protein - yeast (Saccharomyces cerevisiae) ; (X83571) Ribulose-5-Phosphate-Epimerase [Saccharomyces cerevisiae] ; (Z49396) ORF YJL121c [Saccharomyces cerevisiae]
19231	ENU03025	ANI61C1491:	40-61	806-825	NAP		g516124	1027	109	2.00E-32	43	43	(AC004218) unknown protein [Arabidopsis thaliana]
19232	ENU03026	ANI61C7207:	62-81	828-847	NAP		g4103055	827	146	1.00E-73	59	80	
19233	ENU03027	ANI61C1024:	31-52	798-817	NAP		g2624002	213	101	7.00E-21	31	85	
19234	ENU03028	ANI61C9660:	67-86	834-853	NAP		g1173139	546	105	1.00E-50	55	86	
19235	ENU03029	ANI61C2864:	70-89	836-856	NAP		g3355474	359	148	3.00E-35	32	65	

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19236	ENU03030	AN161C1875:	54-74	822-841	NAP		g4539944	218	76	1.00E-20	38	61	(AF133841) aldose reductase (AF133841) aldose reductase
19237	ENU03031	33..862 AN161C819:2	23-53	790-810	NAP		g1477466	612	128	2.00E-57	50	44	ALDRXV4 [Xerophyta viscosa] (U35246) vacuolar protein sorting homolog h-vps45 [Homo sapiens] (U44750) NAD-dependent 15-hydroxyprostaglandin dehydrogenase [Rattus norvegicus]
19238	ENU03032	..831 AN161C1128	22-51	792-811	NAP		g2047309		71	1.00E-11			(AL023780) DNA binding protein [Schizosaccharomyces pombe]
19239	ENU03033	AN161C3329:	27-55	786-816	NAP		g3184115	646	111	5.00E-24	29	52	[Schizosaccharomyces pombe] putative transporter C11D3.18C; (Z68166) unknown
19240	ENU03034	1435..604 AN161C3763:	43-62	811-833	NAP		g1351714	297	71	1.00E-11	31	50	[Schizosaccharomyces pombe] (X83512) Yna1p [Saccharomyces cerevisiae]
19241	ENU03035	AN161C3280:	22-41	786-813	NAP		g603587	1340	404	e-112	70	58	"asparaginyl--TRNA synthetase, cytoplasmic (asparagine--TRNA ligase) (ASNRS) ; hypothetical protein YHR019c - yeast (Saccharomyces cerevisiae) ; (U10399) Ded81p: Asparaginyl-tRNA synthetase [Saccharomyces cerevisiae]" (AB000704) ribosomal protein S11 homolog [Schizosaccharomyces pombe]
19242	ENU03036	1255..2088 AN161C7044:	64-83	835-855	NAP		g731638	1109	380	e-105	65	50	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI] (U59215) cyclin-dependent protein kinase PHOA(M1) [Emmericella nidulans]
19243	ENU03037	AN161C1058	46-66	818-838	NAP		g1813337	491	159	2.00E-38	82	71	36.7 KD protein in CBR5-NOT3 intergenic region ; hypothetical protein YIL041w - yeast (Saccharomyces cerevisiae) ; (Z46861) unknown [Saccharomyces cerevisiae] (AL035539) putative protein [Arabidopsis thaliana] (AC002340) hypothetical protein [Arabidopsis thaliana]
19244	ENU03038	AN161C7997:	22-53	792-815	NAP		g3929362	292	114	7.00E-25	40	36	
19245	ENU03039	AN161C1048	35-56	808-829	NAP		g3643644	1098	194	9.00E-82	70	59	
19246	ENU03040	AN161C566:1	50-69	823-844	NAP		g731801	269	66	4.00E-25	32	80	
19247	ENU03041	AN161C6225:	30-49	802-825	NAP		g4539334		36	0.27			
19248	ENU03042	995..1832 AN161C2571:	45-64	821-840	NAP		g2880049	251	126	2.00E-28	35	54	

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19249	ENNU03043	AN150C346_1:3130..2293	65-87	835-860	NAP		g731285	66	4.00E-10	35	81		hypothetical 27.1 KD protein in ACS1-GCV3 intergenic region ; hypothetical protein YAL049c - yeast (Saccharomyces cerevisiae) ; (U12980) Yal049cp [Saccharomyces cerevisiae] probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (AL035216) probable involvement in ergosterol biosynthesis
19250	ENNU03044	AN161C3044: 852..14	40-60	816-835	NAP		g2132957	310	66	4.00E-10	29	47	[Schizosaccharomyces pombe] (AL035216) probable involvement in ergosterol biosynthesis
19251	ENNU03045	AN161C8498: 45..883	43-62	806-839	NAP		g4160344	682	264	5.00E-70	48	54	[Schizosaccharomyces pombe] DNA-binding protein amda - Emmericella nidulans ; (L28810) regulatory protein [Emmericella nidulans]
19252	ENNU03046	AN161C7244: 133..972	62-81	830-858	NAP		g2133268	575	112	4.00E-49	41	31	hypothetical 35.9 KD protein C56F8.08 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe] (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis] hypothetical oxidoreductase in PTA-ROCC intergenic region ; hypothetical protein - Bacillus subtilis ; (X73124) ipa-82d [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-82d; similar to glucose 1-dehydrogenase [Bacillus subtilis]
19253	ENNU03047	AN161C1118: 6:3..842	23-58	801-820	NAP		g1723440	608	204	8.00E-52	50	74	(D63916) protein phosphatase 2A 65kD regulatory subunit (A subunit) [Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
19254	ENNU03048	AN161C4142: 923..84	22-56	788-819	NAP		g2370322	220	87	1.00E-16	32	70	[Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
19255	ENNU03049	AN161C9321: 3703..2864	33-52	811-830	NAP		g732372	202	97	1.00E-19	33	66	[Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
19256	ENNU03050	AN161C1077: 6:2216..3055	48-72	826-845	NAP		g1235752	1535	215	2.00E-69	65	38	(D63916) protein phosphatase 2A 65kD regulatory subunit (A subunit) [Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
19257	ENNU03051	AN161C4209: 3767..2927	64-83	842-862	NAP		g3560142	454	160	1.00E-38	32	45	[Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
19258	ENNU03052	AN161C2329: 3142..2302	42-61	814-840	NAP		g3183375	284	161	8.00E-39	47	95	putative cytochrome C1 heme lyase (CC1HL) ; (Z98601) cytochrome c1 heme lyase [Schizosaccharomyces pombe]



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19259	ENU03053	ANIS0C1079_1:92..931	32-51	811-830	NAP		g134966		153	1.00E-36	37	27	"STE6 protein ; ste6 protein - fission yeast (Schizosaccharomyces pombe) ; (X53254) ste6 [Schizosaccharomyces pombe] ; (AL049559) guanine-nucleotide releasing factor, Ste6p [Schizosaccharomyces pombe] ; ste6 gene [Schizosaccharomyces pombe]"
19260	ENU03054	ANIS0C7943: 2176..1335	28-47	799-827	NAP		g632081		103	1.00E-21			hypothetical protein 4 - Xanthobacter sp. ; (X79863) orf4 [Xanthobacter sp. Py2]
19261	ENU03055	ANIS0C8446: 6996..6155	47-68	823-846	NAP		g1654074	217	52	0.000005	34	55	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19262	ENU03056	ANIS0C4954: 5249..4407	39-59	820-839	NAP		g2497056	327	105	8.00E-24	31	60	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19263	ENU03057	ANIS0C2666: 4935..4092	45-64	826-845	NAP		g130971	531	193	1.00E-48	47	93	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) precursor - Pseudomonas aeruginosa (strain PAO) ; (M33557) delta-1-pyrroline-5-carboxylate reductase (EC 1.5.1.2) [Pseudomonas aeruginosa] ; (D30688) cytochrome P-450 17 alpha-hydroxylase/C17,20-lyase [Equus caballus]"
19264	ENU03058	ANIS0C4625_4_1:1..844	22-53	796-823	NAP		g1132477		50	9.00E-10			(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19265	ENU03059	ANIS0C3373: 1622..2465	66-87	848-867	NAP		g1654074	1763	246	e-100	78	54	"(Z99113) endo-1,4-beta-xylanase (xylanase D) [Bacillus subtilis]"
19266	ENU03060	ANIS0C9674: 2561..3405	22-49	799-824	NAP		g2634199	426	174	7.00E-43	38	53	lactate 2-monooxygenase (lactate oxidase) ; lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis]
19267	ENU03061	ANIS0C45:26 48..3492	62-81	845-864	NAP		g125886	657	183	1.00E-45	40	70	(AL023634) cyclin [Schizosaccharomyces pombe]
19268	ENU03062	ANIS0C3172: 1727..881	33-54	818-837	NAP		g3150260	169	67	1.00E-10	28	71	

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Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19269	ENU03063	ANI61C2645: 314..1160	22-49	805-826	NAP		g2132011	501	208	5.00E-53	42	94	hypothetical protein YOL080c - yeast (Saccharomyces cerevisiae) ; (Z74822) ORF YOL080c [Saccharomyces cerevisiae]
19270	ENU03064	ANI61C1036 2:2974..3822	58-80	838-864	NAP		g3334212	1108	235	5.00E-97	65	82	delta-aminolevulinic acid dehydratase (porphobilinogen synthase) (ALADH) ; (AF038566) porphobilinogen synthase [Candida glabrata]
19271	ENU03065	ANI61C6401: 104..953	22-54	809-829	NAP		g3880867	728	217	1.00E-55	56	56	(AL032639) predicted using GeneFinder; similar to Iron-containing alcohol dehydrogenases; cDNA EST yk372c11.5 comes from this gene; cDNA EST yk304d8.3 comes from this gene; cDNA EST yk304d8.5 comes from this gene; cDNA EST yk26... UTR2 protein - yeast (Saccharomyces cerevisiae) ; (U18779) Utr2p [Saccharomyces cerevisiae]
19272	ENU03066	ANI61C5735: 923..74	22-46	807-829	NAP		g320712	418	159	2.00E-38	31	60	hypothetical 42.4 KD protein in CDC12-ORC6 intergenic region ; hypothetical protein YHR112c - yeast (Saccharomyces cerevisiae) ; (U00059) Yhr112cp [Saccharomyces cerevisiae]
19273	ENU03067	ANI61C8613: 3511..2662	27-47	800-834	NAP		g731700	817	252	3.00E-66	47	71	"mitogen-activated protein kinase HOG1 (MAP kinase HOG1) (osmosensing protein HOG1) ; protein kinase HOG1 (EC 2.7.1.-), mitogen-activated - yeast (Saccharomyces cerevisiae) ; (X89514) mitogen-activated protein kinase [Saccharomyces cerevisiae] ; (Z73285) ORF YLR113w [Saccharomyces cerevisiae]"
19274	ENU03068	ANI61C8213: 10..859	23-54	805-830	NAP		g2507192	584	158	5.00E-38	63	47	hypothetical 36.7 KD protein C2F7.14C in chromosome I ; hypothetical protein SPAC2F7.14c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe]
19275	ENU03069	ANI61C8076: 852..1	36-55	817-845	NAP		g1175376	475	184	6.00E-46	54	67	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19276	ENU03070	ANI61C1075	59-78	851-870	NAP		g285211	366	128	4.00E-29	40	51	"[3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase (EC 2.7.1.115) - rat ; branched-chain alpha-ketoacid dehydrogenase kinase 44 kda isoform [rats, lung, heart, Peptide Mitochondrial, 412 aa] ; (M93271) branched-chain alpha-ketoacid dehydrogenase kinase [Rattus norvegicus] "
19277	ENU03071	ANI61C1018	52-71	842-864	NAP		g4007783	320	85	7.00E-26	37	72	"(X72850) hydroxyquinol 1,2-dioxygenase [Sphingomonas sp.] "
19278	ENU03072	ANI61C5164	40-59	834-853	NAP		g1169885	966	314	7.00E-85	65	25	putative glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system P-protein) ; hypothetical protein SPAC13G6.06c - fission yeast (Schizosaccharomyces pombe) ; (Z54308) putative glycine dehydrogenase (decarboxylase) [Schizosaccharomyces pombe] (Z64354) unknown
19279	ENU03073	ANI61C8668	58-77	849-871	NAP		g4160354	274	119	3.00E-26	31	93	[Schizosaccharomyces pombe] (Z64354) unknown
19280	ENU03074	ANI61C1132	24-43	819-838	NAP		g2190516	224	99	3.00E-20	34	91	[Schizosaccharomyces pombe] (Y13635) Vip1 protein
19281	ENU03075	ANI61C1081	37-56	832-851	NAP		g632081	285	87	2.00E-23	41	84	[Schizosaccharomyces pombe] (AL009197) hypothetical protein [Schizosaccharomyces pombe]
19282	ENU03076	ANI61C3713	53-72	846-867	NAP		g1894771	362	135	3.00E-31	31	57	hypothetical protein 4 - Xanthobacter sp. ; (X79863) orf4 [Xanthobacter sp. Py2]
19283	ENU03077	ANI61C539	28-47	823-842	NAP		g3183310	235	112	3.00E-24	46	95	(Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] ; (Z99122) similar to metabolite transport protein [Bacillus subtilis]
													hypothetical 23.2 KD protein CSD6.06c in chromosome I ; (Z98056) putative osmotolerance protein [Schizosaccharomyces pombe]

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19284	ENU03078	ANI61C1029:	51-70	838-866	NAP		g1175915	189	64	7.00E-14	44	44	hypothetical 28.8 KD protein in SMC1-SEC4 intergenic region ; probable membrane protein YFL006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL006W [Saccharomyces cerevisiae] ; (D44604) unknown [Saccharomyces cerevisiae]
		1179..322											
19285	ENU03079	ANI61C3377:	22-49	816-837	NAP		g3192044	226	86	3.00E-16	36	80	(AL023796) hypothetical protein [Schizosaccharomyces pombe]
		1390..2247											
19286	ENU03080	ANI61C683:1	22-51	814-837	NAP		g134777	248	128	6.00E-29	29	84	stage V sporulation protein K ; spo VJ protein - Bacillus subtilis ; (X59412) spo VJ [Bacillus subtilis]
		456..599											(Y13623) multifunctional protein2 [Cavia porcellus]
19287	ENU03081	ANI61C1140	43-63	840-859	NAP		g3005897	338	175	4.00E-43	34	38	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
		7:1618..2476											ubiquinol-cytochrome C reductase
19288	ENU03082	ANI61C7321:	61-80	858-878	NAP		g1654074	240	118	5.00E-26	29	57	iron-sulfur subunit precursor (Rieske iron-sulfur protein) (RISP) ; ubiquinol-cytochrome-c reductase (EC 1.10.2.2)
		2751..1892											iron-sulfur protein - Neurospora crassa ; (X02472) cytochrome c reductase
19289	ENU03083	ANI61C9902:	70-89	869-888	NAP		g136704	666	162	1.00E-47	66	85	iron-sulfur subunit [Neurospora crassa]
		639..475											branched-chain amino acid aminotransferase (BCAT) ; (AE000647) branched-chain-amino-acid aminotransferase (ilvE) [Helicobacter pylori 26695]
19290	ENU03084	ANI61C7849:	33-54	819-852	NAP		g3024012	404	184	6.00E-46	36	82	acid aminotransferase (ilvE) (AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]
		1987..1126											probable adenosine deaminase (adenosine aminohydrolase) ; adenosine deaminase homolog YNL141w - yeast (Saccharomyces cerevisiae) ; (Z46843) adenosine deaminase (putative) [Saccharomyces cerevisiae] ; (Z71417) ORF YNL141w [Saccharomyces cerevisiae]
19291	ENU03085	ANI61C1875:	54-74	854-873	NAP		g4539944	218	76	1.00E-20	37	65	
		33..894											
19292	ENU03086	ANI61C8984:	23-42	821-843	NAP		g1703166	704	218	4.00E-56	45	80	
		1974..1112											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19293	ENU03087	AN161C229:3	59-83	857-880	NAP		g549723	738	282	2.00E-75	54	39	hypothetical 75.5 KD protein in SDH1-CIM5/YTA3 intergenic region ; hypothetical protein YKL146w - yeast (Saccharomyces cerevisiae) ; (Z28146) ORF YKL146w [Saccharomyces cerevisiae]
		436..2573											
19294	ENU03088	AN161C6709: 3506..2643	58-76	853-879	NAP		g2104455	456	98	8.00E-38	48	77	(Z95397) unknown [Schizosaccharomyces pombe]
19295	ENU03089	AN161C9444: 1599..735	22-49	825-844	NAP		g1542843	397	162	4.00E-39	34	94	(D87681) acetyltransferase [Aspergillus awamori]
19296	ENU03090	AN161C2926: 4377..3210	67-86	867-890	NAP		g2645229	457	129	3.00E-43	37	58	(U78597) kinesin light chain [Plectonema boryanum]
19297	ENU03091	AN161C5745: 29..894	50-72	854-873	NAP		g1078626	1501	413	e-114	99	19	bimD protein - Emericella nidulans ; (L03200) bimD [Emericella nidulans]
19298	ENU03092	AN161C9795: 3152..2286	24-55	829-848	NAP		g2388966	1410	294	4.00E-79	52	27	(Z98979) putative phosphatidylserine decarboxylase proenzyme [Schizosaccharomyces pombe]
19299	ENU03093	AN161C3270: 1954..2821	22-43	828-847	NAP		g1363743	1110	168	6.00E-41	42	35	probable membrane protein YLR241w - yeast (Saccharomyces cerevisiae) ; (U20865) Ylr241wp [Saccharomyces cerevisiae]
19300	ENU03094	AN161C7067: 928..61	55-74	861-880	NAP		g2494101	628	237	9.00E-62	41	74	mannitol-1-phosphate 5-dehydrogenase ; (U18943) mannitol-1-phosphate dehydrogenase [Bacillus stearothermophilus]
19301	ENU03095	AN161C3705: 2000..1133	53-72	852-878	NAP		g2649289		103	2.00E-21			(AE001015) acyl-CoA dehydrogenase (acid-9) [Archaeoglobus fulgidus]
19302	ENU03096	AN161C1705: 3803..4670	27-52	825-852	NAP		g1546072	1002	112	4.00E-24	31	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
19303	ENU03097	AN161C322:1	26-45	834-853	NAP		g2507070	1257	299	2.00E-80	62	57	N amino acid transport system protein (methyl/tryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19304	ENU03098	AN161C1188: 9136..8271	24-48	832-852	NAP		g4539455	365	154	6.00E-37	40	69	(AL049500) TSC23.70 [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19305	ENU03099	ANI61C9049:	22-52	827-850	NAP		g2500006	708	287	5.00E-77	52	99	formyltetrahydrofolate D-formylase (formyl-FH(4) hydrolase); formyltetrahydrofolate deformylase (EC 3.5.1.10) - Corynebacterium sp.; (U23955) 10-formyltetrahydrofolate hydrolase [Corynebacterium sp.]; (AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]; (AL022197) putative protein [Arabidopsis thaliana]; (AF034260) protein kinase NRC-2 [Neurospora crassa]; "ribosomal protein L31.e.B, cytosolic - yeast (Saccharomyces cerevisiae); (U19729) Y1r406cp: member of L31E ribosomal protein family [Saccharomyces cerevisiae]" (AL022304) eukaryotic translation initiation factor 3 ma-binding subunit [Schizosaccharomyces pombe]; vacuolar protein sorting-associated protein VPS16; vacuolar protein sorting-associated protein VPS16 - yeast (Saccharomyces cerevisiae); (U44030) Vsp16p: Vacuolar sorting protein [Saccharomyces cerevisiae] (AE000715) chormsimate mutase/prephenate dehydratase [Aquifex aeolicus] hypothetical 36.4 KD protein in SMP1-MBA1 intergenic region; probable membrane protein YBR183w - yeast (Saccharomyces cerevisiae); (Z36052) ORF YBR183w [Saccharomyces cerevisiae]; (U02073) unknown [Saccharomyces cerevisiae] (AL022072) arginine n-methyltransferase [Schizosaccharomyces pombe] (AF052566) beta-ketoacyl reductase [Pseudomonas aeruginosa]
		1749..879											
19306	ENU03100	ANI61C2649:	64-86	869-892	NAP		g3184098	307	142	4.00E-33	33	53	
		91..961											
19307	ENU03101	ANI61C1190:	25-44	825-853	NAP		g2980795	379	90	3.00E-40	45	97	
		7048..6177											
19308	ENU03102	ANI61C3127:	40-72	849-869	NAP		g2654106	1056	228	e-111	79	41	
		1166..295											
19309	ENU03103	ANI61C1713:	31-49	840-860	NAP		g1084846	321	96	2.00E-19	68	40	
		253..1124											
19310	ENU03104	ANI61C2402:	68-90	870-898	NAP		g3006180	545	121	8.00E-41	45	90	
		47..918											
19311	ENU03105	ANI61C5793:	33-57	843-863	NAP		g2507153	123	57	2.00E-10	24	33	
		1062..190											
19312	ENU03106	ANI61C212:2	22-53	833-852	NAP		g2983461		139	2.00E-32			
		78..1150											
19313	ENU03107	ANI61C1730:	39-59	851-870	NAP		g586314	199	47	3.00E-12	30	66	
		1945..1072											
19314	ENU03108	ANI61C8793:	24-51	836-855	NAP		g4008547	745	145	3.00E-47	42	55	
		1536..662											
19315	ENU03109	ANI61C6738:	22-49	832-854	NAP		g2970667	293	101	6.00E-21	35	73	
		6151..7026											

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19316	ENU03110	ANI61C6877:	22-46	827-854	NAP	NAP		g3724291	64	8.00E-16				(AB011417) phosphate permease [Gibberella zeae]
19317	ENU03111	1..875	ANI61C9103:	23-46	836-855	NAP		g2951785	248	66	3.00E-11	41	95	(AB011822) clathrin light chain [Schizosaccharomyces pombe]
19318	ENU03112	120..995	ANI61C1065	24-46	837-856	NAP		g3881189	413	103	1.00E-21	52	98	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...
19319	ENU03113	2584..3459	ANI61C4534:	59-78	865-892	NAP		g4164400	574	93	2.00E-18	36	41	(AL035248) putative cell surface protein by similarity [Schizosaccharomyces pombe]
19320	ENU03114	1350..2225	ANI61C9963:	22-46	834-855	NAP		g585956	397	108	5.00E-28	34	95	"probable mitochondrial 40S ribosomal protein S9 precursor; ribosomal protein S9 precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (Z36015) ORF YBR146w [Saccharomyces cerevisiae]"
19321	ENU03115	422..1297	ANI61C2000:	43-70	841-876	NAP		g585695	70	2.00E-11				pisatin demethylase (cytochrome P450 57A2); pisatin demethylase - fungus (Nectria haematococca); (X73145) pisatin demethylase [Nectria haematococca]

# Sequence Comparison

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19322	ENU03116	AN150C5234	28-50	843-862	NAP		g1170012		334	6.00E-91			UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase (GPT) (G1PT) (N-acetylglucosamine-1-phosphate transferase) (GLCNAC-1-P transferase) ; UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase (EC 2.7.8.15) - fission yeast (Schizosaccharomyces pombe) ; (U09454) UDP-N-acetylglucosamine: dolichyl phosphate N-acetylglucosamine-1-phosphate transferase [Schizosaccharomyces pombe] ; (AL031349) N-acetylglucosamine-1-phosphate transferase [Schizosaccharomyces pombe]
19323	ENU03117	AN161C9036	22-50	837-856	NAP		g2132491	210	78	2.00E-24	33	81	probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr284cp [Saccharomyces cerevisiae]
19324	ENU03118	AN161C1093	22-51	835-856	NAP		g286165	498	217	6.00E-56	41	96	"(D14846) endo alpha-1,4 polygalactosaminidase precursor [Pseudomonas sp.] "
19325	ENU03119	AN161C2150	70-89	881-904	NAP		g1723784	264	75	7.00E-13	38	88	hypothetical 31.3 KD protein in TAF145-YOR1 intergenic region ; hypothetical protein YGR280c - yeast (Saccharomyces cerevisiae) ; (Z73065) ORF YGR280c [Saccharomyces cerevisiae]
19326	ENU03120	AN161C8019	66-85	874-903	NAP		g4154817	955	300	4.00E-87	61	86	(AE001466) putative [Helicobacter pylori J99]
19327	ENU03121	AN161C5895	23-46	841-860	NAP		g4490676	643	121	6.00E-63	68	98	(AL035655) ras-related protein [Schizosaccharomyces pombe]



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19328	ENU03122	AN161C538.3	45-65	864-883	NAP		g2132846	476	175	5.00E-43	32	55	probable membrane protein YOL119c-yeast [Saccharomyces cerevisiae] ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]
19329	ENU03123	AN161C1077	22-47	837-860	NAP		g482365	426	175	4.00E-43	51	97	protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) form II - bovine
19330	ENU03124	AN161C8.219	56-78	876-895	NAP		g130858	650	201	2.00E-59			proteasome component C7-alpha (macropain subunit C7-alpha) (proteinase YSCE subunit 7) (multicatalytic endopeptidase complex C7) (component Y8) (SCL1 suppressor protein) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain YC7-alpha - yeast (Saccharomyces cerevisiae) ; (M63641) proteasome Y8 [Saccharomyces cerevisiae] ; (M55440) yeast proteasome subunit YC7-alpha [Saccharomyces cerevisiae] ; (X56732) proteasome Y8 subunit [Saccharomyces cerevisiae] ; (Z72533) ORF YGL011c [Saccharomyces cerevisiae] ; (S58126) Unknown [Saccharomyces cerevisiae] ; proteasome PRS2 [Saccharomyces cerevisiae]
19331	ENU03125	AN161C1097	72-91	887-911	NAP		g1086919		84	1.00E-15			(U41279) similar to E. coli acyl-CoA thioesterase II (SP:P23911) [Caenorhabditis elegans]
19332	ENU03126	AN161C8922.	63-82	881-904	NAP		g2499790	1425	388	e-107	98	94	antigen 1 precursor (ASPND1) ; (Z50175) Aspergillus nidulans antigen 1 [Emmericella nidulans] (X98252) HA Vcr-1 protein [Chlorococcus aethiops]
19333	ENU03127	AN150C6641	40-59	862-881	NAP		g1526574		46	0.0002			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19334	ENU03128	ANI61C8587: 4021..3138	22-47	841-863	NAP		g731865	313	96	4.00E-19	26	50	hypothetical 59.6 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YIL121w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae]
19335	ENU03129	ANI61C905:2 334..3218	22-50	843-864	NAP		g4336889	961	189	2.00E-78	97	92	(AF107254) cyclophilin B; CYPB [Emeticella nidulans]
19336	ENU03130	ANI61C6956: 112..996	53-76	865-895	NAP		g1710852	786	189	2.00E-55	93	94	GTP-binding protein SARA ; (Z67742) sara [Aspergillus niger]
19337	ENU03131	ANI61C8618: 1156..2040	43-62	860-885	NAP		g4038630	523	122	1.00E-47	58	99	(AL032684) ER lumen protein retaining receptor protein [Schizosaccharomyces pombe]
19338	ENU03132	ANI61C1162: 1273..2157	71-90	882-913	NAP		g3702646	625	105	5.00E-25	34	47	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
19339	ENU03133	ANI61C9958: 948..63	47-66	871-890	NAP		g730502	721	277	1.00E-73			activator 1 41 KD subunit (replication factor C 41 KD subunit) ; replication factor C chain RFC2 - yeast (Saccharomyces cerevisiae) ; (D28499) Rfc2 protein [Saccharomyces cerevisiae] ; (U26028) Rfc2p [Saccharomyces cerevisiae] ; (Z49568) ORF YJR068w [Saccharomyces cerevisiae] ; (L47993) ORF YJR068w [Saccharomyces cerevisiae]
19340	ENU03134	ANI61C7904: 526..1411	22-46	846-865	NAP		g585304	596	188	5.00E-47			[Saccharomyces cerevisiae] eukaryotic translation initiation factor 5 (EIF-5) ; translation initiation factor eIF-5 - yeast (Saccharomyces cerevisiae) ; (Z68111) Tif5p [Saccharomyces cerevisiae] ; (Z71255) Tif5p [Saccharomyces cerevisiae] ; (Z73616) eukaryotic translation initiation factor 5 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer 843-870	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19341	ENU03135	ANI61C873:2	26-45			NAP		g1350594	699	136	5.00E-70	79	95	RHO1 protein ; Rho1 protein - fission yeast (Schizosaccharomyces pombe) ; hypothetical protein SPAC1F7.04 - fission yeast (Schizosaccharomyces pombe) ; (D38180) Rho1 [Schizosaccharomyces pombe] ; (Z67998) unknown [Schizosaccharomyces pombe] (U19882) FlbD [Emmericella nidulans] ; Myb-like DNA-binding protein [Emmericella nidulans] (AL034583) putative exonuclease [Schizosaccharomyces pombe] "putative D-3-phosphoglycerate dehydrogenase YIL074W (PGDH) ; hypothetical protein YIL074c - yeast (Saccharomyces cerevisiae) ; (Z37997) orf, len: 469, CAL: 0.23, similar to SERA_ECOLI P08328 D-3-phosphoglycerate dehydrogenase [Saccharomyces cerevisiae] " (D87444) Similar to S.cerevisiae EMP70 protein precursor (S25110) [Homo sapiens] haloacetate dehalogenase H-1 ; haloacetate dehalogenase (EC 3.8.1.3) H-1 - Moraxella sp. plasmid PUO1 ; (D90422) haloacetate dehalogenase H-1 [Moraxella sp.] ribonucleoside-Diphosphate reductase M2 chain (ribonucleotide reductase) ; ribonucleoside-diphosphate reductase (EC 1.17.4.1) chain M2 - mouse ; Protein R2 Of Ribonucleotide Reductase From Mouse ; (X15666) M2 ribonucleotide reductase [Mus musculus] ; (M14223) ribonucleotide reductase subunit M2 [Mus musculus]
19342	ENU03136	ANI61C9705: 4099..3213	45-64			NAP		g642577	1691	592	e-169	99	94	
19343	ENU03137	ANI61C4397: 29..917	50-71			NAP		g4056553	514	145	3.00E-34	42	43	
19344	ENU03138	ANI61C7016: 1144..2032	38-61			NAP		g731830	1371	277	1.00E-81	66	51	
19345	ENU03139	ANI61C7328: 1520..2409	43-63			NAP		g1665777	884	166	1.00E-48	44	41	
19346	ENU03140	ANI61C8058: 439..1327	72-91			NAP		g461925	408	188	4.00E-47	38	95	
19347	ENU03141	ANI61C8183: 2180..3069	25-50			NAP		g132626	877	182	2.00E-70			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19348	ENU03142	ANI61C6083:	63-83	892-911	NAP		g131771	473	179	4.00E-45	36	53	"probable metabolite transport protein GIT1 ; probable membrane protein YCR098c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR098c, len:518 [Saccharomyces cerevisiae] "
		1014..124											putative transporter C11D3.18C ; (Z68166) unknown
19349	ENU03143	ANI61C6144:	43-70	870-892	NAP		g1351714		134	8.00E-31			[Schizosaccharomyces pombe] (AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
		24..915											probable stergmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) ; (U34740) putative p450 monooxygenase [Emenccella nidulans]
19350	ENU03144	ANI61C7133:	35-54	865-884	NAP		g4104775	177	95	6.00E-19	28	70	TRNA-splicing endonuclease subunit SEN2 (TRNA-intron endonuclease) ; tRNA-splicing endonuclease beta chain - yeast (Saccharomyces cerevisiae) ; (M32336) tRNA splicing endonuclease beta-subunit [Saccharomyces cerevisiae] ; (U53876) Sen2p: tRNA-splicing endonuclease beta-subunit [Saccharomyces cerevisiae] ; (Z73277) ORF YLR105c [Saccharomyces cerevisiae]
		2531..3422											(Y16834) hexose transporter [Candida albicans]
19351	ENU03145	ANI61C5627:	53-80	882-902	NAP		g2493389	313	48	5.00E-13	30	45	"(AL031228) dl1033B10.9 (Short-chain alcohol dehydrogenase family member (HKE6, RING2)) [Homo sapiens] "
		952..61											(L07734) DNA polymerase delta [Schizosaccharomyces pombe] (AL021839) topoisomerase ii associated protein [Schizosaccharomyces pombe] (U78319) chitinase [Entamoeba histolytica]
19352	ENU03146	ANI61C1479:	53-75	879-903	NAP		g134427	269	87	1.00E-16			
		1081..189											
19353	ENU03147	ANI61C7638:	64-84	886-915	NAP		g3336839	365	108	8.00E-23	28	44	
		647..1540											
19354	ENU03148	ANI61C5168:	26-45	857-878	NAP		g3820984	239	103	2.00E-21	36	91	
		2742..1848											
19355	ENU03149	ANI61C7755:	63-87	895-916	NAP		g173384	1021	185	3.00E-94	66	25	
		123..1018											
19356	ENU03150	ANI61C363:	32-51	864-885	NAP		g2894266	759	159	4.00E-41	35	35	
		154..4049											
19357	ENU03151	ANI61C9942:	50-70	880-903	NAP		g1685362	459	179	3.00E-44	32	57	
		55..950											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19358	ENU03152	ANI61C7955:	57-76	893-912	NAP		g544276	1444	291	e-110	76	70	glutathione-dependent FORMaldehyde dehydrogenase (FDH) (FALDH); FDH1 protein - yeast (Candida maltosa) ; (M58332) encoding formaldehyde resistance [Candida maltosa]
19359	ENU03153	ANI61C9825:	64-83	900-919	NAP		g3023753	328	138	7.00E-32	35	94	potential formate transporter ; (U52681) FdhC [Methanobacterium thermoformicum]
19360	ENU03154	ANI61C1073	43-62	879-898	NAP		g416643	770	153	1.00E-70	63	69	"aristolochene synthase (sesquiterpene cyclase) (AS) ; sesquiterpene cyclase, aristolochene synthase, AS - Penicillium roqueforti ; (L05193) aristolochene synthase [Penicillium roqueforti] "
19361	ENU03155	ANI61C5905:	61-85	890-916	NAP		g1730741	392	60	0.000000	25	47	hypothetical 65.3 KDa protein in SUN4-MAS5 intergenic region ; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae) ; (U12141) membrane protein [Saccharomyces cerevisiae] ; (Z71341) ORF YNL065w [Saccharomyces cerevisiae]
19362	ENU03156	ANI61C1640:	49-68	883-904	NAP		g2583218	594	212	2.00E-54	51	21	(AF029913) beta glucosidase homolog [Cochliobolus heterostrophus]
19363	ENU03157	ANI61C7916:	72-93	910-929	NAP		g2132851	225	91	9.00E-18	29	55	probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae]
19364	ENU03158	ANI61C9393:	22-45	861-880	NAP		g1706221	106	55	0.000000	25	66	[Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae] cytochrome B5 ; cytochrome b5 - yeast (Saccharomyces cerevisiae) ; (Z69382) Cytochrome B5 [Saccharomyces cerevisiae] ; (Z71387) ORF YNL111c [Saccharomyces cerevisiae]
19365	ENU03159	ANI61C6658:	22-50	847-880	NAP		g2257554	806	210	3.00E-81	57	34	(AB004538) probable membrane protein YOL130w [Schizosaccharomyces pombe] ; (AL021766) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19366	ENU03160	ANI61C7097: 1027..126	69-88	909-928	NAP	g1363775	295	295	136	2.00E-31	40	90	hypothetical protein YDR041w - yeast (Saccharomyces cerevisiae) ; (Z54075) unknown [Saccharomyces cerevisiae]
19367	ENU03161	ANI61C5156: 49..951	53-72	894-913	NAP	g3133108	648	182	4.00E-45	64	93	(AL023554) 40s ribosomal protein s3. [Schizosaccharomyces pombe]	
19368	ENU03162	ANI61C7054: 1789..886	22-49	864-883	NAP	g1749716	1313	367	e-101	60	58	"(D89254) similar to Saccharomyces cerevisiae dihydroxy-acid dehydratase precursor, SWISS-PROT Accession Number P39522 [Schizosaccharomyces pombe]"	
19369	ENU03163	ANI61C7052: 3943..3037	47-68	888-911	NAP	g4587302	1541	226	2.00E-73	54	35	(AB016896) Pec1 [Schizosaccharomyces pombe]	
19370	ENU03164	ANI61C1092: 5:1380..474	46-69	876-911	NAP	g131768	178	62	3.00E-14	28	33	quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]	
19371	ENU03165	ANI61C2278: 1961..2868	22-43	868-887	NAP	g2257524	396	161	5.00E-39	40	95	(AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe]	
19372	ENU03166	ANI61C9199: 1466..557	43-62	882-909	NAP	g730753	863	235	7.00E-83			chromosome segregation protein SMC2 (DA-BOX protein SMC2) ; chromosome segregation protein SMC2 - yeast (Saccharomyces cerevisiae) ; (U05820) Smc2p [Saccharomyces cerevisiae] ; (D50617) chromosome segregation protein SMC2p [Saccharomyces cerevisiae] ; (D44602) DA-box protein Smc2p [Saccharomyces cerevisiae]	
19373	ENU03167	ANI61C1000: 4:4856..5763	22-45	865-888	NAP	g2388953	350	113	3.00E-37	42	96	[Saccharomyces cerevisiae] (Z98979) hypothetical protein [Schizosaccharomyces pombe]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19374	ENU03168	ANI61C6610:	24-59	869-890	NAP		g464862	503	498	e-140			26S protease regulatory subunit 7 homolog (CIM5 protein) (TAT-binding homolog 3) ; tat-binding protein homolog YTA3 - yeast
		1659..1842											(Saccharomyces cerevisiae) ; (X73571) 26S proteasome subunit Rpt1 [Saccharomyces cerevisiae] ; (Z22817) putative ATPase [Saccharomyces cerevisiae] ; (Z28145) ORF YKL145w [Saccharomyces cerevisiae] ; 26S protease [Saccharomyces cerevisiae] (AL033502) uroporphyrinogen-III synthase [Candida albicans] hydroxymethylglutaryl-CoA synthase (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) ; hydroxymethylglutaryl-CoA synthase - fission yeast (Schizosaccharomyces pombe) ; (U32187) 3-hydroxy-3-methylglutaryl coenzyme A synthase [Schizosaccharomyces pombe] ; (Z98530) itr1; myo-inositol transporter [Schizosaccharomyces pombe] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C lactate oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] (AL031525) mitochondrial carrier protein [Schizosaccharomyces pombe] hypothetical 81.2 KD protein in MES1-FOL2 intergenic region ; probable membrane protein YGR266w - yeast (Saccharomyces cerevisiae) ; (Z73051) ORF YGR266w [Saccharomyces cerevisiae] ; (Y07893) ORF YGR266w [Saccharomyces cerevisiae]
19375	ENU03169	ANI61C9449:	53-72	901-920	NAP		g3859663	70	5.00E-16				
19376	ENU03170	ANI61C1038	22-56	866-889	NAP		g1708240	1190	379	e-104			
		2:3308..2399											
19377	ENU03171	ANI61C7185:	36-56	884-904	NAP		g117803	635	169	2.00E-41	38	47	
		648..1558											
19378	ENU03172	ANI61C7334:	22-49	871-890	NAP		g3560163	925	201	8.00E-96	67	89	
		1694..784											
19379	ENU03173	ANI61C5271:	22-56	872-891	NAP		g1723773	128	59	0.000000	23	28	
		67..978								04			

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer 875-894	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19380	ENU03174	ANI61C4304:	25-44			NAP		g3169083	282	116	2.00E-25	34	79	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
19381	ENU03175	ANI61C8225:	22-52			NAP		g4587575	220	77	1.00E-20	28	96	"(AC006550) Belongs to PF01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gb AA585719, gb AA728503 and gb T22272 come from this gene. [Arabidopsis thaliana]"
19382	ENU03176	ANI61C1734:	22-50			NAP		g1351729	388	87	1.00E-17	43	73	MAL3 protein ; (Z68198) putative chromosome segregation protein [Schizosaccharomyces pombe] ; (Y09518) MAL3 protein [Schizosaccharomyces pombe] (AE000705) hypothetical protein [Aquifex aeolicus] (X91837) G1315 [Saccharomyces cerevisiae]
19383	ENU03177	ANI61C1699:	24-55			NAP		g2983324	578	201	4.00E-51	43	89	hypothetical oxidoreductase in MRP144-MTF1 intergenic region ; hypothetical protein YMR226c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae]
19384	ENU03178	ANI61C379:6	23-42			NAP		g1177632	187	91	9.00E-18	32	79	cytochrome P450 51 (CYP11) (P450-L1A1) (sterol 14-alpha demethylase) (eburicol 14-alpha-demethylase) (P450-14DM) ; lanosterol 14alpha-demethylase (EC 1.14.14.-) cytochrome P450 51 - Penicillium italicum ; (Z49750) cytochrome P-450 [Penicillium italicum]
19385	ENU03179	ANI61C499:5	40-59			NAP		g2492763	572	112	1.00E-44	54	94	Phosphatidylinositol-Specific Phospholipase C In Complex With Glucosamine-(Alpha-1-6)-Myo-Inositol
19386	ENU03180	ANI61C9494:	59-78			NAP		g2493386	1608	337	7.00E-92	58	57	Phosphatidylinositol-Specific Phospholipase C In Complex With Myo-Inositol ; Phosphatidylinositol-Specific Phospholipase C ; Phosphatidylinositol-Specific Phospholipase C In Complex With Glucosamine-(Alpha-1-6)-Myo-Inositol
19387	ENU03181	ANI61C8220:	44-64			NAP		g1633139	95	82	6.00E-15	29	91	





Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19399	ENU03193	AN161C1141	65-84	929-949	NAP	g515503	634	192	7.00E-50	43	55		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19400	ENU03194	AN161C6468	48-67	914-933	NAP	g2258125	892	171	6.00E-42	47	46		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19401	ENU03195	AN161C7752	33-52	902-920	NAP	g4049518	592	210	1.00E-62	48	76		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19402	ENU03196	AN161C9305	61-80	928-948	NAP	g2132923	747	287	7.00E-77	45	84		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19403	ENU03197	AN161C4048	41-63	909-928	NAP	g2414604	1119	146	4.00E-46	43	49		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19404	ENU03198	AN161C4601	23-53	893-912	NAP	g1709062	747	221	2.00E-84	55	71		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19405	ENU03199	AN161C1122	25-44	895-914	NAP	g3293547	249	85	1.00E-18	30	95		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19406	ENU03200	AN161C6208	29-50	894-921	NAP	g1709997	214	61	2.00E-17	40	18		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19407	ENU03201	AN161C1094	39-58	913-932	NAP	g2494090	90	90	3.00E-17				(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19408	ENU03202	AN161C2632	27-46	900-921	NAP	g2792328	370	152	3.00E-36	35	96		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]
19409	ENU03203	AN161C8017	36-55	911-930	NAP	g3378273	613	113	5.00E-50	43	79		(U12013) 4-coumarate-CoA ligase [Pinus taeda]; (U39404) 4-enzyme [Pinus taeda]; (U39405) 4-coumarate-CoA ligase [Pinus taeda]

Seq num	Seq id	Contig Source	Primer 3 pos	Primer 5 pos	Selection Basis	Database Hit	nchi gi	act Score	Blast Score	Blast Prob	% id	cvg	Description
19410	ENU03204	AN161S911:1	38-67	914-933	NAP		g4512354	216	98	1.00E-19	29	91	probable membrane protein YLR247c - yeast (Saccharomyces cerevisiae); (U20865) Ylr247cp [Saccharomyces cerevisiae]
19411	ENU03205	AN161C3367: 46-65	922-941	NAP		g2133310	551	139	8.00E-59	46	93	halodurans] 32.0k protein - Neurospora crassa; (L40806) open reading frame [Neurospora crassa]	
19412	ENU03206	AN161C8472: 27-49	901-922	NAP		g2492767		58	4.00E-23	35	98	ORF [Neurospora crassa] putative short-chain type dehydrogenase/reductase Y4mp; (Rhizobium sp. NGR234)	
19413	ENU03207	AN150346_1: 49-68	927-946	NAP		g728797	797	405	e-133	80	77	actin-like protein ro-4 - Neurospora crassa; (L31505) centractin [Neurospora crassa]	
19414	ENU03208	AN161C6286: 59-79	934-957	NAP		g3914053	1151	438	e-122	72	33	DNA mismatch repair protein MSH2; (AF030634) DNA mismatch repair protein [Neurospora crassa]	
19415	ENU03209	AN161C1109 9:12037..1109	939-964	NAP		g2408039	785	196	2.00E-80	56	42	synthesis-associated protein (Z99163) putative beta-glucan synthetase [Schizosaccharomyces pombe]	
19416	ENU03210	AN161C8920: 65-84	921-956	NAP		g131768	232	74	2.00E-12	25	54	quinase permease (quinate transporter), [Schizosaccharomyces pombe]	
19417	ENU03211	AN161C1682: 56-76	914-933	NAP		g4008461		108	6.00E-23			from this gene [Caenorhabditis elegans]	
19418	ENU03212	AN161C5444: 32-51	909-931	NAP		g2980819	226	96	4.00E-19	43	57	(A1224865) IgE-binding protein [Aspergillus fumigatus]	
19419	ENU03213	AN161C4081: 30-49	943-962	NAP		g3647337	268	100	2.00E-20	35	73	endonuclease subunit [Schizosaccharomyces pombe]	
19420	ENU03214	AN161C5488: 61-81											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19421	ENU03215	ANI61C7354:	59-78	938-960	NAP		g2769696	318	143	2.00E-33	33	80	(AC003982) unknown function; 60% similar to Z50177 (PID:g27403) (PID:g27402) [Homo sapiens]
19422	ENU03216	ANI61C1019	63-82	947-966	NAP		g2501598	411	120	2.00E-26	40	89	hypothetical 28.3 KD protein in PPR1-SNF7 intergenic region ; hypothetical protein YLR022c - yeast (Saccharomyces cerevisiae) ; (Z73194) ORF YLR022c [Saccharomyces cerevisiae]
19423	ENU03217	ANI61C5194:	37-56	922-941	NAP		g133961	801	128	2.00E-56	74	90	40S ribosomal protein S4 (omnipotent suppressor protein SUP44) (RP12) (S2E) ; ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) ; (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] ; (Z72645) ORF YGL123w [Saccharomyces cerevisiae] ; (X94106) SUP44 [Saccharomyces cerevisiae] (AL033503) transcription regulatory protein [Candida albicans] (L39639) kievitone hydratase [Fusarium solani] esterase D ; (AF112219) esterase D [Homo sapiens] (Z97204) hypothetical protein [Schizosaccharomyces pombe] ; (D13712) protein phosphatase [Schizosaccharomyces pombe] ; (AL031540) serine-threonine protein phosphatase [Schizosaccharomyces pombe]
19424	ENU03218	ANI61C152:	26-47	912-931	NAP		g3859681	446	198	7.00E-50	34	94	
19425	ENU03219	ANI61C8982:	22-46	898-928	NAP		g755011	263	134	1.00E-30	34	81	
19426	ENU03220	ANI61C7190:	49-67	937-956	NAP		g544254	688	212	3.00E-68	55	95	
19427	ENU03221	ANI61C8388:	22-43	908-929	NAP		g2226414	258	74	9.00E-16	43	99	
19428	ENU03222	ANI61C4017:	30-49	918-938	NAP		g548584	793	228	4.00E-59			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19429	ENU03223	ANI61C7183:	25-56	912-933	NAP		g2498438	58	48	0.00007	18	48	transcriptional coactivator HF11/ADA1 ; HF11 protein - yeast (Saccharomyces cerevisiae) ; (Z67751) putative protein [Saccharomyces cerevisiae] ; (Z73610) ORF YPL254w [Saccharomyces cerevisiae] ; (U76735) putative transcriptional coactivator [Saccharomyces cerevisiae] (AF063095) SEL1L [Mus musculus]
		1667..2617											
19430	ENU03224	ANI61C6626:	72-92	963-982	NAP		g4159995	577	130	2.00E-29	36	29	hypothetical 57.6 KD protein C3OD10.15 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
		5169..6121											
19431	ENU03225	ANI61C1070:	22-50	916-935	NAP		g3219924	276	52	0.000005	29	34	hypothetical 44.9 KD protein in URA10-NRC1 intergenic region ; probable membrane protein YMR272c - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae] (U85909) hydroxylase [Aureobasidium pullulans] (U68040) polyketide synthase [Cochliobolus heterostrophus] (U09358) Rcal1p [Saccharomyces cerevisiae] "(S83228) beta-isopropylmalate dehydrogenase [Aspergillus niger, strain A733, Peptide, 363 aa] [Aspergillus niger] ; (U51130) beta-isopropylmalate dehydrogenase [Aspergillus niger]" sorbitol utilization protein SOU1 ; (AF002134) Sou1p [Candida albicans] (AL033385) transketolase [Schizosaccharomyces pombe] (AC004450) putative carboxyphosphoenolpyruvate mutase [Arabidopsis thaliana]
		6:6101..5146											
19432	ENU03226	ANI61C6762:	70-91	956-984	NAP		g2493967	854	151	2.00E-75	53	72	
		994..1950											
19433	ENU03227	ANI61C8592:	40-59	934-954	NAP		g4099311	604	165	5.00E-40	44	62	
		19..976											
19434	ENU03228	ANI61C2749:	24-46	921-940	NAP		g1546072	373	173	2.00E-42	35	12	
		1407..449											
19435	ENU03229	ANI61C4206:	50-70	944-966	NAP		g508233	1246	191	e-106	67	35	
		76..1034											
19436	ENU03230	ANI61C4920:	51-77	949-969	NAP		g1911741	1223	326	e-121	82	82	
		1744..784											
19437	ENU03231	ANI61C9581:	24-46	925-944	NAP		g2492754	354	111	4.00E-33	38	87	
		3857..4819											
19438	ENU03232	ANI61C4572:	59-78	961-980	NAP		g3850070	1235	434	e-121	63	46	
		3699..2735											
19439	ENU03233	ANI61C1071:	29-48	916-951	NAP		g3763927	329	99	2.00E-41	39	58	
		8:1060..96											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19440	ENU03234	ANI61C8700:	32-49	927-955	NAP		g1703215	399	175	6.00E-43	31	51	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
19441	ENU03235	ANI61C8700:	32-49	927-955	NAP		g1703215	399	175	6.00E-43	31	51	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
19442	ENU03236	ANI61C8861:	50-69	959-978	NAP		g2131729	702	189	7.00E-66	50	36	hypothetical protein YLL029w - yeast (Saccharomyces cerevisiae) ; (Z73134) ORF YLL029w [Saccharomyces cerevisiae]
19443	ENU03237	ANI61C4087:	40-59	949-968	NAP		g464435	1346	507	e-143	69	77	acid phosphatase precursor ; acid phosphatase (EC 3.1.3.2) - Aspergillus ficuum ; (L20566) acid phosphatase [Aspergillus niger] (Z83867) fadB4 [Mycobacterium tuberculosis] hypothetical 103.4 KD TRP-ASP repeats containing protein C3D6.12 in chromosome II ; (Z95620) trp asp repeat protein [Schizosaccharomyces pombe]
19444	ENU03238	ANI61C9249:	22-52	932-952	NAP		g1781226	345	138	8.00E-32	34	92	hypothetical 103.4 KD TRP-ASP repeats containing protein C3D6.12 in chromosome II ; (Z95620) trp asp repeat protein [Schizosaccharomyces pombe]
19445	ENU03239	ANI61C1997:	23-44	933-954	NAP		g3183237	1374	244	8.00E-64	45	34	hypothetical 103.4 KD TRP-ASP repeats containing protein C3D6.12 in chromosome II ; (Z95620) trp asp repeat protein [Schizosaccharomyces pombe]
19446	ENU03240	ANI61C1025	25-46	921-956	NAP		g1351660	526	222	4.00E-57	45	78	endonuclease III homolog (DNA- (apurinic or apyrimidinic site) lyase) ; endonuclease III (EC 3.1.-.-) - fission yeast (Schizosaccharomyces pombe) ; hypothetical protein SPAC30D11.07-fission yeast (Schizosaccharomyces pombe) ; (Z67961) endonuclease III homolog [Schizosaccharomyces pombe]
19447	ENU03241	ANI61C6477:	41-60	951-972	NAP		g3169050	118	68	8.00E-11	32	64	(AL023702) hypothetical protein SC1C3.24 [Streptomyces coelicolor]

# Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19448	ENU03242	ANI61C9181:	51-70	961-983	NAP		g2497056	183	52	6.00E-12			putative dioxxygenase YLL057C; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae); (Z47973) ORF L0572 [Saccharomyces cerevisiae]; (Z73162) ORF YLL057c [Saccharomyces cerevisiae] hypothetical protein C17H9.20 in chromosome I; (Z98597) hypothetical protein [Schizosaccharomyces pombe] (D87681) acetylsterase [Aspergillus awamori]
19449	ENU03243	ANI61C8589:	24-44	926-956	NAP		g3183360	411	155	4.00E-37	27	57	[Saccharomyces cerevisiae] hypothetical protein C17H9.20 in chromosome I; (Z98597) hypothetical protein [Schizosaccharomyces pombe] (D87681) acetylsterase [Aspergillus awamori]
19450	ENU03244	ANI61C8537:	22-51	934-954	NAP		g1542843	1046	206	e-105	66	94	"DNA polymerase beta; Dna Polymerase Beta (Beta Polymerase) (E.C.2.7.7.7) (Apo, Full Protein); Rattus norvegicus; Rattus norvegicus; Rattus norvegicus"
19451	ENU03245	ANI61C266:	41-60	955-974	NAP		g585064	296	146	2.00E-34	28	95	(U59376) N-carbamoyl-D-amino acid amidohydrolase [Agrobacterium radiobacter]
19452	ENU03246	ANI61C9849:	47-67	950-982	NAP		g1401216	471	145	6.00E-34	41	95	"hypothetical 29.7 KD protein in HSPA-ALDA intergenic region; (D90780) ORF_ID:o270#1; similar to [SwissProt Accession Number P34209] [Escherichia coli]; (D90781) ORF_ID:o270#1; similar to [SwissProt Accession Number P34209] [Escherichia coli]; (AE000239) orf. hypothetical protein [Escherichia coli]"
19453	ENU03247	ANI61C4859:	22-46	931-960	NAP		g2506663	339	162	3.00E-39	38	99	(AB017112) mCAC [Mus musculus]
19454	ENU03248	ANI61C1038:	32-58	942-971	NAP		g4239974		68	1.00E-10			hypothetical GTP-binding protein in POP2-HOL1 intergenic region; hypothetical protein YNR053c - yeast (Saccharomyces cerevisiae); (Z71668) ORF YNR053c [Saccharomyces cerevisiae]
19455	ENU03249	ANI61C7390:	22-39	942-961	NAP		g1730685	1466	270	8.00E-72	67	44	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19456	ENU03250	ANI61C7332:	29-48	933-968	NAP		g3122261	843	164	2.00E-84	74	99	eukaryotic translation initiation factor 6 (EIF-6) ; hypothetical protein YPR016c - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz15p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] (AL033391) hypothetical membrane protein [Candida albicans] (Z98944) hypothetical protein [Schizosaccharomyces pombe] (AB010465) lactonohydrolase [Fusarium oxysporum] "hypothetical 67.7 KD protein C23C11.03 in chromosome I ; (Z98559) SPAC23C11.03; len:598aa, similar eg. to YJR002W, YJX2 yeast, P47083, hypothetical 67.0 kd protein, (593aa), fasta scores, opt:855, E0:0, (33.0% identity in 610 aa overlap) [Schizosaccharomyces pombe]"
19457	ENU03251	ANI61C8252:	58-77	977-997	NAP		g3850125	624	199	3.00E-50	35	63	tubulin alpha-2 chain ; tubulin alpha-2 chain - Emeritella nidulans (AL035570) putative nitrilase homolog [Schizosaccharomyces pombe] (AF002660) aflatoxin [Aspergillus parasiticus] probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) ; (Z75170) ORF YOR262w [Saccharomyces cerevisiae] "2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase - Escherichia coli ; (Z47799) 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [Escherichia coli] ; (Z37980) hypothetical 2,4-dihydroxy-hepta-2-ene-1,7-dioate aldolase [Escherichia coli]"
19458	ENU03252	ANI61C1118	31-53	946-971	NAP		g2370496	354	173	1.00E-42	33	35	(AJ223327) rAsp f9 [Aspergillus fumigatus]
19459	ENU03253	ANI61C9343:	60-79	973-1001	NAP		g3810873	478	150	1.00E-35	41	76	
19460	ENU03254	ANI61C9255:	48-78	969-989	NAP		g3183346	559	215	5.00E-55	38	53	
19461	ENU03255	ANI61C3731:	32-51	954-973	NAP		g135407	1617	590	e-168	97	67	
19462	ENU03256	ANI61C1106	31-50	942-977	NAP		g4467274	575	206	2.00E-52	48	97	
19463	ENU03257	ANI61C6325:	45-65	970-991	NAP		g2738309	408	73	1.00E-27	31	70	
19464	ENU03258	ANI61C4666:	51-73	980-998	NAP		g2132930	814	222	3.00E-57	47	83	
19465	ENU03259	ANI61C4278:	42-61	955-990	NAP		g1073302	269	126	3.00E-28	30	100	
19466	ENU03260	ANI61C1072	29-50	955-977	NAP		g2879890	503	220	1.00E-56	37	99	



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19467	ENU03261	AN161C9659:	72-98	1002-1021	NAP		g1723239	784	314	6.00E-85	55	93	hypothetical 35.7 KD protein C26A3.11 in chromosome I ; (Z69240)
		1464..473											putative amidohydrolase [Schizosaccharomyces pombe]
19468	ENU03262	AN161C7455:	65-84				g417090	878	138	2.00E-84			GTP-binding nuclear protein GSP1/CNR1 ; GTP-binding protein GSP1 - yeast (Saccharomyces cerevisiae) ; (L08690) GTP-binding protein [Saccharomyces cerevisiae] ; (X71945) CNR2 [Saccharomyces cerevisiae] ; (U17243) GTP-binding nuclear protein. Highly similar to GSP2_yeast. Belongs to the Ran family of Ras proteins [Saccharomyces cerevisiae]
		6773..7764											[AL031825] putative membrane transport protein [Schizosaccharomyces pombe]
19469	ENU03263	AN161C5172:	33-52				g3702646	298	78	3.00E-26	31	54	(AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]
		3310..2318											hypothetical 33.5 KD protein C1D4.02C in chromosome I ; (Z69239) unknown [Schizosaccharomyces pombe]
19470	ENU03264	AN161C7232:	22-52				g3647335	145	67	2.00E-10	25	74	cytochrome C PEROxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast (Saccharomyces cerevisiae) ; (X62422) Cytochrome c peroxidase [Saccharomyces cerevisiae] ; (Z28291) ORF YKR066c [Saccharomyces cerevisiae]
		5559..4567											hypothetical 32.6 KD protein in DAL5-TH11 intergenic region ; aryl-alcohol dehydrogenase homolog YJR155w - yeast (Saccharomyces cerevisiae) ; (Z49655) ORF YJR155w [Saccharomyces cerevisiae]
19471	ENU03265	AN161C3420:	22-46				g1723224	302	96	5.00E-19	32	99	
		1758..2750											
19472	ENU03266	AN161C9030:	66-85				g543969	478	217	7.00E-56	44	74	
		2449..3441											
19473	ENU03267	AN161C2045:	58-78				g1352946	411	73	2.00E-21	42	94	
		3325..2331											

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19474	ENU03268	ANI61C1109	22-57	953-973	NAP		g1293655	783	249	3.00E-65	44	49	(U51327) versicolorin B synthase [Aspergillus parasiticus]; (U51328) versicolorin B synthase [Aspergillus parasiticus]
		0:630..1622											
19475	ENU03269	ANI61C9633:	38-57	970-989	NAP		g3668160	203	59	0.000000	23	47	(AL031764) hexose transporter. [Schizosaccharomyces pombe]; (AF098076) ght6p [Schizosaccharomyces pombe] (U42349) 39 kDa encoded by N33 [Homo sapiens]
		3640..3430								04			putative thiosulfate sulfoxidase; hypothetical protein YOR251c - yeast (Saccharomyces cerevisiae); (Z75159) ORF YOR251c [Saccharomyces cerevisiae]
19476	ENU03270	ANI61C7613:	22-45	950-974	NAP		g1333673	151	62	2.00E-17	30	75	UDP-glucose--glycoprotein glucosyltransferase (EC 2.7.8.19) - fission yeast (Schizosaccharomyces pombe); (U38417) UDP-Glc:Glycoprotein Glucosyltransferase [Schizosaccharomyces pombe]
		205..1199											
19477	ENU03271	ANI61C1373:	24-43	949-977	NAP		g3122964	432	129	3.00E-50	41	94	
		141..1136											
19478	ENU03272	ANI61C7897:	43-62	976-996	NAP		g2131132	1110	444	e-124	66	22	glucose-6-phosphate 1-dehydrogenase (NADP+) (EC 1.1.1.43) - fission yeast (Schizosaccharomyces pombe); (U38417) UDP-Glc:Glycoprotein Glucosyltransferase [Schizosaccharomyces pombe]
		22..1017											
19479	ENU03273	ANI61C1083	22-46	957-976	NAP		g1708467	333	148	4.00E-35	35	82	branched-chain amino acid aminotransferase (transaminase B) (BCAT); branched-chain-amino-acid transaminase homolog - Haemophilus influenzae (strain Rd KW20); (U32798) branched-chain-amino-acid transaminase (ilvE) [Haemophilus influenzae Rd]
		7:1059..63											lactose permease; lactose permease - yeast [Kluyveromyces marxianus var. lactis]; (X06997) lactose permease (AA1-587) [Kluyveromyces lactis] (AL023780) DNA binding protein [Schizosaccharomyces pombe] (AB010442) PMR1 [Penicillium digitatum] (AF010494) sorbitol dehydrogenase [Callitrix sp.]
19480	ENU03274	ANI61C5227:	46-65	973-1000	NAP		g125935	578	76	2.00E-35	36	46	
		997..1											
19481	ENU03275	ANI61C9066:	26-48	951-981	NAP		g3184115	377	166	3.00E-40	30	63	
		9..1006											
19482	ENU03276	ANI61C4858:	54-74	981-1009	NAP		g3288709	1234	458	e-128	68	22	
		43..1040											
19483	ENU03277	ANI61C1942:	45-65	975-1001	NAP		g2352843	715	104	5.00E-36	42	80	
		3132..2133											

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19484	ENU03278	ANI61C9666:	33-53	965-990	NAP		g2132925	517	263	2.00E-69	41	77	[Saccharomyces cerevisiae] ; (Z75153) ORF YOR245c
		4320..3321											[Saccharomyces cerevisiae] UTR1 protein (unknown transcript 1 protein) ; UTR1 protein - yeast (Saccharomyces cerevisiae) ; (L26347) orf gle530 [Saccharomyces cerevisiae] ; (Z49549) ORF YJR049c
19485	ENU03279	ANI61C4960:	53-72	988-1010	NAP		g729534	739	146	1.00E-75	51	58	[Saccharomyces cerevisiae] ; (L36344) ORF; putative [Saccharomyces cerevisiae]
		3192..2193											histidinol-phosphate aminotransferase (imidazole acetol-phosphate transaminase) ; his 3 protein - fission yeast (Schizosaccharomyces pombe) ; (L19523) imidazoleglycerol-phosphate dehydratase [Schizosaccharomyces pombe] ; (L19524) imidazoleglycerol-phosphate dehydratase
19486	ENU03280	ANI61C6471:	42-61	973-1000	NAP		g547648	949	280	2.00E-92			[Schizosaccharomyces pombe] ; (AB004534) histidinol-phosphate aminotransferase
		11749..10749											[Schizosaccharomyces pombe] (Z99107) similar to hypothetical proteins [Bacillus subtilis] phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa] (AF052688) putative transmembrane transporter Liz1p
19487	ENU03281	ANI61C7553:	40-59	979-998	NAP		g2633013	351	145	1.00E-38	30	93	[Schizosaccharomyces pombe] (Z99107) similar to hypothetical proteins [Bacillus subtilis] phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa] (AF052688) putative transmembrane transporter Liz1p
		299..1299											[Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p
19488	ENU03282	ANI61C1037	49-72	989-1008	NAP		g130117	869	214	7.00E-55	35	56	[Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p
		3:5272..6273											[Schizosaccharomyces pombe] (AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]
19489	ENU03283	ANI61C1131:	34-53	964-994	NAP		g2981103		107	2.00E-22	39	21	[Schizosaccharomyces pombe] (AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]
		1000..250											[Schizosaccharomyces pombe] (AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]
19490	ENU03284	ANI61C7525:	23-47	964-983	NAP		g3169097	190	74	1.00E-12	28	85	[Schizosaccharomyces pombe] (AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]
		7424..8426											[Schizosaccharomyces pombe] (AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]

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19491	ENU03285	AN150C202_3:1765..2767	23-42	950-983	NAP		g2239196	257	6.00E-68	45	98	98	(Z97209) hypothetical protein [Schizosaccharomyces pombe]
19492	ENU03286	AN161C836:3785..4788	38-60	966-999	NAP		g133407	823	341	5.00E-93	60	62	tubulin alpha-2 chain - Emmericella nidulans
19493	ENU03287	AN150C721_1:3356..2353	25-50	967-986	NAP		g116929	272	3.00E-75	49	63	63	hexaprenyl pyrophosphate synthetase precursor (HPS) ; trans-pentaprenyltransferase (EC 2.5.1.33) precursor - yeast (Saccharomyces cerevisiae) ; (J05547) hexaprenyl pyrophosphate synthetase (COQ1) [Saccharomyces cerevisiae] ; (Z35872) ORF YBR003w [Saccharomyces cerevisiae]
19494	ENU03288	AN161C1055:7:3124..4127	34-53	976-995	NAP		g549725	332	126	8.00E-31			"NADH-cytochrome B5 reductase precursor (P34/P32) ; cytochrome-b5 reductase (EC 1.6.2.2), mitochondrial outer membrane form - yeast (Saccharomyces cerevisiae) ; (Z26877) unknown [Saccharomyces cerevisiae] ; (Z28150) ORF YKL150w [Saccharomyces cerevisiae] ; (X81474) NADH-cytochrome b5 reductase [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] "
19495	ENU03289	AN161C562:1854..850	22-48	964-984	NAP		g1346485	889	182	3.00E-54	41	53	malate oxidoreductase (malic enzyme) (ME) (NADP-dependent malic enzyme) (NADP-ME) ; (X56233) malic enzyme [Populus balsamifera subsp. trichocarpa] (M96667) proteosome-related protein [Saccharomyces cerevisiae]
19496	ENU03290	AN161C30:3623..2618	23-52	967-986	NAP		g172260	721	111	6.00E-38	67	52	hypothetical 55.1 KD protein in FAB1-PE54 intergenic region ; probable membrane protein YFR021w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR021W [Saccharomyces cerevisiae] (Z99126) hypothetical oxidoreductase [Schizosaccharomyces pombe]
19497	ENU03291	AN161C8552:8701..9708	72-94	1018-1037	NAP		g1176002	452	164	7.00E-40	32	60	probable serine/threonine-protein kinase C29A4.16 ; (Z97210) protein kinase [Schizosaccharomyces pombe]
19498	ENU03292	AN161C1658:3373..2365	22-44	968-988	NAP		g2398818	192	61	1.00E-23	36	73	
19499	ENU03293	AN161C1649:2056..1048	36-55	976-1002	NAP		g3183055	461	216	2.00E-55	41	47	

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19500	ENU03294	ANI61C1183:	28-47	976-995	NAP		g418391	589	236	1.00E-61	39	88	"ZRT1" protein ; zinc transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (X67787) ORF1 [Saccharomyces cerevisiae] ; (X94357) ORF NRC376; EMBL:SCFZF1;X67787; PIR:DEBY4;S07614 [Saccharomyces cerevisiae] ; (Z72777) ORF YGL255w [Saccharomyces cerevisiae]" (Z98597) hypothetical nadh-cytochrome reductase
19501	ENU03295	ANI61C6843:	46-65	994-1013	NAP		g2330719	105	73	2.00E-12	32	93	[Schizosaccharomyces pombe] ubiquitin--protein ligase RSP5 ; hypothetical protein YER125w - yeast (Saccharomyces cerevisiae) ; (U18916) Rsp5p [Saccharomyces cerevisiae] (AB016895) Pop3 [Schizosaccharomyces pombe] glycerol-3-phosphate dehydrogenase (NAD+) 1 ; glycerol-3-phosphate dehydrogenase (NAD+) (EC 1.1.1.8) precursor - yeast (Saccharomyces cerevisiae) ; (Z24454) glycerol 3-phosphate dehydrogenase [Saccharomyces cerevisiae] ; (U04621) dihydroxyacetone phosphate reductase [Saccharomyces cerevisiae] ; (X76859) glycerol-3-phosphate dehydrogenase (NAD+) [Saccharomyces cerevisiae] ; (Z48432) glycerol-3-phosphate dehydrogenase (NAD+) (X76859) [Saccharomyces cerevisiae] ; (Z74071) ORF YDL022w [Saccharomyces cerevisiae] (AF092576) translation initiation factor eIF3 p40 subunit; eIF3p40 [Homo sapiens] (AB000703) phosphomannomutase [Schizosaccharomyces pombe] (AL023533) hypothetical protein [Schizosaccharomyces pombe]
19502	ENU03296	ANI61C9202:	22-48	968-990	NAP		g730684	2522	226	e-113	73	35	
19503	ENU03297	ANI61C6531:	22-55	971-990	NAP		g3434986	778	255	1.00E-85	62	81	
19504	ENU03298	ANI61C1100	25-45	973-993	NAP		g462197	726	223	6.00E-59			
19505	ENU03299	ANI61C4362:	31-51	980-1000	NAP		g3986482	414	99	2.00E-40	37	80	
19506	ENU03300	ANI61C7112:	31-51	967-1000	NAP		g1813335	721	176	2.00E-75	63	99	
19507	ENU03301	ANI61C1095:	34-55	985-1004	NAP		g3130060	914	115	5.00E-25	32	37	

# Sequence Description

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19508	ENU03302	AN150C66_1	22-51	966-993	NAP		g2879890		245	e-101	70	91	(AJ223327) rAsp f9 [Aspergillus fumigatus]
19509	ENU03303	AN161C9775	33-61	985-1004	NAP		g3873958	194	103	2.00E-21	26	95	(Z81458) similar to transposable element [Caenorhabditis elegans]
19510	ENU03304	AN161C8634	22-51	971-994	NAP		g538066	181	62	0.000000	25	96	(M77661) putative gag protein [Magnaporthe grisea]
19511	ENU03305	AN161C8943	55-80	997-1027	NAP		g3426039	273	127	9.00E-29	49	25	(AC005168) unknown protein [Arabidopsis thaliana]
19512	ENU03306	AN161C1622	29-48	974-1001	NAP		g549739	163	101	9.00E-21	34	37	hypothetical 55.4 KD protein in STE3-GIN10 intergenic region ; hypothetical protein YKL175w - yeast [Saccharomyces cerevisiae] ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28175) ORF YKL175w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] (AF014404) HIV-Nef associated acyl CoA thioesterase [Homo sapiens] ; (AL008726) dJ337O18.3.1 (Thioesterase II) (isoform 1) [Homo sapiens] (AF009672) unknown [Acinetobacter sp. ADP1] (AL022019) putative 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase(3beta-hsd) [Schizosaccharomyces pombe] (AL031786) putative delta-1-pyrroline-5-carboxylate dehydrogenase [Schizosaccharomyces pombe] (AF009418) triphosphate biosynthesis transcription factor [Myrothecium roridum] (AL021815) hypothetical protein [Schizosaccharomyces pombe] ; (AL035675) adducin N terminal domain protein [Schizosaccharomyces pombe] (U68714) isocitrate lyase 1 [Botryotinia fuckeliana]
19513	ENU03307	AN161C9973	38-57	992-1011	NAP		g2318125	316	82	4.00E-18	38	75	
19514	ENU03308	AN161C1292	59-78	1014-1034	NAP		g2271503		64	7.00E-17			
19515	ENU03309	AN161C1011	22-56	978-997	NAP		g2924499	331	124	8.00E-28	35	91	
19516	ENU03310	AN161C1143	68-91	1022-1044	NAP		g3687478	1534	414	e-115	60	61	
19517	ENU03311	AN161C541	23-49	971-999	NAP		g2267603	246	121	9.00E-27	35	54	
19518	ENU03312	AN161C7921	24-58	970-1001	NAP		g2879861	148	84	1.00E-17	25	97	
19519	ENU03313	AN161C8093	33-52	992-1011	NAP		g3282211	1131	211	e-117	70	69	

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19520	ENU03314	ANI61C1147	36-55	1000-1017	NAP		g3318897	337	161	8.00E-39	30	48	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum"
19521	ENU03315	ANI61C1118: 58-78 5506..6530		1020-1040	NAP		g3150262	713	178	4.00E-44	42	85	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
19522	ENU03316	ANI61C7162: 24-44 1316..291		984-1006	NAP		g2492816		74	3.00E-24			uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]
19523	ENU03317	ANI61C4572: 38-71 1170..2195		1002-1021	NAP		g1174417	970	129	5.00E-42	71	65	spermidine synthase (putrescine aminopropyltransferase) (SPDSY) ; (Z54140) putrescine aminopropyltransferase
19524	ENU03318	ANI61C6048: 49-71 28..1055		1013-1034	NAP		g1723920	355	134	1.00E-31	40	77	[Schizosaccharomyces pombe] hypothetical 37.4 KD protein in SEC27-SSM1B intergenic region ; hypothetical protein YGL136c - yeast (Saccharomyces cerevisiae) ; (X92670) G2830 [Saccharomyces cerevisiae] ; (Z72658) ORF YGL136c [Saccharomyces cerevisiae]
19525	ENU03319	ANI61C1082 27-46 6:2111..1083		993-1012	NAP		g1351122	1143	324	e-122	74	98	[Saccharomyces cerevisiae] thiazole biosynthetic enzyme (stress-inducible protein STI35) ; stress-inducible protein sti35 - fungus (Fusarium oxysporum) ; (M33643) STI35 protein [Fusarium oxysporum]
19526	ENU03320	ANI61C1026 55-79 5:1499..471		1012-1041	NAP		g3183345	259	127	1.00E-28	36	61	hypothetical 33.9 KD protein C14C4.12C in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]
19527	ENU03321	ANI61C7819: 25-44 5645..4616		993-1012	NAP		g1083757	781	156	4.00E-55	44	25	plasma membrane Ca2+-ATPase isoform 4 - rat ; (U15408) plasma membrane Ca2+-ATPase isoform 4 [Rattus norvegicus]
19528	ENU03322	ANI61C1019 22-47 3:1386..356		991-1010	NAP		g2624697	1322	155	e-101	73	75	Pectin Lyase A

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19529	ENU03323	AN161C7349:	62-80	1032-1052	NAP	g1657510	628	175	8.00E-62	39	70		(U73857) betaine-aldehyde dehydrogenase [Escherichia coli]
19530	ENU03324	274..1306 AN161C1834:	54-73	1024-1044	NAP	g2500755	486	173	2.00E-47	57	31		response regulator MCS4 (mitotic catastrophe suppressor 4); (Y11927)
		4387..3355											Mcs4 protein [Schizosaccharomyces pombe]; (AF004694) Mcs4 [Schizosaccharomyces pombe]; (AL033388) response regulator mcs4 [Schizosaccharomyces pombe]
19531	ENU03325	AN161C9207:	53-75	1021-1043	NAP	g2894293	822	284	9.00E-76	43	65		(AL021837) hypothetical protein [Schizosaccharomyces pombe]
19532	ENU03326	94..1126 AN161C3172:	38-58	1004-1029	NAP	g1653791	159	104	1.00E-23	32	97		(D90916) hypothetical protein [Synechocystis sp.]
19533	ENU03327	3489..2456 AN161C1086	70-93	1033-1061	NAP	g3738189	314	131	6.00E-30	27	69		(AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe]
19534	ENU03328	5:3495..2461 AN161C8189:	71-101	1043-1062	NAP	g462023	715	129	4.00E-29	65	62		C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus; C-8 sterol isomerase - rice blast fungus; isomerase - rice blast fungus; (Z22775) C-8 sterol isomerase [Magnaporthe grisea]
19535	ENU03329	AN161C9130:	51-71	1022-1043	NAP	g399766	100	78	7.00E-14	29	59		gluconolactonase precursor (D-glucono--delta-lactone lactonohydrolase); gluconolactonase (EC 3.1.1.17) precursor - Zymomonas mobilis; (X67189) gluconolactonase [Zymomonas mobilis]
19536	ENU03330	AN161C9354:	24-49	987-1016	NAP	g1770301	196	71	7.00E-14	36	94		(X95074) Translin [Gallus gallus]
19537	ENU03331	1135..101 AN161C139:	40-62	1011-1032	NAP	g731893	1070	128	9.00E-56	47	54		putative transporter YIL166C; probable membrane protein YIL166C - yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces cerevisiae]
19538	ENU03332	AN161C1034	72-91	1030-1065	NAP	g2370487	1901	444	e-124	65	48		(Z98849) glutaryl-tma synthetase [Schizosaccharomyces pombe]



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19539	ENU03333	AN161C4602:	49-75	1023-1042	NAP		g1723769	269	55	3.00E-11			putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
19540	ENU03334	AN161C7359:	28-47	1002-1021	NAP		g3925755	533	246	2.00E-64	39	65	(AL034352) putative phosphodiesterase-nucleotide pyrophosphatase precursor [Schizosaccharomyces pombe]
19541	ENU03335	AN161C1897:	24-51	999-1018	NAP		g3434937	503	158	5.00E-38	61	94	(AB000281) krev-1 [Neurospora crassa]
19542	ENU03336	AN161C8156:	69-89	1043-1064	NAP		g3551511	910	320	9.00E-87	47	83	(AB016807) flavohemoglobin [Fusarium oxysporum]
19543	ENU03337	AN161C6276:	31-56	1007-1026	NAP		g129781	355	175	4.00E-43	32	87	Pepsinogen II-2/3 precursor (pepsinogen A) ; (M59235) pepsinogen [Oryctolagus cuniculus]
19544	ENU03338	AN161C7530:	22-48	993-1018	NAP		g4008577	348	111	8.00E-24	32	98	(AL034491) conserved hypothetical protein [Schizosaccharomyces pombe]
19545	ENU03339	AN161C5932:	59-78	1033-1055	NAP		g4512354	224	83	5.00E-20			(AB011836) alkyl hydroperoxide reductase large subunit [Bacillus halodurans]
19546	ENU03340	AN161C8268:	32-67	1010-1029	NAP		g2879890	782	185	4.00E-77	52	98	(AJ223327) rAsp f9 [Aspergillus fumigatus]
19547	ENU03341	AN161C1048:	27-47	1005-1024	NAP		g3915140	678	89	2.00E-46	36	63	Isotrichodermin C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides]
19548	ENU03342	AN161C8858:	22-41	996-1020	NAP		g2293194	303	152	3.00E-36	28	89	(AF008220) yreR [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]

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19549	ENU03343	AN161C2233:	24-46	1003-1022	NAP		g585542	541	223	1.00E-57			putative NADH-cytochrome B5 reductase (P35) ; cytochrome-b5 reductase (EC 1.6.2.2) - yeast (Saccharomyces cerevisiae) ; (Z28365)
		3..1043											cytochrome b5 reductase [Saccharomyces cerevisiae] ; (Z46861)
													cytochrome b5 reductase [Saccharomyces cerevisiae] ; (Z46861)
													cytochrome b5 reductase [Saccharomyces cerevisiae] ; (Z46861)
													cytochrome b reductase [Saccharomyces cerevisiae]
19550	ENU03344	AN161C3401:	22-52	998-1021	NAP		g2131525	108	39	0.01	25	94	[Saccharomyces cerevisiae] hypothetical protein YDR489w - yeast (Saccharomyces cerevisiae) ; (U33050) Ydr489wp; CAL: 0.16 [Saccharomyces cerevisiae]
		493..1534											(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe] (AL022071) hypothetical protein [Schizosaccharomyces pombe]
19551	ENU03345	AN161C9825:	47-66	1028-1047	NAP		g3850084	230	63	5.00E-17	29	90	Heat shock protein HSP1 (65 KD IGE-binding protein) ; (U92465) heat shock protein [Aspergillus fumigatus]
19552	ENU03346	AN161C1042	51-77	1032-1051	NAP		g2950464	1087	312	e-102	67	58	glucosamine-6-phosphate isomerase (glucosamine-6-phosphate deaminase) ; glucosamine-6-phosphate deaminase protein (nagB) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32700) glucosamine-6-phosphate isomerase (nagB) [Haemophilus influenzae Rd]
19553	ENU03347	AN161C5619:	65-84	1046-1065	NAP		g2851483	1706	493	e-138	93	78	protein transport protein SEC13 ; SEC13 protein - yeast (Saccharomyces cerevisiae) ; (L05929) Sec13p [Saccharomyces cerevisiae] ; (U14913) Sec13p [Saccharomyces cerevisiae] (AL034583) related to yeast zds family proteins [Schizosaccharomyces pombe] (L39639) kievitone hydratase [Fusarium solani]
		2226..1184											
19554	ENU03348	AN161C41:20	44-64	1025-1044	NAP		g1171641	795	316	1.00E-85	59	96	
		88..1046											
19555	ENU03349	AN161C7807:	64-84	1044-1065	NAP		g417748	807	150	4.00E-77	62	90	
		1969..3013											
19556	ENU03350	AN161C4411:	37-56	1014-1038	NAP		g4056558	130	74	2.00E-12	35	18	
		1439..396											
19557	ENU03351	AN161C3627:	53-73	1032-1054	NAP		g755011	496	217	1.00E-55	36	92	
		6985..5942											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19558	ENU03352	ANI61C5159:	22-47	1008-1027	NAP		g1171024	542	169	9.00E-49	46	87	"mitochondrial RNA splicing protein MRS3 ; splicing protein MRS3, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X56445) MRS3 protein [Saccharomyces cerevisiae] ; (X87371) mitochondrial splicing unit [Saccharomyces cerevisiae] ; (Z49408) ORF YJL133w [Saccharomyces cerevisiae] "
19559	ENU03353	ANI61C1040	23-45	1009-1028	NAP		g3024013	949	203	6.00E-57	66	94	eukaryotic translation initiation factor 2 alpha subunit (EIF-2-alpha) ; (AL021046) translational initiation factor 2 alpha [Schizosaccharomyces pombe]
19560	ENU03354	ANI61C2163:	53-72	1027-1060	NAP		g1523784	140	83	1.00E-25	32	38	(Z79750) acid phosphatase [Emmericella nidulans]
19561	ENU03355	ANI61C766:1	22-49	1008-1030	NAP		g2414631	65	61	0.000000	28	48	(Z99260) hypothetical protein [Schizosaccharomyces pombe]
19562	ENU03356	ANI61C8382:	64-83	1052-1072	NAP		g3135990	765	167	2.00E-50	41	64	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19563	ENU03357	ANI61C9268:	22-55	1011-1031	NAP		g1351310	1415	514	e-145	83	96	Thioredoxin reductase ; 72k broad-range disulfide reductase (NADPH) (EC 1.-.-.-) - Penicillium chrysogenum ; (X76119) thioredoxin reductase [Penicillium chrysogenum]
19564	ENU03358	ANI61C6529:	22-47	1012-1031	NAP		g127112	758	204	6.00E-57	56	97	MAK16 protein ; MAK16 protein - yeast (Saccharomyces cerevisiae) ; (J03852) MAK16 protein [Saccharomyces cerevisiae] ; (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]
19565	ENU03359	ANI61C3092:	23-42	1014-1034	NAP		g125271	1258	389	e-107	72	94	"Casein kinase II, alpha chain (CK II) (CK2-alpha) ; casein kinase II (EC 2.7.1.-) alpha chain - maize ; Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays ; (X61387) casein kinase II alpha subunit [Zea mays] "

# Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19566	ENU03360	ANI61C8693:	59-91	1048-1070	NAP	g1170603	1038	375	e-103	53	32	probable serine/threonine-protein C2F7.03C ; hypothetical protein SPAC2F7.03c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) protein kinase [Schizosaccharomyces pombe] (L35487) mannanase [Aspergillus aculeatus]
19567	ENU03361	ANI61C51:26	47-68	1040-1059	NAP	g558311	1144	254	e-118	65	82	(AF054824) delta 5 microsomal desaturase [Mortierella alpina]
19568	ENU03362	ANI61C980:5	22-57	1001-1034	NAP	g3342268	95	57	0.000000	38	14	GCY protein ; GCY1 protein - yeast (Saccharomyces cerevisiae) ; (X13228)
19569	ENU03363	ANI61C5185:	22-47	1020-1039	NAP	g121087	556	217	5.00E-57			GCY protein (AA 1-312) [Saccharomyces cerevisiae] ; (X90518) ORF O31567 [Saccharomyces cerevisiae] ; (X94335) YOR3269w [Saccharomyces cerevisiae] ; (X96740) GCY protein [Saccharomyces cerevisiae] ; (Z75028) ORF YOR120w [Saccharomyces cerevisiae]
19570	ENU03364	ANI61C1024	65-84	1052-1083	NAP	g417431	604	254	1.00E-66			NADPH dehydrogenase 1 (old yellow enzyme 1) : NADPH dehydrogenase (EC 1.6.99.1) chain OYE1 - yeast (Saccharomyces cerevisiae) ; Old Yellow Enzyme (Oxidized) (Oye) (E.C.1.6.99.1) Complexed With P-Hydroxybenzaldehyde ; Old Yellow Enzyme (Reduced) (Oye) (E.C.1.6.99.1) ; Old Yellow Enzyme (Oxidized) (Oye) (E.C.1.6.99.1) ; (X53597) NADPH dehydrogenase [Saccharomyces pastorianus] (Z11701) putative protein kinase [Saccharomyces cerevisiae] (Y14766) alk8 [Candida albicans]
19571	ENU03365	ANI61C8885:	32-51	1024-1050	NAP	g3836	697	186	2.00E-76	47	29	
19572	ENU03366	ANI61C8063:	22-50	1013-1041	NAP	g3395458	212	56	1.00E-22	39	35	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19573	ENU03367	ANI61C5331	36-56	1027-1056	NAP		g117178	2183	640	0	85	68	Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zuotin like protein [Schizosaccharomyces pombe]
19574	ENU03368	ANI61C9104	49-68	1049-1070	NAP		g3183387	608	109	3.00E-37	40	71	
19575	ENU03369	ANI61C2888	24-42	1029-1048	NAP		g1077195	884	136	3.00E-31	34	56	
19576	ENU03370	ANI61C2922	22-53	1020-1047	NAP		g2276350	899	290	1.00E-77	56	99	
19577	ENU03371	ANI61C6515	38-57	1032-1064	NAP		g1346660		77	4.00E-22			Salicylate hydroxylase (salicylate 1-monoxygenase) ; salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida (strain PpG7) ; (M60055) salicylate hydroxylase [Pseudomonas putida] (AL023534) putative methionine aminopeptidase I [Schizosaccharomyces pombe]
19578	ENU03372	ANI61C9024	29-61	1034-1055	NAP		g3130036	1225	299	e-115	61	87	Salicylate hydroxylase (salicylate 1-monoxygenase) ; salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida (strain PpG7) ; (M60055) salicylate hydroxylase [Pseudomonas putida]
19579	ENU03373	ANI61C6515	44-63	1038-1070	NAP		g1346660		77	4.00E-22			stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata ; (X85963) delta-9 fatty acid desaturase [Ajellomyces capsulatus]
19580	ENU03374	ANI61C8602	27-46	1036-1055	NAP		g1078613	1726	301	e-171	88	74	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19581	ENU03375	ANI61C6203:	25-45	1031-	NAP		g4503653	590	211	8.00E-54	40	52	"fatty-acid-Coenzyme A ligase, very long-chain 1 ; very-long-chain acyl-CoA synthetase (very-long-chain-fatty-acid-CoA ligase) ; (D88308) very-long-chain acyl-CoA synthetase [Homo sapiens] ; (AF096290) very long-chain acyl-CoA synthetase [Homo sapiens]"
		3521..2451		1053									(AL033497) transport protein [Candida albicans]
19582	ENU03376	ANI61C5100:	70-90	1077-	NAP		g3859693		75	7.00E-13			hypothetical 35.1 KD protein in NAM8-GAR1 intergenic region ; hypothetical protein YHR088w - yeast (Saccharomyces cerevisiae) ; (U000060) Yhr088wp [Saccharomyces cerevisiae] (U62917) glucose transporter TGTTP2 [Taenia solium]
19583	ENU03377	ANI61C3804:	50-69	1052-	NAP		g731684	590	192	2.00E-52	42	98	(AB011211) pectin methyl-esterase [Aspergillus oryzae]
		3421..4492		1079									hypothetical 37.0 KD protein in SPOIIR-GLYC intergenic region ; SUA5 homolog ipc-29d - Bacillus subtilis ; (Z38002) Similar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis] ; (Z99122) alternate gene name: ipc-29d, similar to hypothetical proteins [Bacillus subtilis] ; ipc-29d gene [Bacillus subtilis]
19584	ENU03378	ANI61C9031:	63-82	1072-	NAP		g1480799		37	0.000000	03		"proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 ; (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]"
19585	ENU03379	ANI61C3234:	52-71	1063-	NAP		g4514622	469	107	4.00E-44	41	89	(AJ001732) rAsp f4 [Aspergillus fumigatus]
19586	ENU03380	ANI61C8984:	59-81	1054-	NAP		g732384	519	107	8.00E-41			probable calcium-transporting ATPase 9 ; probable membrane protein YOR291w - yeast (Saccharomyces cerevisiae) ; (Z75199) ORF YOR291w [Saccharomyces cerevisiae] (AC000133) ORF [Emericella nidulans]
		3629..2556		1089									
19587	ENU03381	ANI61C1139	65-84	1079-	NAP		g4506223	545	205	5.00E-52	36	84	
		7:730..1805		1098									
19588	ENU03382	ANI61C7637:	50-72	1060-	NAP		g3005839	410	110	1.00E-23	45	31	
		1107..2184		1084									
19589	ENU03383	ANI61C7016:	63-83	1068-	NAP		g2493012	538	99	5.00E-34	41	17	
		6581..5505		1097									
19590	ENU03384	ANI61C567:3	26-48	1029-	NAP		g1870209		46	0.0004			
		434..4511		1061									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19591	ENU03385	ANI61C8963:	26-45	1044-1063	NAP		g2132210	665	268	4.00E-71	41	98	hypothetical protein YPL152w - yeast (Saccharomyces cerevisiae) ; (Z73508) ORF YPL152w [Saccharomyces cerevisiae] ; (X96770) P2591 protein [Saccharomyces cerevisiae]
19592	ENU03386	ANI61C4714:	40-61	1053-1077	NAP		g1836161	530	212	1.00E-56	38	64	"(S83194) Ca2+/calmodulin-dependent protein kinase IV kinase isoform, CaM-kinase kinase alpha [rats, brain, Peptide, 505 aa] [Rattus sp.] ; (AB023658) Calmodulin-dependent protein kinase kinase alpha, CaM-kinase kinase alpha [Rattus norvegicus]
19593	ENU03387	ANI61C129:3	29-48	1036-1066	NAP		g2340046	2589	326	e-105	79	42	(L48074) secreted dipeptidyl peptidase [Aspergillus fumigatus]
19594	ENU03388	ANI61C5996:	22-42	1031-1059	NAP		g2650534	128	74	2.00E-12	29	54	(AE001098) conserved hypothetical protein [Archaeoglobus fulgidus]
19595	ENU03389	ANI61C7595:	23-51	1039-1060	NAP		g2131398	463	120	2.00E-45	37	92	hypothetical protein YDR214w - yeast (Saccharomyces cerevisiae) ; (Z68195) unknown [Saccharomyces cerevisiae] ; (Z68194) unknown [Saccharomyces cerevisiae]
19596	ENU03390	ANI61C1118	47-66	1063-1084	NAP		g1723555		83	2.00E-15			hypothetical 27.0 KD protein C12B10.13 in chromosome I ; (Z70721) conserved hypothetical protein. [Schizosaccharomyces pombe] (AL049522) putative dolichol kinase [Schizosaccharomyces pombe]
19597	ENU03391	ANI61C8085:	52-71	1074-1093	NAP		g4539603	263	91	1.00E-17	36	37	[Schizosaccharomyces pombe] 2-nitropropane dioxygenase precursor (nitroalkane oxidase) (2-NPD) ; (U22530) 2-nitropropane dioxygenase precursor [Neurospora crassa]
19598	ENU03392	ANI61C1118:	22-53	1043-1065	NAP		g2498094	348	162	4.00E-39	34	93	hypothetical 48.0 KD protein C4G8.06C in chromosome I ; hypothetical protein SPAC4G8.06c - fission yeast (Schizosaccharomyces pombe) ; (Z56276) hypothetical protein [Schizosaccharomyces pombe]
19599	ENU03393	ANI61C4327:	27-47	1047-1071	NAP		g1351597	376	203	2.00E-51	40	72	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19600	ENU03394	ANI61C238:1	22-49	1047-1066	NAP		g3135988	201	89	1.00E-19	35	36	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19601	ENU03395	ANI61C7744:	33-54	1058-7338..6252	NAP		g130684	910	314	7.00E-85	66	93	Outer mitochondrial membrane protein porin ; porin - Neurospora crassa ; (X05824) major protein (AA 1-283) [Neurospora crassa]
19602	ENU03396	ANI61C3311:	24-55	1050-1021..2108	NAP		g4581517		83	3.00E-33			(AL049559) putative d-amino acid oxidase [Schizosaccharomyces pombe]
19603	ENU03397	ANI61C2398:	58-77	1084-1506..418	NAP		g113712	600	147	6.00E-40	35	61	Amidase ; amidase (EC 3.5.1.4) - Brevibacterium sp. (strain R312) ; amidase - Rhodococcus sp. (strain N-774) ; (X54074) amidase [Rhodococcus sp.] ; (M60264) enantiomer-selective amidase [Brevibacterium sp.] ; (AB016078) amidase [Rhodococcus sp. N-771] "putative 38.2 KD phosphatase 2C in chromosome I ; (Z98762)
19604	ENU03398	ANI61C7272:	24-43	1046-1840..2929	NAP		g3183379	405	144	9.00E-34	36	83	SPAC4A8.03c, putative protein phosphatase, len:339aa, similar eg. to P2C1_SCHPO, P40371, protein phosphatase 2c homolog 1, (347aa), fasta scores, opt:276, E():3.2e-11, ( 29.4% identity in 282 aa overlap), also simi...."
19605	ENU03399	ANI61C1068	50-70	1079-8:1439..2529	NAP		g4507713	505	203	4.00E-51	36	69	tetratricopeptide repeat domain 2 ; (U46571) tetratricopeptide repeat protein [Homo sapiens]
19606	ENU03400	ANI61C6636:	23-42	1051-268..1358	NAP		g2213547	476	183	1.00E-48	52	59	(Z97052) putative ubiquinone biosynthesis methyltransferase [Schizosaccharomyces pombe]
19607	ENU03401	ANI61C8531:	38-58	1068-1173..79	NAP		g2879890	627	264	7.00E-70	46	89	(AJ223327) rAsp f9 [Aspergillus fumigatus]
19608	ENU03402	ANI61C6472:	69-88	1090-5222..4127	NAP		g3914593	236	132	4.00E-30	39	91	putative ribokinase ; (AL023554) ribokinase [Schizosaccharomyces pombe]
19609	ENU03403	ANI61C2203:	48-67	1083-1130..34	NAP		g1352904	296	69	1.00E-24	34	84	hypothetical 37.5 KD protein in YUH1-URA8 intergenic region ; hypothetical protein YJR100c - yeast (Saccharomyces cerevisiae) ; (Z49600) ORF YJR100c [Saccharomyces cerevisiae]



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19610	ENU03404	ANI61C9708:	58-77	1095-1114	NAP	g1168269	1196	222	e-118	72	95	"Arabian endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]"
		3952..5050										(AC006569) hypothetical protein [Arabidopsis thaliana]
19611	ENU03405	ANI61C9805:	42-61	1079-1098	NAP	g4512702	567	70	3.00E-11	35	24	hypothetical 42.4 KD protein in ENO2-STB5 intergenic region; hypothetical protein YHR176w - yeast (Saccharomyces cerevisiae); (U00027) Yhr176wp [Saccharomyces cerevisiae]
		1380..282										hypothetical zinc-type alcohol dehydrogenase-like protein in AHPF-RNK intergenic region; (U82598) FadH homolog [Escherichia coli]; (AE000166) putative oxidoreductase [Escherichia coli]; (D90701) Glutathione-dependent formaldehyde dehydrogenase (EC 1.2.1.1) (FDH) (FALDH). [Escherichia coli]; (D90702) Glutathione-dependent formaldehyde dehydrogenase (EC 1.2.1.1) (FDH) (FALDH). [Escherichia coli]
19612	ENU03406	ANI61C1031	63-82	1096-1119	NAP	g731746	302	130	2.00E-29	36	80	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae]
		6:2340..3438										"Leucyl-TRNA synthetase, mitochondrial precursor (leucine--TRNA ligase) (LEURS); leucine--TRNA ligase (EC 6.1.1.4) precursor, mitochondrial - Neurospora crassa; (M30472) leucyl-tRNA synthetase [Neurospora crassa]"
19613	ENU03407	ANI61C1067:	69-88	1104-1125	NAP	g3024986	129	59	1.00E-10			
		1112..2210										
19614	ENU03408	ANI50C1743	37-64	1060-1093	NAP	g2132293	157	1.00E-37	32	90		
		6_1:16..1114										
19615	ENU03409	ANI61C7138:	45-65	1082-1102	NAP	g135142	1945	270	9.00E-72	44	36	
		1323..2422										

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19616	ENU03410	ANI61C7147:	56-83	1093-1114	NAP	g128847	1614	603	e-173	90	69	NADH-ubiquinone oxidoreductase 49 KD subunit precursor (complex I-49KD) (C1-49KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 49K chain - Neurospora crassa ; (X54508) NADH dehydrogenase 49 kD subunit [Neurospora crassa]	
19617	ENU03411	ANI61C9007:	22-51	1061-1080	NAP	g3976	198	71	1.00E-11	31	59	(X53840) mitochondrial ribosomal protein Yml20 [Saccharomyces cerevisiae]	
19618	ENU03412	ANI61C6616:	43-61	1081-1102	NAP	g1708464	1270	222	e-108	67	56	"putative dihydroxy-acid dehydratase precursor (DAD) (2,3-Dihydroxy acid hydrolyase) ; (Z69795) unknown [Schizosaccharomyces pombe]"	
19619	ENU03413	ANI61C953:2	55-74	1093-1115	NAP	g584806	1920	661	0	88	66	"ATP synthase alpha chain, mitochondrial precursor ; H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - Neurospora crassa ; (M84191) mitochondrial ATPase alpha-subunit [Neurospora crassa]"	
19620	ENU03414	ANI61C1699:	27-47	1065-1087	NAP	g2808634	3172	522	e-147	80	39	(AJ001909) transcriptional activator [Aspergillus niger]	
19621	ENU03415	ANI61C8652:	34-54	1080-1099	NAP	g2499716	226	77	2.00E-13	29	67	"Exopolysaccharuronase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) ; (X99795) exopolysaccharuronase [Aspergillus tubingensis]"	
19622	ENU03416	ANI61C1106	33-52	1082-1101	NAP	g549759	630	185	5.00E-58	31	78	"hypothetical 52.3 KD protein in FRE2 5'region ; hypothetical protein YKL221w - yeast (Saccharomyces cerevisiae) ; (X75950) ORF4, B473 [Saccharomyces cerevisiae] ; (Z28221) ORF YKL221w [Saccharomyces cerevisiae] ; ORF 4 [Saccharomyces cerevisiae]"	
19623	ENU03417	ANI61C5477:	22-48	1068-1090	NAP	g1834342	750	190	3.00E-78	48	21	(Z68905) A TP-binding cassette multidrug transporter [Emmericella nidulans]	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19624	ENU03418	ANI61C7673:	64-89	1108-1133	NAP	g4495126	1033	1033	269	3.00E-71	37	35	(AL035583) putative helicase [Schizosaccharomyces pombe]
19625	ENU03419	ANI61C8010:	22-51	1056-1091	NAP	g1173405	733	169	2.00E-71				"protein phosphatases PP1 regulatory subunit SDS22 ; protein suppressor sds22 - fission yeast (Schizosaccharomyces pombe) ; (Z98762) SPAC4A8.12c, sds22; protein phosphatases ppl regulat ory subunit, len:332aa, identical to SD22_SCHPO, P22194, (3 32aa), similar eg. to yeast Q15435, SDS22 homolog, (360aa), fasta scores, opt:837, E0:0, (47,6% identi..." (Z99531) ubiquitin system protein [Schizosaccharomyces pombe] (D90917) hypothetical protein [Synechocystis sp.]
19626	ENU03420	ANI61C8479:	62-82	1111-1132	NAP	g2440180	1508	542	e-153	69	11		"uracil-DNA glycosylase precursor (UDG) ; uracil-DNA glycosylase (EC 3.2.2.-) - yeast (Saccharomyces cerevisiae) ; (J04470) uracil-DNA-glycosylase [Saccharomyces cerevisiae] ; (Z46659) UNG1 gene, len: 359, CAl: 0.12, uracil-DNA glycosylase [Saccharomyces cerevisiae]"
19627	ENU03421	ANI61C9176:	22-51	1072-1092	NAP	g1653915	415	203	2.00E-51	32	96		(AL033503) peptide transport protein [Candida albicans] (AL023592) acetamidase [Schizosaccharomyces pombe]
19628	ENU03422	ANI61C1899:	47-66	1098-1117	NAP	g137043	489	149	4.00E-53	44	84		[Schizosaccharomyces pombe] probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
19629	ENU03423	ANI61C8616:	22-47	1066-1093	NAP	g3859684	404	140	1.00E-42	32	53		
19630	ENU03424	ANI61C4044:	23-42	1073-1095	NAP	g3136052	320	147	2.00E-36	33	61		
19631	ENU03425	ANI61C1103:	68-88	1122-1140	NAP	g2132651	664	80	2.00E-33	30	61		
19632	ENU03426	ANI61C6686:	34-56	1085-1106	NAP	g1351714	288	90	3.00E-17	25	68		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19633	ENU03427	ANI61C1032	22-50	1076-1096	NAP	g126918	310	92	9.00E-32	36	95		Mono- and diacylglycerol lipase precursor (MDGL) ; mono- and diacylglycerol lipase (EC 3.1.1.-) precursor - <i>Penicillium camembertii</i> ; (D90315) MDGL precursor [ <i>Penicillium camembertii</i> ] Polygalacturonase precursor (pectinase) (PGL) ; polygalacturonase (EC 3.2.1.15) precursor - <i>Aspergillus parasiticus</i> ; (U17167) polygalacturonase precursor [ <i>Aspergillus parasiticus</i> ] ; (L23523) [ <i>Aspergillus parasiticus</i> ] polygalacturonase [ <i>Aspergillus parasiticus</i> ] (AJ001540) phenylacetyl-CoA ligase [ <i>Penicillium chrysogenum</i> ] (AL035396) SRG1-like protein [ <i>Arabidopsis thaliana</i> ] (AL035076) putative carboxylesterase-lipase family member [ <i>Schizosaccharomyces pombe</i> ] probable membrane protein YOL107w - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z48149) similarity with P. tetraurelia cytochrome C oxidase [ <i>Saccharomyces cerevisiae</i> ] ; (Z74849) ORF YOL107w [ <i>Saccharomyces cerevisiae</i> ] Peroxisomal targeting signal 2 receptor (PTS2 receptor) (peroxisome import protein PAS7) (peroxin-7) ; PAS7 protein - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (X81424) Pas7p [ <i>Saccharomyces cerevisiae</i> ] ; (X83704) Peb1 [ <i>Saccharomyces cerevisiae</i> ] (AL022103) deoxycytidylate deaminase [ <i>Schizosaccharomyces pombe</i> ] (D45893) acr-2 [ <i>Neurospora crassa</i> ]
19634	ENU03428	ANI61C2335	57-75	1111-1132	NAP	g1346703	1482	468	e-142	78	96		
19635	ENU03429	ANI61C6897	66-97	1108-1141	NAP	g3646379	657	161	2.00E-59	41	60		
19636	ENU03430	ANI61C2091	39-58	1087-1114	NAP	g4454019	62	2.00E-12					
19637	ENU03431	ANI61C6093	28-51	1077-1104	NAP	g4107289	467	192	2.00E-50	35	66		
19638	ENU03432	ANI61C9179	35-54	1091-1112	NAP	g1077295	175	102	4.00E-21	31	92		
19639	ENU03433	ANI61C7538	22-46	1081-1100	NAP	g730272	625	238	3.00E-77	43	92		
19640	ENU03434	ANI61C6107	62-82	1122-1141	NAP	g2956780	608	108	1.00E-57	46	90		
19641	ENU03435	ANI61C9017	71-91	1133-1151	NAP	g1754596	398	97	2.00E-19	31	54		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19642	ENU03436	ANI61C9774:	65-85	1127-	NAP		g549443	8521	690	0	99	18	Conidial green pigment synthase ; probable polyketide synthase - Emericella nidulans ; (X65866)
		3928..5051		1146									putative polyketide or fatty acid synthase [Emericella nidulans] ; wA gene [Emericella nidulans] (AJ005253) CIP protease [Mus musculus] ; (AJ012249) CIP protease [Mus musculus]
19643	ENU03437	ANI61C1695:	22-52	1069-	NAP		g3559935	425	141	5.00E-47	55	54	"NMT1 protein homolog ; nmt1 protein - Aspergillus parasiticus ; (U15196) the expression of this gene has been shown to be completely inhibited by thiamine as was observed for the Schizosaccharomyces pombe nmt1, Swiss-Prot Accession Number P36597 [Aspergillus parasiticus] ; nmt1 gene [Aspergillus parasiticus]"
19644	ENU03438	ANI61C6466:	22-57	1085-	NAP		g1171741	1602	512	e-144	92	99	cytochrome C PEROxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast (Saccharomyces cerevisiae) ; (X62422) Cytochrome c peroxidase [Saccharomyces cerevisiae] ; (Z28291) ORF YKR066c [Saccharomyces cerevisiae]
19645	ENU03439	ANI61C1045	70-89	1124-	NAP		g543969	593	135	5.00E-61	42	95	chromosome 22 open reading frame 1 ; (U84894) 239AB [Homo sapiens] (U59214) MAP protein kinase MPKA [Emericella nidulans] (U26463) NADPH-dependent aldehyde reductase [Sporidiobolus salmonicolor] (U41278) contains similarity to G beta repeats (PROsite:PS00670) of the beta-transducin family [Caenorhabditis elegans]
		1:4390..3264		1154									probable membrane protein YOR380w - yeast (Saccharomyces cerevisiae) ; (Z75288) ORF YOR380w [Saccharomyces cerevisiae]
19646	ENU03440	ANI61C7019:	64-83	1128-	NAP		g4502497	280	71	1.00E-11	38	89	
		5621..4493		1149									
19647	ENU03441	ANI61C3212:	38-58	1104-	NAP		g4580577	2092	412	0	97	81	
		2345..1218		1123									
19648	ENU03442	ANI61C1118	46-65	1114-	NAP		g1142698	719	120	3.00E-50	57	94	
		2:2717..3848		1135									
19649	ENU03443	ANI61C8239:	22-52	1090-	NAP		g1086900	178	59	9.00E-12	31	39	
		1151..20		1111									
19650	ENU03444	ANI61C1097	60-79	1131-	NAP		g2132958	353	153	1.00E-36	30	65	
		9:7353..6221		1150									

# Sequence Selection

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19651	ENU03445	ANI61C8387:	72-92	1139-1163	NAP		g3560241	373	85	4.00E-21	40	26	(AL031532) putative amino acid permease [Schizosaccharomyces pombe]
19652	ENU03446	ANI61C5168:	25-52	1088-1116	NAP		g1171946	615	183	1.00E-71	41	93	NADPH dehydrogenase 3 (old yellow enzyme 3) ; NADPH dehydrogenase (EC 1.6.99.1) OYE3 - yeast (Saccharomyces cerevisiae) ; (L29279) NADPH dehydrogenase [Saccharomyces cerevisiae] ; (Z73527) ORF YPL171c [Saccharomyces cerevisiae]
19653	ENU03447	ANI61C1113	46-65	1110-1139	NAP		g1730251	724	192	4.00E-84	56	91	GTP cyclohydrolase II ; GTP-cyclohydrolase - Pichia guilliermondii ; GTP-cyclohydrolase - Pichia guilliermondii ; (Z49093) GTP-cyclohydrolase [Pichia guilliermondii] Triosephosphate isomerase (TIM) ; triose-phosphate isomerase (EC 5.3.1.1) - Emericella nidulans ; (D10019) triosephosphate isomerase [Emericella nidulans]
19654	ENU03448	ANI61C2332:	27-50	1094-1120	NAP		g136053	1099	187	e-111	98	99	hypothetical 30.0 K D protein C13F4.14 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (AL031322) conserved hypothetical protein [Schizosaccharomyces pombe]
19655	ENU03449	ANI61C6376:	58-77	1131-1151	NAP		g1723274	275	96	4.00E-19	36	94	[Schizosaccharomyces pombe] hypothetical 51.6 K D protein in SSB2-SPX18 intergenic region ; hypothetical protein YNL206c - yeast (Saccharomyces cerevisiae) ; (X78898) (Saccharomyces cerevisiae) ; possibly expressed during the late G1 /S phase; homology with the SS RP proteins [Saccharomyces cerevisiae] ; (Z71482) ORF YNL206c [Saccharomyces cerevisiae]
19656	ENU03450	ANI61C2623:	71-89	1145-1164	NAP		g732190		81	6.00E-16			(AF031376) LIM-domain binding factor 2; LDB2 [Danio rerio]
19657	ENU03451	ANI61C9329:	69-88	1142-1162	NAP		g3078001		36	0.66			Hexokinase ; (L04480) hexokinase [Schistosoma mansoni]
19658	ENU03452	ANI61C3576:	55-75	1120-1150	NAP		g2833327		76	4.00E-13			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19659	ENU03453	AN161C4140:	43-63	1116-1139	NAP		g1705465	1079	414	e-119	58	88	Biotin synthetase (biotin synthetase); biotin synthetase - yeast (Saccharomyces cerevisiae); (Z73071) ORF YGR286c [Saccharomyces cerevisiae]
19660	ENU03454	AN161C9438:	31-50	1100-1127	NAP		g3929362	362	174	9.00E-43	32	70	pisatin demethylase (cytochrome P450 57A1); pisatin demethylase - fungus (Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpVI]
19661	ENU03455	AN161C6611:	30-57	1105-1127	NAP		g2492777	604	220	1.00E-56	47	88	hypothetical zinc-type alcohol dehydrogenase-like protein in PRE5-FET4 intergenic region; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae); (Z54141) unknown [Saccharomyces cerevisiae] Polyalgalacturonase precursor (PG) (pectinase); (L02239) endopolyalgalacturonase [Gibberella fujikuroi] putative disulfide isomerase TIGA precursor; (X98748) tlgA [Aspergillus niger]
19662	ENU03456	AN161C7326:	23-45	1093-1122	NAP		g585668	807	192	5.00E-48	49	90	(U61983) benzyl alcohol dehydrogenase [Acinetobacter calcoaceticus] (X95720) O6357 [Saccharomyces cerevisiae] Pectin lyase precursor; (L22857) pectin lyase [Colletotrichum gloeosporioides]
19663	ENU03457	AN161C5335:	22-41	1103-1125	NAP		g2501210	1300	420	e-135	69	99	"glucoamylase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosyltransferase); glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus sp; (D10460) glucoamylase [Aspergillus shirousami]
19664	ENU03458	AN161C2777:	52-71	1137-1156	NAP		g1408294	565	220	1.00E-56	39	94	
19665	ENU03459	AN161C4098:	72-91	1154-1176	NAP		g1199853	292	140	2.00E-32	36	90	
19666	ENU03460	AN161C3743:	67-86	1152-1171	NAP		g3914390	685	150	2.00E-35	45	91	
19667	ENU03461	AN161C1756:	50-79	1134-1156	NAP		g113792	1500	466	e-130	63	59	
19668	ENU03462	AN161C9390:	67-94	1149-1175	NAP		g3915606	251	86	1.00E-24	30	52	Armitte oxidase [flavin-containing] (monoamine oxidase) (MAO)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19669	ENU03463	ANI61C348:2	23-58	1109-1133	NAP		g3493591	647	279	3.00E-74	44	56	(AF063231) cytoplasmic dynein intermediate chain 2 [Mus musculus]
19670	ENU03464	..1154 ANI61C323:2	25-44	1118-1136	NAP		g140479	785	148	9.00E-35	36	37	"probable transporter FEN2 ; probable membrane protein YCR028c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR028c, len:512 [Saccharomyces cerevisiae]"
19671	ENU03465	ANI61C1037	29-50	1121-1140	NAP		g66290	554	217	9.00E-56	34	59	laccase (EC 1.10.3.2) I - Emericella nidulans
19672	ENU03466	2:81..1234 ANI61C843:3	23-46	1111-1134	NAP		g3913072	143	86	5.00E-16	39	24	probable 2-dehydropanioate 2-reductase (ketopantoate reductase) (KPA reductase) ; (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus]
19673	ENU03467	768..2614 ANI61C843:3	41-64	1129-1152	NAP		g3913072	143	86	5.00E-16	39	24	probable 2-dehydropanioate 2-reductase (ketopantoate reductase) (KPA reductase) ; (AE000986) thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus]
19674	ENU03468	45..1198 ANI61C9542:2	28-53	1120-1139	NAP		g3183308	392	143	2.00E-33	37	38	hypothetical 49.6 KD protein C5D6.04 in chromosome I ; (Z98056) hypothetical protein
19675	ENU03469	1884..728 ANI61C6702:2	36-60	1129-1150	NAP		g2132851	146	53	9.00E-12	29	44	[Schizosaccharomyces pombe] probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w
19676	ENU03470	1289..133 ANI61C9502:2	55-74	1150-1169	NAP		g3323397	1563	518	e-163	83	92	[Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae] (U89991) mannose-1-phosphate guanylyltransferase [Hypocrea jecorina]
19677	ENU03471	4..1171 ANI61C546:1	35-55	1129-1150	NAP		g2499517	578	181	3.00E-66	41	56	hypothetical 71.1 KD protein in DSK2-CAT8 intergenic region ; hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae) ; (Z49704) unknown [Saccharomyces cerevisiae]



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19678	ENU03472	ANI61C11:71	67-87	1163-	NAP		g1730840	935	190	1.00E-47	36	45	putative cysteinyl-TRNA synthetase C29E6.00C (cysteine--TRNA ligase) (CYSRS) ; probable membrane protein YNL247w - yeast (Saccharomyces cerevisiae) ; (X96722) ORF N0885 [Saccharomyces cerevisiae] ; (Z71523) ORF YNL247w [Saccharomyces cerevisiae]
19679	ENU03473	ANI61C8853: 29-48		1114-	NAP		g1730193	703	291	5.00E-78			UDP-glucose 4-epimerase (galactowaldenase) (UDP-GALactose 4-epimerase) ; (X99339) UDP-glucose 4-epimerase [Bacillus subtilis] ; (D83026) highly homologous to UDP-glucose 4-epimerases (SwissProt:GALE_HAEIN and GALE_ECOLI); hypothetical [Bacillus subtilis] ; (Z99123) UDP-glucose 4-epimerase [Bacillus subtilis] (M11621) putative [Saccharomyces cerevisiae]
19680	ENU03474	ANI61C676:4 44-65		1145-	NAP		g806323	295	93	2.00E-27	39	58	"(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]"
19681	ENU03475	ANI61C9629: 22-43		1124-	NAP		g4006818	832	135	9.00E-80	55	96	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae] (AF007270) contains similarity to syntaxin [Arabidopsis thaliana] (AL033497) unknown hypothetical protein [Candida albicans]
19682	ENU03476	ANI61C1097 49-68		1152-	NAP		g2132942		112	4.00E-24			N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
		5:5843..4679		1171									
19683	ENU03477	ANI50C1823 27-46		1128-	NAP		g2191179		72	6.00E-12	31	72	
		_6:2180..3345		1150									
19684	ENU03478	ANI61C5073: 39-58		1143-	NAP		g3859696	361	123	4.00E-38	34	78	
		1205..40		1162									
19685	ENU03479	ANI61C4357: 53-73		1159-	NAP		g2507070	383	105	4.00E-38	36	65	
		1174..6		1179									

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer 1173-	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19686	ENU03480	ANI61C11:71	67-87	1173-	1193	NAP		g1730840	935	196	2.00E-49	36	45	putative cysteinyl-TRNA synthetase C29E6.06C (cysteine--TRNA ligase) (CVSR5) ; probable membrane protein YNL247w - yeast (Saccharomyces cerevisiae) ; (X96722) ORF N0885 [Saccharomyces cerevisiae] ; (Z71523) ORF YNL247w [Saccharomyces cerevisiae]
19687	ENU03481	ANI61C7427:	32-54	1139-	1158	NAP		g4038613	681	184	8.00E-46	50	91	(Z98602) conserved uncharacterized protein domain-containing protein [Schizosaccharomyces pombe]
19688	ENU03482	ANI61C4324:	71-94	1180-	1199	NAP		g3821271	1076	351	4.00E-96	64	66	(AJ009956) alpha-galactosidase 1 [Penicillium simplicissimum]
19689	ENU03483	ANI61C9384:	37-63	1148-	1169	NAP		g2981103	375	140	1.00E-32	33	64	(AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe]
19690	ENU03484	ANI61C1005	59-78	1173-	1192	NAP		g131768	568	159	4.00E-38	32	69	quinate permease (quinate transporter) ; quinate transport protein - Emeritella nidulans ; (X13525) quinate permease [Emeritella nidulans] (Z98974) putative small nuclear ribonucleoprotein [Schizosaccharomyces pombe]
19691	ENU03485	ANI61C1024:	26-45	1143-	1161	NAP		g2388912	499	80	1.00E-36	49	99	(Z98974) putative small nuclear ribonucleoprotein [Schizosaccharomyces pombe]
19692	ENU03486	ANI61C6064:	52-71	1159-	1187	NAP		g3581921	198	53	0.000004	45	58	(AL031546) ubiquinol-cytochrome c reductase complex subunit [Schizosaccharomyces pombe]
19693	ENU03487	ANI61C7603:	67-87	1173-	1202	NAP		g3859693	68	68	1.00E-10			(AL033497) transport protein [Candida albicans]
19694	ENU03488	ANI61C7603:	67-87	1173-	1202	NAP		g3859693	68	68	1.00E-10			(AL033497) transport protein [Candida albicans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19695	ENU03489	ANI61C7187:	65-84	1167-1201	NAP		g112940	532	134	1.00E-40			Acyl-coenzyme A:6-aminopenicillanic-acid-acyltransferase precursor (isopenicillin N acyltransferase); acyltransferase AAT - Emericella nidulans; isopenicillin N acyltransferase (EC 2.3.1.-) - Emericella nidulans; (X53310) Acyl-CoA [Emericella nidulans]; (M58293) acyl-coenzyme A:isopenicillin N acyltransferase [Emericella nidulans] (AL031603) putative glycosyl transferase [Schizosaccharomyces pombe]
19696	ENU03490	ANI61C9634:	52-71	1165-1189	NAP		g3646449	753	206	3.00E-62	48	69	hypothetical 61.8 KD protein C12B10.03 in chromosome 1; (Z70721) WD repeat protein [Schizosaccharomyces pombe]
19697	ENU03491	ANI61C352:	5-22-48	1142-1161	NAP		g1723547	701	170	8.00E-80	46	59	hypothetical 61.8 KD protein C12B10.03 in chromosome 1; (Z70721) WD repeat protein [Schizosaccharomyces pombe]
19698	ENU03492	ANI61C8306:	60-79	1180-1202	NAP		g1351809	956	397	e-109	53	94	membrane protein YDR331w - yeast (Saccharomyces cerevisiae); (U32517) Ydr331 wp [Saccharomyces cerevisiae] (Z80108) lip1 [Mycobacterium tuberculosis]
19699	ENU03493	ANI61C1105	37-56	1161-1180	NAP		g1542908		96	6.00E-19			(AL031532) hypothetical protein [Schizosaccharomyces pombe]
19700	ENU03494	ANI61C1056	59-89	1180-1202	NAP		g3560245	168	79	5.00E-14	26	51	(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
19701	ENU03495	ANI61C2603:	22-48	1138-1165	NAP		g4490992	188	76	3.00E-13	30	79	hypothetical 47.0 KD protein in PET117-CEM1 intergenic region; hypothetical protein YER059w - yeast (Saccharomyces cerevisiae); (U18813) Yer059wp [Saccharomyces cerevisiae]
19702	ENU03496	ANI61C6589:	55-74	1174-1199	NAP		g731468	299	114	1.00E-24	38	56	hypothetical 39.0 KD protein in GLNQ-ANSR intergenic region; (D84432) YqkA [Bacillus subtilis]; (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
19703	ENU03497	ANI61C9095:	22-50	1147-1166	NAP		g1731087	67	56	0.000000	21	59	hypothetical 39.0 KD protein in GLNQ-ANSR intergenic region; (D84432) YqkA [Bacillus subtilis]; (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
19704	ENU03498	ANI61C1082:	63-82	1181-1208	NAP		g1929089	393	133	3.00E-30	30	65	hypothetical 39.0 KD protein in GLNQ-ANSR intergenic region; (D84432) YqkA [Bacillus subtilis]; (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
19705	ENU03499	ANI61C4013:	34-55	1161-1181	NAP		g2804298	792	241	6.00E-63	36	70	hypothetical 39.0 KD protein in GLNQ-ANSR intergenic region; (D84432) YqkA [Bacillus subtilis]; (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19706	ENU03500	ANI61C410:1	55-74	1179-1204	NAP	g2131476	626	626	210	7.00E-69	44	89	hypothetical protein YDR415c - yeast (Saccharomyces cerevisiae) ; (U133007) Ydr415cp; CAl: 0.14 [Saccharomyces cerevisiae]
19707	ENU03501	ANI61C8114: 64-83		1181-1215	NAP	g1706694	609	609	178	1.00E-46	35	49	"Lanosterol synthase (oxidosqualene—lanosterol cyclase) (2,3-epoxysqualene-lanosterol cyclase) (OSC) ; lanosterol synthase (EC 5.4.99.7) - fission yeast (Schizosaccharomyces pombe) ; (U41368) lanosterol synthase [Schizosaccharomyces pombe]"
19708	ENU03502	ANI61C9917: 22-41		1153-1173	NAP	g3581896	443	443	138	8.00E-32	24	70	[Schizosaccharomyces pombe]" (AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
19709	ENU03503	ANI61C6104: 28-47		1158-1179	NAP	g4106687	432	432	86	6.00E-20	34	97	(AL035065) putative nadh-dependent flavin oxidoreductase [Schizosaccharomyces pombe]"
19710	ENU03504	ANI61C6105: 57-75		1190-1209	NAP	g3560215	956	956	252	2.00E-80	49	81	"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe]"
19711	ENU03505	ANI61C650:3	22-49	1155-1176	NAP	g1711370	326	326	107	5.00E-34	32	96	nuclear pore protein SEH1 ; SEC13 protein homolog YGL100w - yeast (Saccharomyces cerevisiae) ; (X90994) Sec13p-like protein [Saccharomyces cerevisiae] ; (Z72622) ORF YGL100w [Saccharomyces cerevisiae]"
19712	ENU03506	ANI61C1054	24-43	1148-1179	NAP	g2648302	290	290	108	1.00E-32	42	97	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpce-2) [Archaeoglobus fulgidus]"
19713	ENU03507	ANI61C8859: 22-41		1153-1178	NAP	g4587097	104	65	0.000000	001	32	67	(AB019045) OMPdecarboxylase [Rhizomucor pusillus]"
19714	ENU03508	ANI61C9217: 22-41		1150-1180	NAP	g1169696		36	0.7				Flagellin 1 ; flagellin flhC-1 - Proteus mirabilis ; (L07270) flagellin [Proteus mirabilis]
19715	ENU03509	ANI61C6534: 23-47		1166-1183	NAP	g549699	427	41	0.021	27	89		hypothetical 50.5 KD protein in MDH1-VMA5 intergenic region ; hypothetical protein YKL082c - yeast (Saccharomyces cerevisiae) ; (Z28082) ORF YKL082c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19716	ENU03510	AN161C6741:	48-67	1186-1209	NAP		g1174552	564	99	1.00E-54	43	95	tryptophan YL-TRNA synthetase (tryptophan--TRNA ligase) (TRPRS); tryptophan--TRNA ligase (EC 6.1.1.2) - Haemophilus influenzae (strain Rd KW20); (U32746) tryptophanyl-TRNA synthetase (trpS) [Haemophilus influenzae Rd]
19717	ENU03511	AN161C1046	22-49	1152-1184	NAP		g3123677	610	254	1.00E-66	46	99	(AJ005824) Ufd1 protein [Schizosaccharomyces pombe]; (AJ005825) Ufd1 protein [Schizosaccharomyces pombe]
19718	ENU03512	AN161C8443:	24-55	1154-1186	NAP		g1352074	792	282	3.00E-77			type II proteins geranylgeranyltransferase beta subunit (type II protein geranyl-geranyltransferase beta subunit) (GGTASE-II-beta) (PGGT) (YPT1/SEC4 proteins geranylgeranyltransferase beta subunit); probable protein prenyltransferase (EC 2.5.1.-) BET2 - yeast (Saccharomyces cerevisiae); (U25842) Protein Geranyl-geranyltransferase beta subunit (Swiss Prot. accession number P20133; P32433) [Saccharomyces cerevisiae]
19719	ENU03513	AN161C3364:	56-76	1185-1219	NAP		g603955	1280	349	e-122	71	64	(D43950) KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. [Homo sapiens]
19720	ENU03514	AN161C5704:	24-50	1159-1187	NAP		g1351659	766	311	5.00E-84	46	88	hypothetical 49.3 KD protein C30D11.06C in chromosome I; hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe); (Z67961) hypothetical protein [Schizosaccharomyces pombe]
19721	ENU03515	AN161C7052:	67-87	1213-1233	NAP		g2131781	369	102	8.00E-44	35	42	hypothetical protein YLR114c - yeast (Saccharomyces cerevisiae); (U53878) Ylr114cp [Saccharomyces cerevisiae]; (X89514) putative orf [Saccharomyces cerevisiae]; (Z73286) ORF YLR114c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19722	ENU03516	ANI61C9393:	62-81	1208-	NAP	g3261633	452	200	2.00E-50	35	95		(Z79700) fadE13 [Mycobacterium tuberculosis]
19723	ENU03517	2303..3511 ANI61C8651:	23-44	1172-	NAP	g2499591	1035	296	2.00E-79	69	68		mitogen-activated protein kinase HOG1 (MAP kinase HOG1); (X90586) unnamed protein product [Candida albicans]
19724	ENU03518	579..1789 ANI61C9381:	45-67	1194-	NAP	g135025	905	297	7.00E-84	69	83		"succinyl-CoA ligase (GDP-FORMING), alpha-chain precursor (succinyl-CoA synthetase, alpha chain) (SCS-alpha); succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain precursor - rat; (J03621) succinyl-CoA synthetase alpha subunit (EC 6.2.1.4) [Rattus norvegicus]" (AF054512) endoglucanase V [Aspergillus aculeatus]
19725	ENU03519	14274..13064 ANI61C1227:	44-63	1193-	NAP	g2997731	992	229	3.00E-59	64	92		putative DNA repair protein C12B10.12C; (Z70721) putative dna repair protein [Schizosaccharomyces pombe]
19726	ENU03520	4360..3149 ANI61C1227:	69-95	1216-	NAP	g1723554	619	237	1.00E-61	39	60		(AL031536) hypothetical zinc finger protein [Schizosaccharomyces pombe]
19727	ENU03521	2..1:1300..88 ANI50C7567	22-54	1172-	NAP	g3560212		68	5.00E-25	29	20		(Z75532) similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans]
19728	ENU03522	418..2631 ANI61C263:1	22-40	1159-	NAP	g3875242	181	66	3.00E-22	30	90		(X16609) alt. ankyrin (variant 2.2) [Homo sapiens]
19729	ENU03523	8:3268..2054 ANI61C1056	71-90	1223-	NAP	g747710	231	117	1.00E-25	30	20		hypothetical 70.5 KD protein in AGP3-DAK3 intergenic region; probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae); (D50617) YFL054C [Saccharomyces cerevisiae]; (D44603) unknown [Saccharomyces cerevisiae]
19730	ENU03524	3065..4279 ANI61C1086:	41-60	1194-	NAP	g1175958	571	233	1.00E-60	36	55		(AC000132) F21M12.7 gene product [Arabidopsis thaliana]
19731	ENU03525	376..1591 ANI61C5132:	22-51	1170-	NAP	g2160161		43	0.003				(AL034565) putative transcription initiation factor ttf1f small subunit [Schizosaccharomyces pombe]
19732	ENU03526	4:6301..5085 ANI61C1064	63-88	1209-	NAP	g4049527	391	71	1.00E-30	45	97		

# Gene ID: 2633018

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	at Score	Blast Score	Blast Prob	% id	% cvrg	Description
19733	ENU03527	AN161C6659	61-80	1238	NAP	g2633018	395	205	7.00E-52	32	63		(Z99107) similar to hypothetical proteins from <i>B. subtilis</i> [Bacillus subtilis]
19733	ENU03527	1179..2398			NAP	g465483	869	261	7.00E-69	48	61		protein kinase WIS1 ; protein kinase wsi1 (EC 2.7.1.-) - fission yeast [Schizosaccharomyces pombe] ; (X62631) protein kinase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AL032684) putative pre-tRNA nuclear export receptor [Schizosaccharomyces pombe]
19734	ENU03528	AN161C9013	22-41	1180-1199	NAP	g3810833	405	132	6.00E-30	33	36		pombe] peroxisomal membrane protein PEX13 (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] peroxin-13 ; (U70067) integral peroxisomal membrane protein [Schizosaccharomyces pombe] Ppex13p [Pichia pastoris] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] phosphatidate cytidyltransferase (CDP-phosphatidate cytidyltransferase) (CDP-diglyceride pyrophosphorylase) (CDP-diglyceride synthase) (CDS) diacylglycerol synthase (CDS) (CTP:phosphatidate (CDP-DAG cytidyltransferase) (CDP-DAG cytidyltransferase) ; probable membrane protein synthase) ; yeast [Saccharomyces YBR029c - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0313 [Saccharomyces cerevisiae] ; (Z35898) [Saccharomyces cerevisiae] ; ORF YBR0313 ORF YBR029c [Saccharomyces cerevisiae] ; ORF YBR0313 [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL023634) GTPase activating protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AE001038) acyl-CoA dehydrogenase (acd-6) [Archaeoglobus fulgidus]
19735	ENU03529	AN161C6231	23-46	1182-1201	NAP	g2498763	496	142	5.00E-46	41	89		
19736	ENU03530	AN161C7020	65-84	1226-1245	NAP	g1351714	223	73	2.00E-16	35	59		
19737	ENU03531	AN161C1021	45-64	1201-1225	NAP	g586479	934	294	e-105				
19738	ENU03532	AN161C1046	22-52	1177-1202	NAP								
19739	ENU03533	AN161C9016	27-49	1189-1208	NAP	g3150248	797	304	3.00E-91	53	65		
19740	ENU03534	AN161C6369	63-82	1226-1245	NAP	g2649648	601	208	3.00E-62	37	95		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19741	ENU03535	AN161C2490:	35-54	1199-67..1292	NAP	g2507436	922	333	1.00E-90	49	46		glutaminyl-TRNA synthetase (GLNRS); glutamine--tRNA ligase (EC 6.1.1.18) - yeast (Saccharomyces cerevisiae); (U55021) Gln4p [Saccharomyces cerevisiae]; (Z75076) ORF YOR168w [Saccharomyces cerevisiae]
19742	ENU03536	AN161C5804:	22-47	1183-1205	NAP	g125886	618	169	2.00E-53	41	86		lactate 2-monoxygenase (lactate oxidase); lactate 2-monoxygenase (EC 1.13.12.4) - Mycobacterium smegmatis; (J05402) L-lactate 2-monoxygenase [Mycobacterium smegmatis]
19743	ENU03537	AN161C1809:	22-47	1174-1207	NAP	g2498337	722	242	2.00E-64	42	78		squalene monoxygenase (squalene epoxidase) (SE); (D88252) squalene epoxidase [Candida albicans]; (U69674) squalene epoxidase [Candida albicans]
19744	ENU03538	AN161C7512:	64-84	1228-1251	NAP	g2408022	357	125	8.00E-28	47	35		(Z99162) ER protein-translocation complex subunit [Schizosaccharomyces pombe]
19745	ENU03539	AN161C7486:	57-75	1225-1246	NAP	g117803	1224	452	e-126	62	67		cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome) (L-lactate ferricytochrome C oxidoreductase) (L-LCR); L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala); (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]
19746	ENU03540	AN161C676:	32-51	1203-1221	NAP	g544261	46	0.0006					RNA-binding protein EWS; RNA-binding protein EWS - human; (X66899) RNA binding protein [Homo sapiens]; (X72990) EWS [Homo sapiens]; (Y07848) RNA binding protein [Homo sapiens]; EWS gene [Homo sapiens]
19747	ENU03541	AN161C5627:	55-74	1227-1246	NAP	g3914984	208	113	3.00E-24	25	10		ferrichrome siderophore peptide synthetase; (U62738) ferrichrome siderophore peptide synthetase [Ustilago maydis]



# Sequence Alignment

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19748	ENU03542	ANI61C164:1	36-55	1195-1227	NAP	g1750122	1071	163	3.00E-64	42	75		"(U66480) xylan beta-1,4-xylosidase [Bacillus subtilis] ; (Z99113) xylan beta-1,4-xylosidase [Bacillus subtilis]"
19749	ENU03543	ANI61C9610: 72-96	1578..347	1244-1264	NAP	g118298	463	200	2.00E-50				S-adenosylmethionine decarboxylase PROenzyme (ADOMETDC) ; adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - yeast (Saccharomyces cerevisiae) ; (M38434) S-adenosylmethionine decarboxylase [Saccharomyces cerevisiae] ; (X91067) adenosylmethionine decarboxylase [Saccharomyces cerevisiae] ; (Z74794) ORF YOL052c [Saccharomyces cerevisiae]
19750	ENU03544	ANI61C5499: 57-77	269..1504	1215-1250	NAP	g2132395	346	150	3.00E-48	36	71		polyadenylated RNA-binding protein PUB1 - yeast (Saccharomyces cerevisiae) ; (Z71292) ORF YNL016w [Saccharomyces cerevisiae]
19751	ENU03545	ANI61C3215: 72-91	1248..12	1247-1266	NAP	g730251	626	208	5.00E-64	49	89		protein phosphatase 2C homolog 1 (PP2C-1) ; phosphoprotein phosphatase (EC 3.1.3.16) 2C - fission yeast (Schizosaccharomyces pombe) ; (L26970) protein phosphatase 2C [Schizosaccharomyces pombe]
19752	ENU03546	ANI61C9596: 22-56	2267..3504	1196-1216	NAP	g1078613	1662	534	e-151	69	80		stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata ; (X85963) delta-9 fatty acid desaturase [Ajellomyces capsulatus]
19753	ENU03547	ANI61C6355: 38-57	17..1253	1207-1232	NAP	g730615	978	393	e-108	47	28		DNA-directed RNA polymerase mitochondrial precursor ; (L25087) mitochondrial RNA polymerase [Neurospora crassa] ; cyt-5 gene [Neurospora crassa]
19754	ENU03548	ANI61C1028	33-55	1207-1228	NAP	g1723906	542	206	3.00E-52	39	48		hypothetical 80.0 KD protein in SNF4-TAF60 intergenic region ; probable membrane protein YGL114w - yeast (Saccharomyces cerevisiae) ; (Z72636) ORF YGL114w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19755	ENU03549	ANI61C1118:	69-88	1246-	NAP		g2132958	354	110	2.00E-23	26	73	probable membrane protein YOR380w - yeast (Saccharomyces cerevisiae) ; (Z75288) ORF YOR380w
		4267..3029		1264									[Saccharomyces cerevisiae]
19756	ENU03550	ANI61C5525:	26-45	1201-	NAP		g2271503	247	83	1.00E-20	30	91	(AF009672) unknown [Acinetobacter sp. ADP1]
19757	ENU03551	ANI61C8624:	47-68	1223-	NAP		g114699	158	85	9.00E-16	29	67	ATP10 protein ; (J05463) ATP10 protein [Saccharomyces cerevisiae]
19758	ENU03552	ANI61C1080	72-92	1242-	NAP		g2645229	358	95	1.00E-18	34	29	(U78597) kinesin light chain [Plectonema boryanum]
19759	ENU03553	ANI61C431:3	22-44	1200-	NAP		g1176586	579	157	1.00E-37	36	36	hypothetical 102.3 KD protein in DAL82-RFA2 intergenic region ; hypothetical protein YNL313c - yeast (Saccharomyces cerevisiae) ; (Z46259) NO364 [Saccharomyces cerevisiae] ; (Z71589) ORF YNL313c
		219..1979		1220									[Saccharomyces cerevisiae]
19760	ENU03554	ANI61C1007	44-63	1223-	NAP		g731740	990	363	1.00E-99	50	91	probable ATP-dependent RNA helicase DBP8 ; helicase homolog - yeast (Saccharomyces cerevisiae) ; (U00027) Yhr169wp [Saccharomyces cerevisiae]
19761	ENU03555	ANI61C1111:	66-88	1232-	NAP		g3184115	634	250	1.00E-65	35	80	(AL023780) DNA binding protein [Schizosaccharomyces pombe]
19762	ENU03556	ANI61C3965:	66-86	1242-	NAP		g1703172	1802	433	e-163	98	93	alcohol dehydrogenase II ; alcohol dehydrogenase (EC 1.1.1.1) II - Emericella nidulans ; (Z48000) alcohol dehydrogenase II [Emericella nidulans] ; alcohol dehydrogenase II [Emericella nidulans]
		1636..394		1265									(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]
19763	ENU03557	ANI61C290:9	26-47	1207-	NAP		g3646450	1005	148	9.00E-35	41	53	zinc finger protein 207 ; (AF046001) zinc finger transcription factor [Homo sapiens]
19764	ENU03558	ANI61C7312:	66-85	1250-	NAP		g4508017	242	58	4.00E-18	27	76	
		1222..2467		1269									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19765	ENU03559	AN161C1036	25-55	1209-	NAP		g549077	974	375	e-103	51	98	"3-ketoacyl-CoA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica) ; (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica] "
		6:1735..490		1228									(Z79750) acid phosphatase [Emmericella nidulans]
19766	ENU03560	AN161C170:3	55-74	1232-	NAP		g1523784	2260	840	0	97	67	Uroporphyrinogen decarboxylase (UPD) ; uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (Saccharomyces cerevisiae) ; (X63721) uroporphyrinogen decarboxylase [Saccharomyces cerevisiae] ; (Z19089) uroporphyrinogen decarboxylase [Saccharomyces cerevisiae] ; (Z49209) Hem12p [Saccharomyces cerevisiae] (AL035076) putative glutamate-1-semialdehyde aminotransferase [Schizosaccharomyces pombe]
19767	ENU03561	AN161C9890: 23-44		1195-	NAP		g416894	1069	392	e-112			(Y16748) malate dehydrogenase [Piromyces sp. E2]
		1251..4		1228									(AL034393) predicted using GeneFinder; cDNA EST yk343c12.5 comes from this gene; cDNA EST yk402e12.5 comes from this gene; cDNA EST yk457e8.5 comes from this gene; cDNA EST yk470f2.5 comes from this gene; cDNA EST yk281e3.5 com...
19768	ENU03562	AN161C8571: 71-94		1257-	NAP		g4107288	922	216	5.00E-84	52	88	(A1007712) replication factor C subunit [Arxula adenivorans]
		1770..523		1276									(AL031788) uv excision repair protein rad23 homolog [Schizosaccharomyces pombe]
19769	ENU03563	AN161C3737: 51-70		1236-	NAP		g4029338	627	112	5.00E-41	49	95	probable serine/threonine-protein kinase CID4.11C ; (Z69239) unknown [Schizosaccharomyces pombe]
		2726..3975		1257									
19770	ENU03564	AN161C8574: 24-48		1204-	NAP		g3979938	105	36	0.73	34	31	
		85..1333		1230									
19771	ENU03565	AN161C1023	33-56	1220-	NAP		g3367626	867	163	7.00E-87	59	94	
		5:1602..354		1239									
19772	ENU03566	AN161C6252: 31-52		1219-	NAP		g3687502	605	65	3.00E-20	48	90	
		5320..4069		1239									
19773	ENU03567	AN161C1155: 22-48		1211-	NAP		g1708616	896	175	3.00E-82	57	48	
		4035..2784		1231									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19774	ENU03568	AN161C4414:	22-40	1207-	NAP	g1077358	523	196	6.00E-55	37	66	probable membrane protein YLR361c-yeast (Saccharomyces cerevisiae); (U19103) Y11361cp [Saccharomyces cerevisiae]
19775	ENU03569	AN161C7023:	59-78	1254-	NAP	g1351643	674	161	2.00E-70	41	93	hypothetical 43.0 KD protein C8A4.09C in chromosome I; hypothetical protein SPAC8A4.09c-fission yeast (Schizosaccharomyces pombe); (Z66569) unknown [Schizosaccharomyces pombe]; (AL032824) hypothetical protein [Schizosaccharomyces pombe] (AL033385) conserved hypothetical protein [Schizosaccharomyces pombe] (X58121) SMP3 protein [Saccharomyces cerevisiae] (AL031743) putative protein transport protein [Schizosaccharomyces pombe] (AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe] "hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region; FUN49 protein - yeast (Saccharomyces cerevisiae); (U12980) Yal060wp [Saccharomyces cerevisiae] (AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus] (AE001684) Oxononate Synthase [Chlamydia pneumoniae] probable serine/threonine-protein kinase C24B11.11C; hypothetical protein SPAC24B11.11c - fission yeast (Schizosaccharomyces pombe); (Z67757) unknown [Schizosaccharomyces pombe]
19776	ENU03570	AN161C8693:	37-56	1232-	NAP	g3850069	254	85	1.00E-15	32	95	
19777	ENU03571	AN161C6252:	60-83	1257-	NAP	g4498	445	163	3.00E-45	35	69	
19778	ENU03572	AN161C3740:	55-75	1242-	NAP	g3650391	831	201	1.00E-50	50	78	
19779	ENU03573	AN161C672:	36-59	1235-	NAP	g3850111	561	94	2.00E-45	41	98	
19780	ENU03574	AN161C2194:	46-65	1246-	NAP	g731293	286	138	1.00E-31	33	90	
19781	ENU03575	AN161C5263:	32-51	1231-	NAP	g4585221	330	101	3.00E-24	39	88	
19782	ENU03576	AN161C1054:	42-61	1243-	NAP	g4377376	462	165	1.00E-52	39	94	
19783	ENU03577	AN161C7707:	59-78	1256-	NAP	g1346360	542	231	6.00E-60	47	31	

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19784	ENU03578	AN161C4008:	58-77	1259-1280	NAP	g2276351	329	93	4.00E-18	55	42		Description (Z97992) putative transcriptional regulator [Schizosaccharomyces pombe]
19785	ENU03579	AN161C1160:	32-51	1225-1255	NAP	g585007	63	57	0.000000	2			cell division protein kinase 2 homolog CRK1 ; protein kinase (EC 2.7.1.37) cdc2-related CRK1 - Leishmania mexicana ; (X60385) cdc2-like protein [Leishmania mexicana]
19786	ENU03580	AN161C4268:	22-42	1228-1247	NAP	g400766	447	201	1.00E-50	36	62		phenol 2-monooxygenase (phenol hydroxylase) ; phenol 2-monooxygenase (EC 1.14.13.7) - Pseudomonas sp. plasmid EST1412 (AL031534) protein kinase kin1 [Schizosaccharomyces pombe]
19787	ENU03581	AN161C8771:	22-48	1213-1247	NAP	g3560139	157	50	0.00003	27	39		maackiain detoxification protein 1 - fungus (Nectria haematococca) ; (U35892) predicted flavin-containing mono-oxygenase [Nectria haematococca]
19788	ENU03582	AN161C4868:	71-90	1279-1299	NAP	g2133295	1263	182	4.00E-96	54	77		Meiotic recombination protein DLH1 (DMC1 homolog) ; DMC1/LIM15 homolog 1 - yeast (Candida albicans) ; (U39808) Dlh1p [Candida albicans]
19790	ENU03584	AN161C1113	22-46	1225-1250	NAP	g1351604	337	123	2.00E-35	35	96		hypothetical 40.0 KD protein C4G8.14C in chromosome I ; hypothetical protein SPAC4G8.14c - fission yeast (Schizosaccharomyces pombe)
19791	ENU03585	AN161C9449:	29-48	1235-1259	NAP	g1279911	1596	555	e-167	91	99		(U52963) mitogen-activated protein kinase [Nectria haematococca var. brevicornis]
19792	ENU03586	AN161C6804:	50-77	1262-1281	NAP	g1084946	276	96	4.00E-25	29	83		hypothetical protein YPR023c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
19793	ENU03587	AN161C1101:	26-51	1235-1257	NAP	g434759	1403	232	e-147	64	41		(D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]
19794	ENU03588	AN161C1171:	25-52	1240-1259	NAP	g3184099	637	193	5.00E-51	36	69		(AL023777) hypothetical protein [Schizosaccharomyces pombe]

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19795	ENU03589	AN161C7713:	22-43	1234-1258	NAP		g3185342	519	135	5.00E-31	38	96	hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein
19796	ENU03590	AN161C8371:	22-46	1235-1259	NAP		g1805251	366	166	4.00E-40	29	74	[Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori]
19797	ENU03591	AN161C1137	25-47	1241-1262	NAP		g2388971	1133	260	e-119	57	99	(Z98979) hypothetical protein [Schizosaccharomyces pombe]
19798	ENU03592	AN161C822:1	22-45	1228-1260	NAP		g2739168	229	148	7.00E-35	31	98	(AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum]
19799	ENU03593	AN161C1918:	22-55	1241-1261	NAP		g2764614	510	128	7.00E-58	40	98	(AJ001330) orfT [Lactobacillus sakei]
19800	ENU03594	AN161C9032:	22-41	1242-1262	NAP		g2144467	1212	135	2.00E-84	59	52	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae)
19801	ENU03595	AN161C5905:	70-89	1292-1311	NAP		g2499312	2312	591	e-168	92	77	NADH-ubiquinone oxidoreductase 51 KD subunit precursor (complex I-51KD) (C1-51KD) ; (X64402) NADH dehydrogenase [Aspergillus niger]
19802	ENU03596	AN161C6334:	63-83	1272-1304	NAP		g3925778	835	78	1.00E-17	44	26	(AL034353) probable metabolite transport protein
19803	ENU03597	AN161C3320:	35-55	1246-1276	NAP		g2808725	159	78	1.00E-13	34	53	[Schizosaccharomyces pombe] (AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis]
19804	ENU03598	AN161C2332:	64-87	1283-1307	NAP		g2407968	415	164	9.00E-40	35	87	(Y14749) MDM10 [Podospira anserinal]
19805	ENU03599	AN161C5370:	23-42	1237-1266	NAP		g2315453	463	123	5.00E-43	40	98	(AF016448) Similar to glycolate oxidase; coded for by C. elegans cDNA yk151h10.5; coded for by C. elegans cDNA yk151h10.3 [Caenorhabditis elegans]
19806	ENU03600	AN161C6496:	22-56	1247-1266	NAP		g135746	730	182	2.00E-83	46	93	"3-ketoacyl-CoA thiolase peroxisomal A precursor (beta-ketothiolase A) (acetyl-CoA acyltransferase A) (peroxisomal 3-oxoacyl-CoA thiolase A) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16) A precursor, peroxisomal - rat ; (D90058) 3-ketoacyl-CoA thiolase A [Rattus norvegicus] "
19807	ENU03601	AN161C1837:	71-90	1296-1315	NAP		g2625138	2012	190	5.00E-94	48	23	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]

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19808	ENU03602	ANI61C9767: 3929..2643	23-56	1248-1267	NAP	g1723533	220	109	4.00E-23	38	39		hypothetical 33.6 KD protein C25G10.01 in chromosome I ; (Z70691) ma binding protein [Schizosaccharomyces pombe] (Z75532) similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans]
19809	ENU03603	ANI61C263:1 584..2871	22-41	1242-1267	NAP	g3875242	181	66	3.00E-22	30	96		
19810	ENU03604	ANI61C526:3 333..2046	72-93	1290-1317	NAP	g125935	165	65	0.000000	26	64		lactose permease ; lactose permease - yeast (Kluveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluveromyces lactis] "(D83732) endo-1,4-beta-glucanase [Aspergillus oryzae] "
19811	ENU03605	ANI61C1086 7.367..1654	24-56	1243-1269	NAP	g2467375	1275	527	e-149	63	98		probable membrane protein YOR161c - yeast (Saccharomyces cerevisiae) ; (U55021) O3568p [Saccharomyces cerevisiae] ; (Z75069) ORF YOR161c [Saccharomyces cerevisiae]
19812	ENU03606	ANI61C3295: 10..1297	31-52	1255-1277	NAP	g2132901	833	178	4.00E-75	40	78		hypothetical 56.4 KD protein in RPL32-CWH41 intergenic region precursor ; probable membrane protein YGL028c - yeast (Saccharomyces cerevisiae) ; (Z72550) ORF YGL028c [Saccharomyces cerevisiae]
19813	ENU03607	ANI61C435:4 685..3397	49-68	1269-1295	NAP	g1723809	380	152	7.00E-36	27	78		hypothetical 56.4 KD protein in RPL32-CWH41 intergenic region precursor ; probable membrane protein YGL028c - yeast (Saccharomyces cerevisiae) ; (Z72550) ORF YGL028c [Saccharomyces cerevisiae]
19814	ENU03608	ANI61C2205: 2001..712	64-84	1290-1310	NAP	g3850125	458	131	9.00E-31	33	76		protein [Candida albicans] Arginine metabolism regulation protein III ; regulatory protein ARGR111 - yeast (Saccharomyces cerevisiae) ; (X05328) ARGR111 protein (AA 1-355) [Saccharomyces cerevisiae] ; (Z46727) Arg3p [Saccharomyces cerevisiae] (AE001015) acyl-CoA dehydrogenase (acd-9) [Archaeoglobus fulgidus]
19815	ENU03609	ANI61C80:12 97..8	55-74	1283-1302	NAP	g114134	236	93	4.00E-18	33	86		hypothetical 34.2 KD protein in CUS1-RPL18A1 intergenic region ; hypothetical protein YMR241w - yeast (Saccharomyces cerevisiae) ; (Z48756) unknown [Saccharomyces cerevisiae]
19816	ENU03610	ANI61C9725: 1421..131	53-72	1282-1301	NAP	g2649289	300	118	8.00E-26	33	88		
19817	ENU03611	ANI61C6152: 1746..3037	45-64	1273-1293	NAP	g2497200	1006	332	1.00E-92	70	97		

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19818	ENU03612	ANI61C1077	67-86	1295-	NAP	g13363051	468	113	2.00E-24	28	76		P58 protein - bovine ; (U04631) PKR inhibitor P58 [Bos taurus]
19819	ENU03613	4:5799..4508 ANI61C8876: 43-63		1316 1271-	NAP	g1170767	1490	383	e-154	77	96		26S protease regulatory subunit 8 homolog (LET1 protein) ; transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) ; (U02280) Let1 [Schizosaccharomyces pombe] ; (A1035065) 26s protease regulatory subunit 8 homolog [Schizosaccharomyces pombe]
19820	ENU03614	ANI61C59:19 26-45 80..3274		1259- 1278	NAP	g2492825	374	141	5.00E-41	32	96		"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus]"
19821	ENU03615	ANI61C59:19 26-45 80..3274		1259- 1278	NAP	g2492825	374	141	5.00E-41	32	96		"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus]"
19822	ENU03616	ANI61C1100 29-49 1:3092..4388		1256- 1283	NAP	g1854443	474	180	2.00E-44	39	92		(D83970) CPRD8 protein [Vigna unguiculata]
19823	ENU03617	ANI61C9270: 26-51 52..207		1249- 1280	NAP	g2500938	115	71	2.00E-11	32	42		Myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
19824	ENU03618	ANI61C9270: 26-51 52..207		1249- 1280	NAP	g2500938	115	71	2.00E-11	32	42		Myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
19825	ENU03619	ANI61C3627: 22-42 1747..450		1257- 1277	NAP	g4240421	99	1.00E-22					[Schizosaccharomyces pombe] (AF080225) reductase homolog [Streptomyces cyanogenus]



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19826	ENU03620	AN161C9039:	28-51	1264-	NAP		g2330781	972	328	e-103	51	84	"(Z98559) SPAC23C11.17; len:485aa, similar eg. to YPR125W, Q06493, chromosome xvi orf, (454aa), fasta scores, opt:1063, E0:0, (43.5% identity in 418 aa overlap)
		3292..4589		1283									[Schizosaccharomyces pombe] "
19827	ENU03621	AN161C3441:	72-93	1292-	NAP		g731716	646	270	4.00E-73	42	88	hypothetical 49.8 KD protein in ACT3-YCK1 intergenic region precursor ;
		705..2002		1327									hypothetical protein YHR132c - yeast (Saccharomyces cerevisiae) ; (U10398)
19828	ENU03622	AN161C1057	23-42	1262-	NAP		g731846	159	53	0.000003	27	70	Ecml4p [Saccharomyces cerevisiae] "
		2:2746..1446		1281									hypothetical 39.4 KD protein in SGA1-KTR7 intergenic region ;
													hypothetical protein YIL096c - yeast (Saccharomyces cerevisiae) ; (Z38125) orf, len: 336, CAl: 0.14
19829	ENU03623	AN150C1282	50-69	1277-	NAP		g137471		134	1.00E-30	38	94	[Saccharomyces cerevisiae] "
		7_1:1701..400		1309									"vacuolar ATP synthase subunit C (V-ATPase C subunit) ; H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar - bovine ; (J05681) H+ - ATPase C subunit [Bos taurus] "
19830	ENU03624	AN161C5190:	68-90	1310-	NAP		g1172616	1087	326	2.00E-88	49	54	probable ATP-dependent RNA helicase PRH1 ; PRH1 protein - fission yeast (Schizosaccharomyces pombe) ; (Z54354) probable atp-dependent mna helicase prh1 [Schizosaccharomyces pombe]
		2421..1118		1329									(Y16748) malate dehydrogenase [Piromyces sp. E2]
19831	ENU03625	AN161C8056:	65-84	1306-	NAP		g4029338	632	145	6.00E-65	57	96	(AB016720) carboxylesterase precursor [Aphis gossypii]
		641..1944		1326									putative polyketide biosynthesis protein PKSJ ; (U11039) unknown [Bacillus subtilis] ; (Z99112) pksJ [Bacillus subtilis] ; (Z99113) pksJ [Bacillus subtilis]
19832	ENU03626	AN161C6841:	22-42	1267-	NAP		g3426006	302	140	2.00E-32	39	32	(AB011157) KIAA0585 protein [Homo sapiens]
		5143..3838		1285									(Y14749) MDM10 [Podospira anserina]
19833	ENU03627	AN161C5500:	50-71	1299-	NAP		g730334	379	173	2.00E-42	28	76	
		2517..1207		1318									
19834	ENU03628	AN161C1029	22-42	1271-	NAP		g3043694	243	137	2.00E-31	29	64	
		4:4056..2745		1290									
19835	ENU03629	AN161C2332:	64-87	1315-	NAP		g2407968	415	164	9.00E-40	34	88	
		3982..2670		1334									

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19836	ENU03630	AN161C8090:	22-41	1277-	NAP	g2984184	398	157	2.00E-37	29	82	82	(AE000763) N-methylhydantoinase B [Aquifex aeolicus]
19837	ENU03631	1445..129 AN161C4285:	46-68	1302-	NAP	g2664292	1594	447	e-171	81	95	95	(Y15744) cellular aspartic protease [Aspergillus fumigatus] ; (AJ132504) aspartic protease [Aspergillus fumigatus]
19838	ENU03632	AN161C7950:	57-77	1304-	NAP	g2493391	96	4.00E-19					probable stergmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emmericella nidulans]
19839	ENU03633	AN161C4230:	47-75	1289-	NAP	g1351673	367	113	6.00E-32	38	96	96	hypothetical 37.7 KD protein C1F7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast [Schizosaccharomyces pombe] ; (Z67998) unknown [Schizosaccharomyces pombe]
19840	ENU03634	AN161C3599:	29-52	1288-	NAP	g522302	4000	589	e-167	63	36	36	[Schizosaccharomyces pombe] (L35053) endonuclease [Magnaporthe grisea]
19841	ENU03635	5916..4596 AN161C4299:	57-80	1307 1316-	NAP	g1351606	196	67	3.00E-10	29	25	25	hypothetical 54.3 KD protein C23D3.03C in chromosome I ; hypothetical protein SPAC23D3.03c - fission yeast [Schizosaccharomyces pombe] ; (Z64354) unknown [Schizosaccharomyces pombe]
19842	ENU03636	AN161C406:2	30-57	1290-	NAP	g135184	2357	266	e-118	54	38	38	"Valyl-TRNA synthetase, mitochondrial precursor (valine--TRNA ligase) (VALRS) ; valine--tRNA ligase (EC 6.1.1.9) - Neurospora crassa "
19843	ENU03637	AN161C4412:	45-65	1307-	NAP	g1469396	692	226	8.00E-75	43	94	94	(U43775) secreted aspartic proteinase precursor [Glomerella cingulata]
19844	ENU03638	7822..6499 AN161C1527:	25-56	1326 1290-	NAP	g730338	1840	565	e-160	58	72	72	Lysophospholipase precursor (phospholipase B) ; lysophospholipase (EC 3.1.1.5) - Penicillium notatum (fragment) ; (X60348) lysophospholipase [Penicillium chrysogenum]
19845	ENU03639	AN161C188:1	56-77	1321-	NAP	g1346290	802	166	2.00E-81	45	69	69	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
		375..49		1340									

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19846	ENU03640	ANI61C1118	71-94	1334-1355	NAP	g2621739	762	227	2.00E-87	51	68		(AE000845) long-chain-fatty-acid-CoA ligase [Methanobacterium thermoautotrophicum]
19847	ENU03641	ANI61C3898: 1348..20	65-90	1331-1351	NAP	g2498971	627	130	3.00E-29	34	75		putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740)
19848	ENU03642	ANI61C1085 7:1133..2463	22-51	1282-1310	NAP	g3738167	452	173	2.00E-42	41	100		putative FAD-containing monooxygenase [Emmericella nidulans] (AL031856) putative golgi uridine diphosphate-N-acetylglucosamine transporter [Schizosaccharomyces pombe]
19849	ENU03643	ANI61C1018 7:4272..2941	44-63	1314-1333	NAP	g1723948	1150	469	e-131	55	95		probable histone DEacetylase HOS2 ; probable transcription regulator YGL194c - yeast (Saccharomyces cerevisiae) ; (Z72716) ORF YGL194c [Saccharomyces cerevisiae] (AB010714) salicylate hydroxylase [Pseudomonas putida]
19850	ENU03644	ANI61C8914: 1895..3227	51-70	1315-1341	NAP	g2826168		62	7.00E-13				hypothetical protein YDR322w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr322wp [Saccharomyces cerevisiae] (AL023596) hypothetical protein MLCB2407.16c [Mycobacterium leprae]
19851	ENU03645	ANI61C1926: 59..1393	22-42	1295-1314	NAP	g2131429	236	119	4.00E-26	25	96		probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae) ; (U43491) hypothetical protein UNE378 [Saccharomyces cerevisiae] ; (Z74745) ORF YOL003c [Saccharomyces cerevisiae]
19852	ENU03646	ANI61C8043: 2221..884	65-84	1340-1360	NAP	g3150104	251	129	4.00E-29	36	33		putative glycyl-TRNA synthetase (glycine--TRNA ligase) (GLYRS) ; (Z69369) glycyl tRNA synthetase [Schizosaccharomyces pombe]
19853	ENU03647	ANI61C7152: 4223..2886	40-61	1314-1335	NAP	g2132817	222	75	2.00E-21	33	41		
19854	ENU03648	ANI61C3804: 2043..705	22-41	1299-1318	NAP	g1711632	2083	396	e-149	62	65		

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19855	ENU03649	ANI61C4864:	57-76	1333-	NAP		g1176339	517	136	4.00E-57	36	87	"hypothetical 50.8 KD protein in MIR1-STE18 intergenic region ; indoleamine-pyrrole 2,3-dioxygenase homolog YJR078w - yeast (Saccharomyces cerevisiae) ; (Z49578) ORF YJR078w [Saccharomyces cerevisiae] ; (L47993) ORF YJR078w [Saccharomyces cerevisiae]"
		635..1973		1353									(AL033534) carbamoyl-phosphate synthase [Schizosaccharomyces pombe]
19856	ENU03650	ANI61C7945:	72-91	1349-	NAP		g3873545	3360	293	e-150	66	36	(Y13975) phospholipase C [Candida albicans]
		1416..2755		1369									(U62917) glucose transporter TGT2 [Taenia solium]
19857	ENU03651	ANI61C1092	47-66	1323-	NAP		g2462982	244	103	8.00E-35	34	23	hypothetical protein YDR322w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr322wp [Saccharomyces cerevisiae]"
		8:3792..2452		1345									(U62928) multidrug resistance protein, ABC transporter protein [Aureobasidium pullulans] ; (U85909) multidrug resistance-like protein [Aureobasidium pullulans]"
19858	ENU03652	ANI61C9031:	63-82	1335-	NAP		g1480799		37	0.000000			(U31348) G4p1 [Saccharomyces cerevisiae]
		342..579		1362									(X81067) probable mitochondrial protein; nearly identical to YME1 [Saccharomyces cerevisiae]
19859	ENU03653	ANI61C1926:	22-42	1302-	NAP		g2131429	236	119	4.00E-26	25	96	Galactose-1-phosphate uridylyltransferase ; UDPglucose--hexose-1-phosphate uridylyltransferase (EC 2.7.7.12) - yeast (Kluveromyces marxianus var. lactis) ; (X07039) epimerase (GAL 7) (AA 1 - 370) [Kluveromyces lactis]
		59..1401		1322									(AB025252) reverse transcriptase [Magnaporthe grisea]
19860	ENU03654	ANI61C6211:	49-71	1324-	NAP		g4097503	1671	313	2.00E-84	42	34	
		1869..3212		1350									
19861	ENU03655	ANI61C3588:	64-84	1347-	NAP		g1002712	351	64	0.000000	54	12	
		2903..2660		1366									
19862	ENU03656	ANI61C4066:	58-77	1342-	NAP		g531752	1288	418	e-116	56	57	
		1651..306		1361									
19863	ENU03657	ANI61C7448:	22-48	1305-	NAP		g120909	856	314	2.00E-92	51	96	
		1277..2623		1325									
19864	ENU03658	ANI61C5998:	50-69	1334-	NAP		g4586458	151	108	1.00E-22	32	62	
		5415..4069		1354									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19865	ENU03659	AN161C8751:	22-45	1307-	NAP		g2498440	926	297	4.00E-99	48	88	"Homogentisate 1,2-dioxygenase (homogentisicase) (homogentisate oxygenase) (homogentisic acid oxidase) ; 3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15) - Emericella nidulans ; (U30797) 2,5 dihydroxyphenylacetate oxidase [Emericella nidulans] ; (AJ001836) homogentisate dioxygenase [Emericella nidulans]"
19866	ENU03660	AN161C2872:	28-50	1315-	NAP		g1717973	1184	499	e-140	61	56	"Glycogen (starch) synthase, isoform 2 ; UDPglucose--starch glucosyltransferase (EC 2.4.1.11) 2-yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae]"
19867	ENU03661	AN161C5204:	42-61	1325-	NAP		g4558826	2307	553	e-156	99	98	(AF076691) aureobasidin-resistance protein; AurA [Emericella nidulans]
19868	ENU03662	AN161C4343:	39-69	1328-	NAP		g1176967	88	71	1.00E-11	28	32	hypothetical 37.6 KD protein in GNTR-HTPG intergenic region ; (AB005554) see SWISS_PROT ACC#: P42106 [Bacillus subtilis] ; (Z99124) yxaG [Bacillus subtilis]
19869	ENU03663	AN161C236:	1 45-65	1328-	NAP		g2266941	1681	559	e-168	87	93	(AF009036) NAD(+)-isocitrate dehydrogenase subunit I [Ajellomyces capsulatus]
19870	ENU03664	AN161C4864:	57-76	1333-	NAP		g1176339	517	136	4.00E-57	35	88	"hypothetical 50.8 KD protein in MIR1-STE18 intergenic region ; indoleamine-pyrrrole 2,3-dioxygenase homolog YJR078w - yeast (Saccharomyces cerevisiae) ; (Z49578) ORF YJR078w [Saccharomyces cerevisiae] ; (L47993) ORF YJR078w [Saccharomyces cerevisiae]"

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19871	ENU03665	AN161C8878:	23-42	1307-	NAP	g1351651	784	220	1.00E-56	45	99		hypothetical 43.7 KD protein C24B11.08C in chromosome 1; hypothetical protein SPAC24B11.08c - fission yeast (Schizosaccharomyces pombe) ; (Z67757) unknown [Schizosaccharomyces pombe] (AC000133) ORF [Emerticella nidulans] (AL021748) major facilitator superfamily protein
19872	ENU03666	AN161C3420:	37-56	1326-	NAP	g1870209	419	158	7.00E-38	95	13		[Schizosaccharomyces pombe] DNA-3-methyladenine glycosylase (3-methyladenine DNA glycosylase) (3MEA DNA glycosylase) ; DNA-3-methyladenine glycosylase 1 (EC 3.2.2.20) - fission yeast (Schizosaccharomyces pombe) ; (U76637) 3-methyladenine DNA glycosylase [Schizosaccharomyces pombe]
19873	ENU03667	AN161C6436:	57-76	1350-	NAP	g2842516	589	83	1.00E-34	30	66		[Schizosaccharomyces pombe] DNA-3-methyladenine glycosylase (3-methyladenine DNA glycosylase) (3MEA DNA glycosylase) ; DNA-3-methyladenine glycosylase 1 (EC 3.2.2.20) - fission yeast (Schizosaccharomyces pombe) ; (U76637) 3-methyladenine DNA glycosylase [Schizosaccharomyces pombe]
19874	ENU03668	AN161C6064:	22-41	1315-	NAP	g2494171		80	3.00E-14				Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae] (AL021710) hypothetical protein [Arabidopsis thaliana] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] protein kinase C-like ; protein kinase C homolog PKCA - Aspergillus niger ; (U10549) protein kinase C [Aspergillus niger]
19875	ENU03669	AN161C313:2	22-41	1319-	NAP	g1711561		105	3.00E-27				Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae] (AL021710) hypothetical protein [Arabidopsis thaliana] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] protein kinase C-like ; protein kinase C homolog PKCA - Aspergillus niger ; (U10549) protein kinase C [Aspergillus niger]
19876	ENU03670	AN161C8049:	69-90	1367-	NAP	g2832659	249	100	2.00E-20	27	71		(AL021710) hypothetical protein [Arabidopsis thaliana] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] protein kinase C-like ; protein kinase C homolog PKCA - Aspergillus niger ; (U10549) protein kinase C [Aspergillus niger]
19877	ENU03671	AN161C8377:	50-69	1344-	NAP	g117803	591	262	3.00E-69	39	71		(AL021710) hypothetical protein [Arabidopsis thaliana] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] protein kinase C-like ; protein kinase C homolog PKCA - Aspergillus niger ; (U10549) protein kinase C [Aspergillus niger]
19878	ENU03672	AN161C722:3	42-61	1342-	NAP	g2499576	2827	357	e-177	85	35		(AL021710) hypothetical protein [Arabidopsis thaliana] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] protein kinase C-like ; protein kinase C homolog PKCA - Aspergillus niger ; (U10549) protein kinase C [Aspergillus niger]

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19879	ENU03673	AN161C9491:	27-46	1328-	NAP	g4154089	286	98	2.00E-32	35	100	100	(Z98981) putative pyridoxal kinase [Schizosaccharomyces pombe]
19880	ENU03674	AN161C9160:	68-95	1370-	NAP	g4512109	470	176	2.00E-43	36	40	40	(AF125185) origin recognition complex subunit 4-related protein Orp4p [Schizosaccharomyces pombe]
19881	ENU03675	AN161C2242:	56-75	1356-	NAP	g729014	1043	146	1.00E-95	46	74	74	Arginine permease ; arginine transport protein - yeast (Saccharomyces cerevisiae) ; (M11724) amino acid permease [Saccharomyces cerevisiae] ; (U18795) Can1p: arginine permease [Saccharomyces cerevisiae]
19882	ENU03676	AN161C7470:	65-84	1366-	NAP	g3135990	1056	287	1.00E-76	42	78	78	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19883	ENU03677	AN161C1036	35-58	1343-	NAP	g2465156	701	255	5.00E-67	45	94	94	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
19884	ENU03678	AN161C1018	22-50	1334-	NAP	g2058345	1215	168	e-110	70	96	96	(Y12693) oxysterol-binding protein [Neurospora crassa]
19885	ENU03679	AN161C310:1	64-83	1380-	NAP	g3261633	321	83	5.00E-17	33	94	94	(Z79700) fadE13 [Mycobacterium tuberculosis]
19886	ENU03680	AN161C1090	36-56	1352-	NAP	g3122213	667	236	3.00E-61	39	96	96	histidinol dehydrogenase (HDH) ; (AE000809) histidinol dehydrogenase [Methanobacterium thermoautotrophicum]
19887	ENU03681	AN161C4094:	22-55	1339-	NAP	g1465805	274	87	7.00E-21	32	85	85	(U64852) coded for by C. elegans cDNA cm17d4; Similar to epoxide hydrolase. [Caenorhabditis elegans]
19888	ENU03682	AN161C3456:	70-99	1388-	NAP	g2492816	582	156	5.00E-62	32	73	73	uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]
19889	ENU03683	AN161C7433:	35-54	1354-	NAP	g121855	1110	182	7.00E-76				"Exoglucanase II precursor (exocellobiohydrolase II) (CBHII) (1,4-beta-cellobiohydrolase) ; cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) ; cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride) ; (M16190) cellobiohydrolase II [Trichoderma reesei] ; cellobiohydrolase II [Trichoderma reesei] "

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19890	ENU03684	ANI61C1092	57-76	1376-1395	NAP		g461915	829	108	2.00E-43			Dipeptidyl aminopeptidase A (DPAP A) (YSCIV); dipeptidyl aminopeptidase (EC 3.4.14.-) - yeast (Saccharomyces cerevisiae); (L21944) dipeptidyl aminopeptidase [Saccharomyces cerevisiae]; (U08230) dipeptidyl aminopeptidase A [Saccharomyces cerevisiae]; (X92441) YOR50-9 [Saccharomyces cerevisiae]; (Z75127) ORF YOR219c [Saccharomyces cerevisiae]
19891	ENU03685	ANI61C2498	47-67	1367-1388	NAP		g2315524	682	129	1.00E-67	37	81	[Saccharomyces cerevisiae] (AF016452) Similar to aldehyde dehydrogenase; coded for by C. elegans cDNA yk144e3.3; coded for by C. elegans cDNA CESAC55R; coded for by C. elegans cDNA yk144e3.5 [Caenorhabditis elegans] hypothetical protein YOR197w - yeast (Saccharomyces cerevisiae); (Z75105) ORF YOR197w [Saccharomyces cerevisiae]
19892	ENU03686	ANI61C8615	23-42	1329-1364	NAP		g2132083	929	353	2.00E-96	49	95	(AF140505) DEAD box RNA helicase [Candida albicans] "Endo-1,4-beta-xylanase (xylanase) (1,4-beta-D-xyilan xylohydrolyase)" "ARG-6 protein precursor (contains: N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-glutamate smilaldehyde dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-...; acetylglutamate kinase (EC 2.7.2.8) / N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) precursor, mitochondrial - Neurospora crassa; (L27746) arg-6 gene product [Neurospora crassa] "
19893	ENU03687	ANI61C8941	64-83	1388-1407	NAP		g4589366	542	226	3.00E-58	39	65	(Z29102) putative transposase [Drosophila hydei]; transposase [Drosophila hydei]
19894	ENU03688	ANI61C7867	69-88	1391-1413	NAP		g3123294	781	79	2.00E-70	61	97	
19895	ENU03689	ANI61C1061	35-56	1360-1380	NAP		g1703361	1592	467	e-169			
19896	ENU03690	ANI61C7037	22-56	1337-1368	NAP		g436466	162	68	1.00E-10	25	89	



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19897	ENU03691	AN161C3244:	25-46	1344-1371	NAP		g1708319	820	349	4.00E-95	45	82	cell cycle protein kinase HSK1 ; protein kinase hsk1 (EC 2.7.1.1) - fission yeast [Schizosaccharomyces pombe] ; (D50493) hsk1 + protein kinase [Schizosaccharomyces pombe] ; (AL035263) cell cycle protein kinase hsk1 [Schizosaccharomyces pombe] (Z29102) putative transposase [Drosophila hydei] ; transposase [Drosophila hydei]
19898	ENU03692	AN161C9575:	22-56	1337-1368	NAP		g436466	143	64	0.000000	24	89	NADPH dehydrogenase 2 (old yellow enzyme 2) ; NADPH dehydrogenase (EC 1.6.99.1) chain OYE2 - yeast (Saccharomyces cerevisiae) ; (L06124) NAD(P)H:oxidoreductase [Saccharomyces cerevisiae] ; (U00027) Oye2p: NAD(P)H oxidoreductase (Old Yellow Enzyme) [Saccharomyces cerevisiae]
19899	ENU03693	AN161C9932:	32-59	1359-1379	NAP		g417432	613	280	1.00E-74	40	91	Conidium-specific protein ; SpoC1-C1D protein - Emerella nidulans ; (X54668) SpoC1-C1D product [Emerella nidulans] (AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]
19900	ENU03694	AN161C7763:	26-45	1353-1376	NAP		g134270	146	54	0.000003	33	31	Zn/Cd resistance gene [Saccharomyces cerevisiae]
19901	ENU03695	AN161C1560:	44-64	1376-1395	NAP		g2648355	167	60	0.000000	38	96	hypothetical protein YDR330w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr330wp [Saccharomyces cerevisiae]
19902	ENU03696	AN161C410:5	41-62	1371-1394	NAP		g227157	333	107	2.00E-22	32	85	ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae) ; (Z73153) ORF YLL048c [Saccharomyces cerevisiae]
19903	ENU03697	AN161C1048	59-79	1387-1412	NAP		g2131432	441	155	5.00E-37	32	83	
19904	ENU03698	AN161C1128	67-87	1401-1420	NAP		g3915963	742	159	3.00E-73	38	26	

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19905	ENU03699	AN161C2134:	26-45	1347-4169..5564	NAP		g730893	283	54	7.00E-13			tryptophan permease (tryptophan amino acid transporter) ; tryptophan transport protein - yeast
													(Saccharomyces cerevisiae) ; (L33461) tryptophan permease [Saccharomyces cerevisiae] ; (X79150) tryptophan amino acid permease [Saccharomyces cerevisiae] ; (Z74762) ORF YOL020w [Saccharomyces cerevisiae] ; (U66834) suppressor of ABF1 [Saccharomyces cerevisiae]
19906	ENU03700	AN161C2438:	72-93	1407-160..1556	NAP		g731880	520	191	8.00E-48	27	64	"hypothetical 80.5 KD protein in SLN1-RAD25 intergenic region ; hypothetical protein YIL144w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 691, CAI: 0.15, possible coiled-coil [Saccharomyces cerevisiae] "
19907	ENU03701	AN161C2438:	72-93	1407-160..1556	NAP		g731880	520	191	8.00E-48	27	64	"hypothetical 80.5 KD protein in SLN1-RAD25 intergenic region ; hypothetical protein YIL144w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 691, CAI: 0.15, possible coiled-coil [Saccharomyces cerevisiae] "
19908	ENU03702	AN161C1724:	30-51	1356-2191..3589	NAP		g461508	925	393	e-108			"vacuolar aminopeptidase I precursor (polypeptidase) (leucine aminopeptidase IV) (LAPIV) (aminopeptidase III) (aminopeptidase YSCI) ; aminopeptidase yscI (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae) ; (M25548) aminopeptidase I [Saccharomyces cerevisiae] ; (X71133) vacuolar aminopeptidase YSCI [Saccharomyces cerevisiae] ; (Z28103) ORF YKL103c [Saccharomyces cerevisiae] "
19909	ENU03703	AN161C7948:	41-60	1375-5069..4253	NAP		g3925779	71	47	0.0003	28	35	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]

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19910	ENU03704	ANI61C3294:	58-77	1401-1421	NAP	g3201958	368	159	4.00E-40	39	62		(AF068116) eIF4E-like protein 4E-LP [Mus musculus]
19911	ENU03705	ANI61C3573:	68-90	1398-1431	NAP	g1078218	961	195	3.00E-80	45	93		probable membrane protein YDR105c - yeast (Saccharomyces cerevisiae) ; (Z47746) unknown [Saccharomyces cerevisiae] ; (Z48758) unknown [Saccharomyces cerevisiae]
19912	ENU03706	ANI61C7316:	30-57	1375-1394	NAP	g4388565	1265	424	e-125	52	91		[Saccharomyces cerevisiae] (Z35875) ORF YBR006w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae]
19913	ENU03707	ANI61C2435:	51-71	1386-1417	NAP	g1749554	618	213	7.00E-64	47	95		"(D89173) similar to Saccharomyces cerevisiae hypothetical 36.4KD protein in SOD1-CPA2 intergenic region, SWISS-PROT Accession Number P47143 [Schizosaccharomyces pombe] ; (AL023781) adenosine kinase [Schizosaccharomyces pombe] "
19914	ENU03708	ANI61C9254:	23-52	1370-1389	NAP	g3738169	1087	314	7.00E-99	58	97		[Schizosaccharomyces pombe] (AL031856) putative mitochondrial protein import protein - DNAJ protein [Schizosaccharomyces pombe]
19915	ENU03709	ANI61C1115	22-48	1370-1390	NAP	g3183342	353	130	2.00E-29	38	96		hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]
19916	ENU03710	ANI61C3949:	66-85	1415-1434	NAP	g1345704	233	62	0.000000	27	33		[Schizosaccharomyces pombe] cell division control protein 15 ; cell division control protein cdc15 - fission yeast (Schizosaccharomyces pombe) ; (Z95334) Cdc15p [Schizosaccharomyces pombe]
19917	ENU03711	ANI61C9367:	22-42	1362-1391	NAP	g131828	998	282	5.00E-98	44	79		[Schizosaccharomyces pombe] LOW-affinity glucose transporter ; glucose transport protein RAG1 - yeast (Kluyveromyces marxianus var. lactis) ; (X53752) putative sugar transporter [Kluyveromyces lactis]
19918	ENU03712	ANI61C212.3	23-42	1367-1393	NAP	g2996008	1881	666	0	85	99		(AF053983) translation release factor subunit 1 [Podospira anserina]
19919	ENU03713	ANI61C7848:	37-55	1384-1408	NAP	g3023951	470	205	5.00E-52	30	43		Histone transcription regulator 1 homolog ; (Z97204) putative hiira protein; histone transcription regulator [Schizosaccharomyces pombe]
19920	ENU03714	ANI61C9794:	23-50	1367-1394	NAP	g2271477	1012	194	e-106	49	97		(AF009631) AP47/50p [Arabidopsis thaliana]

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19921	ENU03715	ANI61C7561:	45-64	1391-1421	NAP		g117619	135	50	0.00004	34	18	choleline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
		258..87											choleline transport protein [Saccharomyces cerevisiae] ; (Z72599)
													ORF YGL077c [Saccharomyces cerevisiae]
19922	ENU03716	ANI61C9917:	22-41	1380-1399	NAP		g3581896	443	138	9.00E-32	24	75	(AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
19923	ENU03717	ANI61C7944:	36-55	1392-1414	NAP		g1077336	466	127	2.00E-52	35	96	hypothetical protein YLR380w - yeast (Saccharomyces cerevisiae) ; (U19104)
		3165..4585											Ylr380wp [Saccharomyces cerevisiae]
19924	ENU03718	ANI61C2369:	22-44	1380-1402	NAP		g586465	233	88	2.00E-20	26	94	hypothetical 50.8 KD protein in COQ1-FLR1 intergenic region precursor ; probable membrane protein YBR004c - yeast (Saccharomyces cerevisiae) ; (Z35873) ORF YBR004c [Saccharomyces cerevisiae]
19925	ENU03719	ANI61C1133	22-44	1383-1403	NAP		g2746775	414	139	9.00E-37	36	82	(AF040640) similar to peptidase family C19 (ubiquitin carboxyl-terminal hydrolase) [Caenorhabditis elegans]
19926	ENU03720	ANI61C7948:	42-61	1391-1424	NAP		g125407	523	179	1.00E-47	36	95	mevalonate kinase (MVK) ; mevalonate kinase (EC 2.7.1.36) - yeast (Saccharomyces cerevisiae) ; (X55875) mevalonate kinase [Saccharomyces cerevisiae] ; (X06114) ORF1 (put. RAR1 protein) (AA 1-443) [Saccharomyces cerevisiae] ; (Z49809)
19927	ENU03721	ANI61C316:3	58-84	1423-1442	NAP		g2492782	551	219	5.00E-56	38	97	Rar1p [Saccharomyces cerevisiae] alpha-galactosidase precursor (melibiase) (alpha-D-galactoside galactohydrolase) ; (L27992) alpha-galactosidase [Coffea arabica]
		290..1864											"DLTE protein ; hypothetical protein - Bacillus subtilis ; dlte product[putative cytosolic oxidoreductase [Bacillus subtilis, Peptide, 252 aa] ; (X73124)
19928	ENU03722	ANI61C1271:	22-44	1379-1408	NAP		g729344		45	0.000000		01	ipa-1r [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-1r [Bacillus subtilis]
		2312..2792											"

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19929	ENU03723	ANI61C8203:	68-88	1429-	NAP		g4249560	1229	291	e-133	52	96	(AB003109) beta-glucosidase [Humicola grisea var. thermoides]
19930	ENU03724	ANI61C1036	49-68	1421-	NAP		g1730771	1269	330	1.00E-89	41	43	hypothetical 110.9 KD protein in SPC98-TOM70 intergenic region ; probable membrane protein YNL123w - yeast (Saccharomyces cerevisiae) ; (Z69382) N1897 [Saccharomyces cerevisiae] ; (Z71399) ORF YNL123w [Saccharomyces cerevisiae]
19931	ENU03725	ANI61C8805:	24-49	1396-	NAP		g4105567	184	105	9.00E-22	31	93	(AF047707) UDP-glucose:ceramide glycosyltransferase [Rattus norvegicus]
19932	ENU03726	ANI61C1038	23-42	1397-	NAP		g2894272	351	141	1.00E-32	38	76	(AL021839) hypothetical protein [Schizosaccharomyces pombe]
19933	ENU03727	ANI61C9835:	51-69	1425-	NAP		g2132357	148	84	2.00E-15	40	35	NBP2 protein - yeast (Saccharomyces cerevisiae) ; (Z50046) Nbp2p [Saccharomyces cerevisiae] ; (D43693) Nap1-binding protein [Saccharomyces cerevisiae]
19934	ENU03728	ANI61C8985:	57-75	1432-	NAP		g3915140	562	127	2.00E-54	34	94	isotrichoderm C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichoderm C-15 hydroxylase [Fusarium sporotrichioides]
19935	ENU03729	ANI61C7943:	40-59	1419-	NAP		g632081		103	3.00E-21			hypothetical protein 4 - Xanthobacter sp. ; (X79863) orf4 [Xanthobacter sp. Py2]
19936	ENU03730	ANI61C9526:	22-44	1401-	NAP		g2501674	185	61	2.00E-18	39	20	DRAP deaminase ; RIB2 protein - yeast (Saccharomyces cerevisiae) ; (Z21618) DRAP deaminase [Saccharomyces cerevisiae] ; (Z74808) ORF YOL066c [Saccharomyces cerevisiae]
19937	ENU03731	ANI61C8286:	55-74	1426-	NAP		g1172703	484	191	8.00E-48	44	32	"peptide transporter PTR2-A ; (U01171) similar to S. cerevisiae PTR2 gene, GenBank Accession Number L11994 [Arabidopsis thaliana]" (X63029) Uhu [Drosophila heteroneural]
19938	ENU03732	ANI61C408:	52-79	1425-	NAP		g7464		75	1.00E-12			(Z98529) putative RNA-binding protein [Schizosaccharomyces pombe]
19939	ENU03733	ANI61C9882:	22-49	1405-	NAP		g2462671	413	129	4.00E-29	33	97	
		3530..4974		1424									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
19940	ENU03734	ANI61C2898:	72-91	1458-1477	NAP		g1709679	753	238	6.00E-85	40	59	probable mitochondrial intermediate peptidase precursor (MIP) ; (Z70690) unknown [Schizosaccharomyces pombe]
19941	ENU03735	ANI61C6436:	57-76	1436-1463	NAP		g2842516	589	92	3.00E-37	30	72	(AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe]
19942	ENU03736	ANI61C8998:	39-58	1427-1446	NAP		g2398820	524	221	8.00E-57	34	43	(Z99126) hypothetical protein. [Schizosaccharomyces pombe]
19943	ENU03737	ANI61C8998:	39-58	1427-1446	NAP		g2398820	524	221	8.00E-57	34	43	(Z99126) hypothetical protein. [Schizosaccharomyces pombe]
19944	ENU03738	ANI61C7853:	22-48	1411-1430	NAP		g1345707	387	108	6.00E-42	38	73	CCC1 protein ; CCC1 protein - yeast (Saccharomyces cerevisiae) ; (U19027) CCC1p: putative transmembrane Ca2+ transporter [Saccharomyces cerevisiae] ; (L24112) Ccc1p [Saccharomyces cerevisiae]
19945	ENU03739	ANI61C5260:	62-81	1441-1474	NAP		g1709784	955	347	8.00E-95			gamma-glutamyl phosphate reductase (GPR) (glutamate-5-semialdehyde dehydrogenase) (glutamyl-gamma-semialdehyde dehydrogenase) ; glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41) - yeast (Saccharomyces cerevisiae) ; (X90565) orf 06155 [Saccharomyces cerevisiae] ; (U43565) gamma-glutamyl phosphate reductase [Saccharomyces cerevisiae] ; (Z75231) ORF YOR323c [Saccharomyces cerevisiae] (AF127176) trichothecene 3-O-acetyltransferase [Fusarium sporotrichoides]
19946	ENU03740	ANI61C7017:	22-55	1409-1434	NAP		g4378882		150	3.00E-35			hypothetical 42.3 KD protein in YTA2-DIT1 intergenic region ; hypothetical protein YDR400w - yeast (Saccharomyces cerevisiae) ; (U32274) Ydr400wp; CAI: 0.14 [Saccharomyces cerevisiae]
19947	ENU03741	ANI61C6489:	24-50	1417-1437	NAP		g2497466	344	73	3.00E-34	35	98	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19948	ENU03742	AN161C1056	22-41	1406-1439	NAP		g3881508	259	75	1.00E-12	33	91	(Z47357) cDNA EST EMBL: T00822 comes from this gene, cDNA EST EMBL: T00823 comes from this gene [Caenorhabditis elegans]
19949	ENU03743	AN161C7184:	32-53	1428-1450	NAP		g1710597	292	121	2.00E-30	33	73	"mitochondrial 60S ribosomal protein L7 precursor (YML7) ; ribosomal protein Yml7, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49701) unknown [Saccharomyces cerevisiae]" (AF095898) siderophore biosynthesis repressor SREA [Emericella nidulans] "3-ketoacyl-CoA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica) ; (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica]" choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19950	ENU03744	AN161C9446:	67-86	1452-1486	NAP		g4585213	2852	484	0	99	81	
19951	ENU03745	AN161C6203:	68-87	1465-1491	NAP		g549077	840	275	1.00E-75	53	95	
19952	ENU03746	AN161C3969:	29-48	1420-1452	NAP		g117619	632	213	2.00E-54	33	82	
19953	ENU03747	AN161C1041	69-90	1467-1493	NAP		g2507070	369	88	1.00E-18	35	61	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19954	ENU03748	AN161C9290:	55-86	1460-1481	NAP		g1237183	434	146	2.00E-53	33	83	(D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
19955	ENU03749	AN161C6471:	24-50	1432-1451	NAP		g3947853	663	232	9.00E-65	53	73	(AL034381) transcriptional regulator [Schizosaccharomyces pombe]
19956	ENU03750	AN161C222:	1 23-43	1430-1450	NAP		g403179	263	129	5.00E-29	37	25	(L24441) kinesin light chain [Loligo pealii]

# Genomic Annotation

Seq num	Seq id	Contig	Source	5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19957	ENU03751	AN161C7471:	65-84	6428..4957	1474-1494	NAP		g2507070	442	113	1.00E-50	35	83	N amino acid transport system protein (methyltryptophan resistance protein); neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19958	ENU03752	AN161C1144	35-64	6:2721..1249	1442-1465	NAP		g127024	1418	417	e-163	60	93	homoserine O-acetyltransferase (homoserine O-trans-acetylase); homoserine O-acetyltransferase (EC 2.3.1.31) - fungus (Ascobolus immersus) ; (M26662) met2 [Ascobolus immersus]
19959	ENU03753	AN161C2369:	58-77	810..2283	1467-1489	NAP		g586465	233	88	2.00E-20	26	94	hypothetical 50.8 KD protein in COQ1-FLR1 intergenic region precursor; probable membrane protein YBR004c - yeast (Saccharomyces cerevisiae) ; (Z35873) ORF YBR004c [Saccharomyces cerevisiae]
19960	ENU03754	AN161C1056	62-81	5:1164..2638	1474-1494	NAP		g3881508	259	76	7.00E-13	32	96	(Z47357) cDNA EST EMBL.T00822 comes from this gene; cDNA EST EMBL.T00823 comes from this gene [Caenorhabditis elegans]
19961	ENU03755	AN161C5215:	27-54	4956..3482	1440-1459	NAP		g1172824	337	57	0.000000	56	11	DNA repair and recombination protein RAD52 ; (X75086) K.lactis Rad52 [Kluyveromyces lactis]
19962	ENU03756	AN161C9290:	55-86	3960..2484	1470-1489	NAP		g1237183	434	146	2.00E-53	33	84	(D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
19963	ENU03757	AN161C1118	22-53	5:6237..4760	1438-1457	NAP		g3025028	482	217	2.00E-55	33	83	"hypothetical 47.3 KD protein in OMPX-MOEB intergenic region ; (AE000184) orf, hypothetical protein [Escherichia coli] ; (D90719) ORF_ID:o207#4 [Escherichia coli] ; (D90720) ORF_ID:o207#4 [Escherichia coli]"
19964	ENU03758	AN161C9356:	23-42	1498..19	1440-1460	NAP		g3150152	1177	372	e-121	70	78	(A1006219) clathrin-associated protein [Drosophila melanogaster]
19965	ENU03759	AN161C3300:	22-41	478..1957	1440-1459	NAP		g2388977	152	56	0.000000	39	16	(Z98980) hypothetical protein [Schizosaccharomyces pombe]



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19966	ENU03760	AN161C7237:	42-63	1451-1481	NAP		g1708578	63	0.000000	006			myo-inositol transporter I ; myo-inositol transport protein ITR1 - yeast (Saccharomyces cerevisiae) ; (U33057)
		3570..5051											It r1p: myo-inositol transporter; YDR497C; CAL: 0.19 [Saccharomyces cerevisiae]
19967	ENU03761	AN161C8669:	46-68	1453-1485	NAP		g1176670	262	90	4.00E-17	33	96	hypothetical 37.7 KD protein C08B11.7 in chromosome II ; (Z46676) similar to thiolesterase; cDNA EST yk221d9.5 comes from this gene [Caenorhabditis elegans] (U59421) Band 17 [Gallus gallus]
19968	ENU03762	AN161C9412:	54-74	1471-1494	NAP		g2795769	36	0.0004				dicarboxylic amino acid permease ; dicarboxylic amino acid permease DIP5 - yeast (Saccharomyces cerevisiae) ; (X95802) dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae] ; (Z73621) ORF YPL265w [Saccharomyces cerevisiae]
19969	ENU03763	AN161C3441:	37-59	1450-1480	NAP		g1706439	1343	469	e-131	56	77	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19970	ENU03764	AN161C5996:	30-55	1454-1475	NAP		g2507070	323	101	1.00E-35	28	93	(AC003027) lclprt_seq No definition line found [Arabidopsis thaliana] probable eukaryotic initiation factor C17C9.03 ; (Z73099) probable initiation factor [Schizosaccharomyces pombe]
19971	ENU03765	AN161C3862:	68-95	1495-1515	NAP		g4204312	652	271	1.00E-71	38	42	(U59234) biotin carboxylase [Synechococcus PCC7942] (AJ006487) propionyl-CoA carboxylase [Homo sapiens] (AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
19972	ENU03766	AN161C2424:	72-96	1503-1522	NAP		g1723562	778	291	2.00E-81	46	30	
19973	ENU03767	AN161C2430:	39-58	1470-1489	NAP		g1399818	863	337	1.00E-96	45	98	
19974	ENU03768	AN161C276:	72-94	1505-1524	NAP		g4127990	375	142	5.00E-33	34	83	
19975	ENU03769	AN161C7856:	26-49	1449-1478	NAP		g3702646	458	81	5.00E-26			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19976	ENU03770	AN161C1113	38-57	1476-1495	NAP		g416582	1318	276	e-127			actin-like protein ARP2 ; actin-like protein ACT2 - yeast (Saccharomyces cerevisiae) (strain X2180) ; (X61502)
		3:1690..192											actin-like protein [Saccharomyces cerevisiae] ; (Z71781) actin-like protein ACT2 [Saccharomyces cerevisiae] ; (Z74077) ORF YDL029w [Saccharomyces cerevisiae] ; actin-like protein ACT2 [Saccharomyces cerevisiae]
19977	ENU03771	AN161C1093	53-79	1480-1510	NAP		g3006137	942	324	9.00E-88	44	53	(AL022229) Cu++-transporting ATPase [Schizosaccharomyces pombe]
		5:1563..64											(U51327) versicolorn B synthase [Aspergillus parasiticus] ; (U51328) versicolorn B synthase [Aspergillus parasiticus]
19978	ENU03772	AN161C3308	58-77	1495-1517	NAP		g1293655	880	347	1.00E-94	41	73	Vitellogenin II precursor (major vitellogenin) [contains: lipovitellin I (LV1); phosvitin (PV); lipovitellin II (LVII); YGP40] ; vitellogenin II precursor - chicken ; (X13607)
		2458..957											vitellogenin [Gallus gallus] "hypothetical 43.7 KD protein in OST6-PSP2 intergenic region ; probable membrane protein YML018c - yeast (Saccharomyces cerevisiae) ; (Z46659) unknown orf, len: 393, CAI: 0.13 [Saccharomyces cerevisiae] "
19979	ENU03773	AN161C6810	32-60	1473-1492	NAP		g138595	57	41	0.02	26	8	maackiain detoxification protein 1 - fungus (Nectria haematococca) ; (U35892) predicted flavin-containing mono-oxygenase [Nectria haematococca]
		6538..8040											nuclear polyadenylated RNA-binding protein NAB2 ; RNA-binding protein NAB2 - yeast (Saccharomyces cerevisiae) ; (L10288) RNA-binding protein [Saccharomyces cerevisiae] ; (Z72644) ORF YGL122c [Saccharomyces cerevisiae]
19980	ENU03774	AN161C5895	43-63	1474-1504	NAP		g2497105	546	166	4.00E-40	38	97	
		2179..672											
19981	ENU03775	AN161C9701	65-84	1501-1526	NAP		g2133295	664	187	2.00E-73	38	96	
		1300..2803											
19982	ENU03776	AN161C3368	22-41	1467-1486	NAP		g417337	77	3.00E-13				
		5624..4118											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19983	ENU03777	AN161C7316:	28-47	1463-1493	NAP		g2132651	161	2.00E-45				probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae); (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
19984	ENU03778	AN161C4256:	52-71	1497-1517	NAP		g2143220	1826	681	0	79	93	(Y13338) cellular serine proteinase [Aspergillus fumigatus]
19985	ENU03779	AN161C905:2	22-53	1458-1489	NAP		g3328946	155	80	4.00E-14	34	30	(AE001323) S13 Ribosomal Protein [Chlamydia trachomatis]
19986	ENU03780	AN161C6340:	22-48	1472-1492	NAP		g2132374	501	205	5.00E-52	34	57	p-aminobenzoate synthase (EC 4.1.3.-) - yeast (Saccharomyces cerevisiae); (Z71648) ORF YNR033w [Saccharomyces cerevisiae]
19987	ENU03781	AN161C1036	47-65	1499-1520	NAP		g4502041	818	147	1.00E-75	44	83	"aldehyde dehydrogenase 6; aldehyde dehydrogenase 6; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 6 precursor, salivary - human; (U07919) aldehyde dehydrogenase 6 [Homo sapiens]" (M95300) csGA [Stigmatella aurantiaca]
19988	ENU03782	AN161C1098	26-51	1483-1503	NAP		g152650		54	0.000000	009		(U62028) negative acting factor [Fusarium solani f. sp. psii]
19989	ENU03783	AN161C6204:	71-90	1525-1549	NAP		g1470090	243	64	0.000000	30	72	serine/threonine-protein kinase COT-1; probable protein kinase cot-1 (EC 2.7.1.-) - Neurospora crassa
19990	ENU03784	AN161C5953:	68-88	1520-1547	NAP		g729186	474	194	2.00E-51	38	52	"met-10+ protein - Neurospora crassa; (L40806) Restriction enzyme inactivation of met-10 complementation in this region. Sequence similarity to S. cerevisiae chromosome VIII cosmid 9205, accession no. U10556 CDS residues 22627-24126 [Neurospora crassa]; met-10 gene [Neurospora crassa]; "glutathione reductase (GR) (GRASE); glutathione reductase (NADPH) (EC 1.6.4.2) - yeast (Saccharomyces cerevisiae); (U43281) G1r1p, Lpg17p [Saccharomyces cerevisiae]"
19991	ENU03785	AN161C9152:	61-80	1522-1541	NAP		g2133315	914	330	2.00E-89	45	94	fumarate hydratase (EC 4.2.1.2) - Rhizopus oryzae
19992	ENU03786	AN161C800:1	22-56	1476-1502	NAP		g1708060	1088	179	e-107	53	94	
19993	ENU03787	AN161C6075:	72-91	1535-1554	NAP		g2118296	1531	550	e-159	69	87	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19994	ENU03788	ANI61C357.2	27-47	1491-1510	NAP		g4160574	528	127	3.00E-49	33	83	(AL035226) major facilitator superfamily protein
19995	ENU03789	ANI61C7020.6795..5263	49-69	1520-1539	NAP		g1351917	422	68	8.00E-20	41	24	[Schizosaccharomyces pombe] probable amidase ; amidase (EC 3.5.1.4) - yeast (Saccharomyces cerevisiae) ; (Z49701) Amdyp [Saccharomyces cerevisiae] (AB010714) salicylate hydroxylase [Pseudomonas putida]
19996	ENU03790	ANI61C7125.1703..166	24-53	1484-1519	NAP		g2826168	67	57	0.000000	45	10	Similar to fumarylacetoacetate hydrolase, gblL41670 from Emericella nidulans. [Arabidopsis thaliana] "
19997	ENU03791	ANI61C3681.2420..2906	22-53	1496-1518	NAP		g3157928	455	152	4.00E-45	38	96	Similar to fumarylacetoacetate hydrolase, gblL41670 from Emericella nidulans. [Arabidopsis thaliana] "
19998	ENU03792	ANI61C3681.2420..2906	24-55	1498-1520	NAP		g3157928	455	152	4.00E-45	38	96	Similar to fumarylacetoacetate hydrolase, gblL41670 from Emericella nidulans. [Arabidopsis thaliana] "
19999	ENU03793	ANI61C59.1735..3274	23-42	1501-1520	NAP		g2492825	374	141	7.00E-41	32	88	"N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus] "
20000	ENU03794	ANI61C7924.618..2163	50-69	1529-1553	NAP		g121146	766	162	5.00E-80	45	94	geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (Dimethylallyltransferase / geranyltranstransferase / farnesyltranstransferase ; geranylgeranyl pyrophosphate synthetase - Neurospora crassa ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]
20001	ENU03795	ANI61C2480.4201..5746	24-43	1502-1527	NAP		g3738166	561	172	4.00E-50	41	97	"(AL031856) STAM-like protein, VHS domain containing, putative signal transducing adaptor [Schizosaccharomyces pombe] "

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20002	ENU03796	ANI61C3788:	72-96	1544-1577	NAP		g1351102	1128	342	4.00E-93	65	57	putative agmatinase precursor (agmatine ureohydrolase) (AUH); (Z68166) unknown
20003	ENU03797	ANI61C7597:	45-64	1527-1550	NAP		g549620	349	122	7.00E-27	33	85	[Schizosaccharomyces pombe] hypothetical 46.5 KD protein in MRS4-DYN1 intergenic region; hypothetical protein YKR053c - yeast (Saccharomyces cerevisiae); (Z28278) ORF YKR053c [Saccharomyces cerevisiae]
20004	ENU03798	ANI61C9849:	24-54	1513-1531	NAP		g3122249	687	296	3.00E-79	41	97	"D-hydantoinase (dihydropyrimidinase) (DHPASE); dihydropyrimidinase (EC 3.5.2.2) - Bacillus stearothermophilus; (S73773) hydantoinase [Bacillus stearothermophilus, NS1122A, Peptide, 471 aa] [Bacillus stearothermophilus]; hydantoinase [Bacillus stearothermophilus]" (Z97211) probable inosine-5'-monophosphate dehydrogenase [Schizosaccharomyces pombe]
20005	ENU03799	ANI61C1077	24-43	1512-1531	NAP		g2239243	1343	374	e-103	64	82	26S protease regulatory subunit 6A homolog 1 (TBP-1); (D88663) Tat binding protein 1 [Brassica rapa] hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [Schizosaccharomyces pombe]
20006	ENU03800	ANI61C1086	42-62	1521-1551	NAP		g3024434	1475	344	e-151	69	99	"aldehyde dehydrogenase (ALDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans]"
20007	ENU03801	ANI61C821:	4	25-48	NAP		g1351702	608	149	2.00E-62	35	84	tubulin alpha-2 chain; tubulin alpha-2 chain - Emericella nidulans (AL031543) stxbp-unc-18-sec1 family protein [Schizosaccharomyces pombe]
20008	ENU03802	ANI61C5992:	47-66	1547-1568	NAP		g118498	1272	437	e-142	54	96	
20009	ENU03803	ANI61C5357:	57-76	1560-1579	NAP		g135407	1608	455	e-156	73	94	
20010	ENU03804	ANI61C1612:	22-57	1522-1545	NAP		g3581893	1005	336	e-112	51	70	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20011	ENU03805	ANI61C2135:	32-52	1543-1562	NAP		g2493387	804	261	1.00E-93	43	96	probable stergmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emericella nidulans] (AF130355) Pad-1 [Neurospora crassa]
20012	ENU03806	ANI61C486:1	35-58	1537-1566	NAP		g4530579	1474	483	e-151	71	79	"(AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda]"
20013	ENU03807	ANI61C1046	26-46	1532-1558	NAP		g2245570	437	89	1.00E-36	32	63	PRL1/PRL2-like protein ; (AB004535)
20014	ENU03808	ANI61C385:3	45-64	1558-1578	NAP		g3122623	1340	511	e-144	56	98	PRL1 [Schizosaccharomyces pombe] (Z98951) hypothetical protein [Schizosaccharomyces pombe] ; (AL031546) putative dna-binding protein [Schizosaccharomyces pombe] (D49827) alpha-mannosidase [Aspergillus phoenicis]
20015	ENU03809	ANI61C4744:	22-47	1534-1556	NAP		g2370467	1132	441	e-123	49	75	putative dioxxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae] (Z95436) hypothetical protein Ry3633 [Mycobacterium tuberculosis] hypothetical 54.2 KD TRP-ASP repeats containing protein C29A4.08C in chromosome I ; (Z97210) beta-transducin [Schizosaccharomyces pombe]
20016	ENU03810	ANI61C1035	70-89	1583-1606	NAP		g1171477	1118	724	0	72	95	serine/threonine-protein kinase PRP4 ; (L10739) serine/threonine kinase [Schizosaccharomyces pombe] ; (AL031532) mRNA splicing-associated serine-threonine protein kinase [Schizosaccharomyces pombe]
20017	ENU03811	ANI61C5378:	22-52	1540-1559	NAP		g2497056	557	202	5.00E-51	44	35	hypothetical 51.9 KD protein C27F1.04C in chromosome I ; (Z69368) unknown [Schizosaccharomyces pombe]
20018	ENU03812	ANI61C9607:	25-46	1544-1563	NAP		g2105061	180	85	2.00E-15	30	40	
20019	ENU03813	ANI61C1014	36-55	1552-1574	NAP		g3219948	474	123	4.00E-43	33	96	
20020	ENU03814	ANI61C1559:	64-82	1585-1604	NAP		g2851498	1058	386	e-109	49	90	
20021	ENU03815	ANI61C7:410	25-46	1548-1570	NAP		g1723245	419	131	1.00E-29	28	89	

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20022	ENU03816	ANI61C318:8	22-41	1548-1572	NAP	g1063421	412	95	5.00E-28	27	89		(L48797) toxin pump [Cochiobolus carbonum]
20023	ENU03817	077..6485 ANI61C7785: 53-72 1218..2811		1583-1604	NAP	g4507707	330	144	1.00E-33	37	60		thiosulfate sulfoxidation (rhodanese) ; 3-mercaptothiosulfate sulfoxidation (MST) ; thiosulfate sulfoxidation (EC 2.8.1.1) - human ; (X59434) rhodanese [Homo sapiens] Nucleolar protein NOP5 ; hypothetical protein YOR310c - yeast
20024	ENU03818	ANI61C1069 33-52 9:841..2435		1557-1585	NAP	g2833225	1329	275	e-113	60	85		(Saccharomyces cerevisiae) ; (X90565) orf 06108 [Saccharomyces cerevisiae] ; (Z75217) ORF YOR310c [Saccharomyces cerevisiae] ; (AF056070) nucleolar protein Nop5p [Saccharomyces cerevisiae] putative transporter YGR260w ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae] (Z99295) aminoalcoholphosphotransferase [Schizosaccharomyces pombe] (AB006052) RNA polymerase I second-largest subunit [Neurospora crassa]
20026	ENU03820	ANI61C6527: 22-48 7678..9277		1557-1579	NAP	g2414603	443	89	3.00E-31	38	99		"putative GTP-binding protein C1B3.04C ; (Z98598) putative gtp binding protein, gtpase; Elongation factor Tu family [Schizosaccharomyces pombe] "
20027	ENU03821	ANI61C30:82 23-47 ..1681		1561-1580	NAP	g3668171	2167	531	e-150	69	41		(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe] (AC000133) ORF [Emmericella nidulans] tubulin-specific chaperone e ; (U61232) cofactor E [Homo sapiens] (AL031907) trp-asp repeat containing protein [Schizosaccharomyces pombe]
20028	ENU03822	ANI61C1185: 69-88 5480..3878		1599-1629	NAP	g3219963	1564	235	e-135	53	78		
20029	ENU03823	ANI61C1894: 36-64 166..1770		1566-1598	NAP	g3650387	510	170	3.00E-41	35	20		
20030	ENU03824	ANI61C1794: 22-49 1735..1340		1570-1594	NAP	g1870209	1025	324	e-102	42	94		
20031	ENU03825	ANI61C7709: 43-64 1050..2669		1594-1618	NAP	g4507375	255	65	8.00E-19	30	84		
20032	ENU03826	ANI61C4819: 62-82 446..2063		1609-1637	NAP	g3766367	1267	338	e-125	52	97		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20033	ENU03827	ANI61C6841:	26-47	1581-1602	NAP		g3702646	681	280	2.00E-74	33	98	(AL031825) putative membrane transport protein
		4850..6468											[Schizosaccharomyces pombe]
20034	ENU03828	ANI61C9043:	22-45	1584-1603	NAP		g1346290	750	282	2.00E-80	40	82	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
		645..2268											(AL022103) hypothetical protein [Schizosaccharomyces pombe]
20035	ENU03829	ANI61C3809:	48-76	1603-1631	NAP		g2956784	549	228	1.00E-58	44	79	"ATP synthase beta chain, mitochondrial precursor ; H+-transporting ATP synthase (EC 3.6.1.34) beta chain - Neurospora crassa ; (X53720) F(1)-ATPase beta-subunit precursor (519 AA)
		3146..4771											[Neurospora crassa] ; (M84192) mitochondrial A TPase beta-subunit [Neurospora crassa] "
20036	ENU03830	ANI61C896:	34-54	1592-1617	NAP		g114555	2077	439	0	86	83	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
		3..1638											Maltose permease MAL6T (maltose transport protein MAL6T) ; maltose transport protein MAL61 - yeast (Saccharomyces cerevisiae) ; (X17391) maltose permease [Saccharomyces cerevisiae] ; (M27823) maltose permease [Saccharomyces carlsbergensis]
20037	ENU03831	ANI61C1139	22-53	1588-1608	NAP		g1346290	456	125	3.00E-50	31	88	glutathione synthetase (glutathione synthetase) (GSH synthetase) (GSH-S) ; hypothetical protein YOL049w - yeast (Saccharomyces cerevisiae) ; (Z74791) ORF YOL049w [Saccharomyces cerevisiae] ; (Y13804) Glutathione synthetase [Saccharomyces cerevisiae] (AL034564) hypothetical protein [Schizosaccharomyces pombe] (AF009417) cytochrome P450 [Myrothecium roridum]
		6:500..2128											
20038	ENU03832	ANI61C6331:	59-78	1630-1651	NAP		g126694	225	103	4.00E-21	27	62	
		7851..6217											
20039	ENU03833	ANI61C4568:	37-56	1598-1629	NAP		g2495096	629	250	2.00E-65	39	98	
		2950..1316											
20040	ENU03834	ANI61C1188:	72-91	1645-1667	NAP		g4049539	85	57	0.000000	34	18	
		4935..6572											
20041	ENU03835	ANI61C3095:	61-80	1636-1656	NAP		g2267601	723	233	1.00E-74	34	93	
		1688..3330											



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20042	ENU03836	AN161C9933:	28-47	1607-1626	NAP	g127289	1692	458	0	73	99		mitochondrial processing peptidase beta subunit precursor (beta-MPP) (ubiquinol-cytochrome C reductase complex CORE protein I) ; mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - Neurospora crassa ; (M20928) processing enhancing protein precursor [Neurospora crassa]
20043	ENU03837	AN161C2470:	52-71	1632-1651	NAP	g3395585	735	129	5.00E-65	49	86		(AL031179) hypothetical protein [Schizosaccharomyces pombe]
20044	ENU03838	AN161C1647:	72-94	1651-1672	NAP	g1169291	1259	277	e-116	54	96		aldehyde dehydrogenase (ALDDH) ; (M32351) aldehyde dehydrogenase [Aspergillus niger]
20045	ENU03839	AN161C349:3	22-48	1594-1622	NAP	g2132652	1240	222	7.00E-57	34	41		probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) ; (Z73136) ORF YLL031c [Saccharomyces cerevisiae]
20046	ENU03840	AN161C6338:	23-47	1606-1625	NAP	g2330697	400	52	0.000000	24	43		(Z98529) mating and morphogenesis protein Scd1p. [Schizosaccharomyces pombe]
20047	ENU03841	AN161C9837:	69-89	1649-1675	NAP	g1351714	588	146	2.00E-60	33	94		putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
20048	ENU03842	AN161C54:20	23-46	1603-1631	NAP	g3915154	602	156	4.00E-68	33	96		Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20049	ENU03843	AN161C7279:	30-60	1621-1641	NAP	g399006	844	232	3.00E-64	48	98		potential transcriptional adaptor ; probable transcriptional adaptor ADA2 - yeast (Saccharomyces cerevisiae) ; (M95396) ADA2 [Saccharomyces cerevisiae] ; (U33007) Ada2p: probable transcriptional adaptor; YDR448W; CAI: 0.12 [Saccharomyces cerevisiae] (AL021815) hypothetical protein [Schizosaccharomyces pombe] ; (AL035675) adducin N terminal domain protein [Schizosaccharomyces pombe]
20050	ENU03844	AN161C1109	44-64	1639-1657	NAP	g2879861	59	1.00E-10					

# Database "Description"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20051	ENU03845	AN161C1085	46-66	1640-	NAP		g2132080	918	230	1.00E-71	37	29	hypothetical protein YOR191w - yeast (Saccharomyces cerevisiae) ; (Z75099) ORF YOR191w [Saccharomyces cerevisiae]
20052	ENU03846	AN161C1145	22-50	1616-1637	NAP		g3560233	582	182	5.00E-45	32	54	(AL031530) putative b-zip transcription factor [Schizosaccharomyces pombe]
20053	ENU03847	AN161C8860	40-61	1638-1657	NAP		g3184114	344	61	0.000000	34	17	(AL023780) hypothetical protein [Schizosaccharomyces pombe]
20054	ENU03848	AN161C3943	50-69	1647-1668	NAP		g3874345	84	48	0.0001			(Z81035) predicted using GeneFinder; Similarity to dehydrogenases; cDNA EST EMBL: D65800 comes from this gene; cDNA EST EMBL: D76184 comes from this gene; cDNA EST EMBL: D69322 comes from this gene; cDNA EST EMBL: C08158 comes from...
20055	ENU03849	AN161C6208	51-70	1650-1669	NAP		g4502169	673	189	4.00E-69	34	95	unknown ; (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens] ; (AC004638) amyloid precursor protein-binding protein 1 (APP-B1) [Homo sapiens] (AC000133) ORF [Emmericella nidulans] (AC000133) ORF [Emmericella nidulans] (AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
20056	ENU03850	AN161C9150	23-44	1606-1641	NAP		g1870209	2694	1027	0	94	99	"(AL034358) predicted using hexExon; L4830.1, Hypothetical protein, len: 1107 [Leishmania major]"
20057	ENU03851	AN161C1229	23-44	1606-1641	NAP		g1870209	2917	1107	0	99	99	(AF041049) 4-coumarate:CoA ligase [Populus tremuloides]
20058	ENU03852	AN161C6693	24-47	1621-1642	NAP		g3702646	66	2.00E-29				(U33265) complement fixation antigen [Coccidioides immitis] ; (U51271) complement-fixation antigen [Coccidioides immitis]
20059	ENU03853	AN161C5910	67-95	1665-1686	NAP		g4493738	35	1.3				
20060	ENU03854	AN161C5282	42-69	1641-1661	NAP		g3258635	526	218	3.00E-60	32	97	
20061	ENU03855	AN161C1045	22-47	1621-1643	NAP		g1255728	1081	195	1.00E-94	56	96	

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20062	ENU03856	AN161C1000: 4222..2557	23-48	1619-1645	NAP	g2498883	821	821	363	2.00E-99	43	50	Spliceosome associated protein 145 (SAP 145) (SF3B150) ; (U41371) spliceosome associated protein [Homo sapiens]
20063	ENU03857	AN161C4380: 1178..2844	38-59	1643-1662	NAP	g2791647	700	168	3.00E-78	41	90	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]	
20064	ENU03858	AN161C6812: 2103..437	25-44	1623-1650	NAP	g2635698	234	74	3.00E-25	37	49	(Z99120) yu1l [Bacillus subtilis]	
20065	ENU03859	AN161C6552: 1967..299	60-79	1666-1686	NAP	g137461	2306	363	0	80	80	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit) ; H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa ; (J03955) vacuolar ATPase vma-1 [Neurospora crassa]"	
20066	ENU03860	AN161C5299: 1205..2876	61-81	1671-1690	NAP	g2804298	813	261	2.00E-88	38	94	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous]	
20067	ENU03861	AN161C4054: 1151..2824	31-50	1644-1662	NAP	g1176239	470	207	2.00E-52	36	62	hypothetical ABC transporter ATP-binding protein YHES ; (U18997) ORF_o637 [Escherichia coli] ; (AE000411) putative ATP-binding component of a transport system [Escherichia coli]	
20068	ENU03862	AN161C7785: 3418..5091	27-47	1639-1658	NAP	g3850071	823	260	3.00E-74	48	56	(AL033385) cadmium resistance protein [Schizosaccharomyces pombe]	
20069	ENU03863	AN161C9135: 2422..4097	40-59	1654-1673	NAP	g171085	1225	276	e-121	66	96	(M35237) argininosuccinate synthetase (ARG1; E.C. 6.8.4.5) [Saccharomyces cerevisiae]	
20070	ENU03864	AN161C1100: 2732..1056	22-48	1623-1656	NAP	g1703220	57	38	0.2	30	38	AI02 protein ; (U40857) AI02 [Arabidopsis thaliana]	
20071	ENU03865	AN161C6528: 30..1710	23-43	1641-1660	NAP	g2131358	588	166	3.00E-40	52	28	hypothetical protein YDL201w - yeast (Saccharomyces cerevisiae) ; (X99000) ORF D1075 [Saccharomyces cerevisiae] ; (Z74249) ORF YDL201w [Saccharomyces cerevisiae]	
20072	ENU03866	AN161C1117: 5555..7234	22-54	1638-1659	NAP	g3560142	651	167	2.00E-40	31	83	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]	

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20073	ENU03867	AN161C8874:	49-76	1667-1687	NAP		g1170324	1662	422	e-170	56	64	Heavy metal tolerance protein precursor ; vacuolar membrane protein HMT1 - fission yeast
		2557..877											(Schizosaccharomyces pombe) ; (Z14055) HMT1
20074	ENU03868	AN161C9789:	22-55	1630-1663	NAP		g543187	46	0.000003				[Schizosaccharomyces pombe] "ankyrin, erythrocyte - mouse ; (X69063) erythroid ankyrin [Mus musculus]"
		3347..5030											(AJ223630) homocitrate synthase [Penicillium chrysogenum]
20075	ENU03869	AN161C5161:	22-52	1645-1664	NAP		g4165570	1971	551	0	86	99	"hypothetical 23.6 KD protein C23C11.13C in chromosome I ; (Z98559) SPAC23C11.13c; len:206aa; similar eg. to YJR133W, YJ9B_yeast, P47165, hypothetical 23.7 kd protein, (209aa), fasta scores, opt:737, E(0.0, (59.0% identity in 200 aa overlap) [Schizosaccharomyces pombe]"
20076	ENU03870	AN161C6798:	25-45	1650-1670	NAP		g3183352	490	104	2.00E-32	64	26	(AL035076) putative carboxylesterase-lipase family member [Schizosaccharomyces pombe] (AF010145) hexose transporter [Aspergillus parasiticus]
		3320..5007											unknown ; (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens] ; (AC004638) amyloid precursor protein-binding protein 1 (APP-B1) [Homo sapiens] (AB003102) 26S proteasome subunit p44.5 [Homo sapiens]
20077	ENU03871	AN161C2287:	26-54	1652-1672	NAP		g4107289	569	237	1.00E-61	35	96	(Z50044) similar to phenylalanyl-tRNA synthetase; cDNA EST EMBL:701401 comes from this gene; cDNA EST yk303c5.3 comes from this gene; cDNA EST yk303c5.5 comes from this gene; cDNA EST yk452d5.3 comes from this gene; cDNA EST yk...
		340..2028											
20078	ENU03872	AN161C903:1	23-43	1650-1669	NAP		g2306977	1793	432	e-176	72	98	
		894..206											
20079	ENU03873	AN161C6208:	25-54	1659-1678	NAP		g4502169	673	189	5.00E-72	35	97	
		1181..2876											
20080	ENU03874	AN161C7715:	60-84	1698-1717	NAP		g1945609	951	328	5.00E-89	55	65	
		3303..1604											
20081	ENU03875	AN161C5156:	22-55	1648-1681	NAP		g3876233	1161	223	e-112	48	83	
		3261..1560											

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20082	ENU03876	AN161C5447:	30-49	1682-2892..1180	NAP		g2493011	1294	434	e-145	48	33	probable calcium-transporting ATPase 8; probable membrane protein YMR162c - yeast (Saccharomyces cerevisiae) ; (Z49705) unknown [Saccharomyces cerevisiae]
20083	ENU03877	AN161C7051:	34-63	1686-2926..1213	NAP		g1778093	334	134	4.00E-40	27	89	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]
20084	ENU03878	AN161C1717:	55-76	1708-86..183	NAP		g124159	1022	205	e-107			"isocitrate dehydrogenase [NAD], mitochondrial subunit 2 precursor (isocitric dehydrogenase) (NAD+-specific ICDH) ; isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) chain IDH2 precursor - yeast (Saccharomyces cerevisiae) ; (M74131) isocitrate dehydrogenase kinase/phosphatase [Saccharomyces cerevisiae] ; (X94335) YOR3326w [Saccharomyces cerevisiae] ; (Z75043) ORF YOR136w [Saccharomyces cerevisiae] "
20085	ENU03879	AN161C5779:	22-54	1677-1281..2998	NAP		g4127832	513	163	2.00E-51	29	97	(Y17243) cytochrome P450 [Gibberella fujikuroi]
20086	ENU03880	AN161C2392:	28-48	1683-100..1817	NAP		g417726	667	179	7.00E-71			Recessive suppressor of secretory defect ; RSD1 protein - yeast (Saccharomyces cerevisiae) ; (X75951) RSD1 (SAC1) [Saccharomyces cerevisiae] ; (Z28212) ORF YKL212w [Saccharomyces cerevisiae] ; (X51672) recessive suppressor of secretory defect [Saccharomyces cerevisiae] ; RSD1 gene [Saccharomyces cerevisiae]
20087	ENU03881	AN161C9372:	22-56	1666-155..1872	NAP		g1723769	297	92	8.00E-18	27	88	putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]

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20088	ENU03882	ANI61C54:20	22-51	1663-1698	NAP		g3915154	602	156	1.00E-67	33	99	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20089	ENU03883	ANI50C2738	24-46	1682-1701	NAP		g114303		300	e-125	47	53	Calcium-transporting ATPase 3 ; Ca2+-transporting ATPase (EC 3.6.1.38) - fission yeast (Schizosaccharomyces pombe) ; (J05634) Ca-2+-ATPase (cia3) [Schizosaccharomyces pombe] ; (AL021816) calcium-transporting atpase 3 [Schizosaccharomyces pombe]
20090	ENU03884	ANI61C6494:	48-67	1706-1726	NAP		g125349	591	277	2.00E-73	40	46	Carboxypeptidase KEX1 precursor (carboxypeptidase D) ; KEX1 protein precursor - yeast (Saccharomyces cerevisiae) ; (M17231) carboxypeptidase B-like peptide [Saccharomyces cerevisiae] ; (Z72725) ORF YGL203c [Saccharomyces cerevisiae]

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20091	ENU03885	AN161C1084	33-52	1689-1711	NAP	g2914624		152	9.00E-39		61	94	"Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl[cyclo-7(2r)-((N-Valyl) Amino)-2-(Hydroxyl-(1s)-1-Methoxycarbonyl)-2-Phenylethoxy] Phosphinyloxy-Ethyl]-1-Naphthalenacetamide] Sodium Sa... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl (2s)-[1-(((N-Formyl)-L-Valyl)amino-2-(2-Naphthyl)ethyl) Hydroxyphosphinyloxy]-3-Phenylpropanoate, Sodium Salt Hydrolase, Penicillopepsin,... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl (2s)-[1-(((N-(1-Naphthalenacetyl))-L-Valyl)aminomethyl) Hydroxyphosphinyloxy]-3-Phenylpropanoate, Sodium Salt Hydrolase, Penicillopepsin... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Macrocyclic Inhibitor: Methyl[cyclo-7(2r)-((N-Valyl)amino)-2-(Hydroxyl-(1s)-1-Methoxycarbonyl)-2-Phenylethoxy] Phosphinyloxy-Ethyl]-1-Naphthalenacetamid..."
20092	ENU03886	AN161C717	61-80	1722-1741	NAP	g548494		1662	539	0	61	94	Phosphoglucumutase 2 (glucose phosphomutase 2) (PGM 2) ; phosphoglucumutase (EC 5.4.2.2) PGM2 - yeast (Saccharomyces cerevisiae) ; (X74823) phosphoglucumutase [Saccharomyces cerevisiae] ; (U09499) phosphoglucumutase [Saccharomyces cerevisiae] ; (Z49702) Pgm2p [Saccharomyces cerevisiae]

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20093	ENU03887	AN161C6918:	22-49	1683-1703	NAP	g4154078	253	122	7.00E-27	29	55	55	(AL035161) putative efflux protein [Streptomyces coelicolor]
20094	ENU03888	AN161C593:6	71-90	1723-1753	NAP	g731613	558	196	3.00E-49	32	88	88	hypothetical 60.6 KD protein in CBP2-SSBR1 intergenic region ; hypothetical protein YHL036w - yeast (Saccharomyces cerevisiae) ; (U11583) Small region of weak similarity to ectopic retrovirus receptor [Saccharomyces cerevisiae]
20095	ENU03889	AN161C1065:	55-79	1718-1737	NAP	g4218005	95	59	0.000000	1			(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
20096	ENU03890	AN161C3446:	72-92	1730-1756	NAP	g585356	268	61	1.00E-15	32	40	40	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) ; kdud protein - Erwinia chrysanthemi ; (X62073) 2-keto-3-deoxygluconate oxidoreductase [Erwinia chrysanthemi]
20097	ENU03891	AN161C8444:	22-54	1691-1710	NAP	g4160583	626	273	2.00E-72	47	58	58	(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]
20098	ENU03892	AN161C1118	69-89	1738-1758	NAP	g3876093	650	148	5.00E-43	40	77	77	(Z69635) cDNA EST yk472e10.5 comes from this gene; cDNA EST yk473c9.5 comes from this gene; cDNA EST yk472e10.3 comes from this gene [Caenorhabditis elegans]
20099	ENU03893	AN161C6296:	65-84	1741-1760	NAP	g1711561	535	59	1.00E-12	34	37	37	Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20100	ENU03894	AN161C1948:	23-52	1695-1719	NAP	g2250699	289	128	1.00E-28	36	16	16	(AB001517) PWP2 protein [Homo sapiens]
20101	ENU03895	AN161C7713:	23-43	1703-1722	NAP	g2293058	324	94	4.00E-21	33	93	93	(AJ000318) putative RNA-binding protein [Schizosaccharomyces pombe] ; (AL022304) putative mna-binding protein. [Schizosaccharomyces pombe] (Z98979) hypothetical protein [Schizosaccharomyces pombe]
20102	ENU03896	AN161C884:1	50-70	1727-1750	NAP	g2388969	162	76	5.00E-13	30	50	50	[Schizosaccharomyces pombe]



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20103	ENU03897	ANI61C6290:	66-85	1748-	NAP		g4103070	597	277	2.00E-73	45	37	(AF020705) protein kinase homolog [Schizosaccharomyces pombe]
20104	ENU03898	2282..538 ANI61C8572:	24-44	1768 1710-	NAP		g2388980	1225	233	5.00E-84	40	62	[Schizosaccharomyces pombe] (Z98980) hypothetical protein [Schizosaccharomyces pombe]
20105	ENU03899	1062..2809 ANI61C1026	71-106	1729 1757-	NAP		g2132053	568	237	1.00E-61	46	49	hypothetical protein YOR091w - yeast (Saccharomyces cerevisiae) ; (X94335) YOR3160w [Saccharomyces cerevisiae] ; (Z74999) ORF YOR091w [Saccharomyces cerevisiae]
20106	ENU03900	ANI61C9080:	43-62	1726-	NAP		g2258125	399	87	2.00E-33	27	97	(Z83828) ArmMst-1 [Amanita muscaria]
20107	ENU03901	5119..3369 ANI61C9442:	39-58	1751 1734-	NAP		g3881018	389	210	3.00E-53	34	79	(AL032621) similar to Acyl-CoA dehydrogenase; cDNA EST EMBL:D75425 comes from this gene; cDNA EST EMBL:M89392 comes from this gene; cDNA EST EMBL:M89303 comes from this gene; cDNA EST EMBL:D27766 comes from this gene; cDNA EST ...
20108	ENU03902	226..2469 ANI61C498:4	65-84	1751- 1780	NAP		g3915154	868	304	1.00E-81	39	96	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20109	ENU03903	514..4757 ANI61C382:6	55-74	1744- 1770	NAP		g2131246	1035	247	e-119	49	70	EMP70 protein precursor - yeast (Saccharomyces cerevisiae) ; (U53880) Emp7Op: P24A protein [Saccharomyces cerevisiae] ; (Z73255) ORF YLR083c [Saccharomyces cerevisiae]
20110	ENU03904	2069..3837 ANI61C2254:	29-48	1736- 1755	NAP		g3953471	288	146	3.00E-34	32	35	(AC002328) F22O2.16 [Arabidopsis thaliana]
20111	ENU03905	4110..2337 ANI61C9764:	41-60	1745- 1772	NAP		g2132443	124	75	2.00E-12	30	21	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae) ; (Z74192) ORF YDL144c [Saccharomyces cerevisiae]

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20112	ENU03906	ANI61C9185:	45-65	1753-1776	NAP		g121855	1258	176	2.00E-87			"Exoglucanase II precursor (exocellobiohydrolase II) (CBHII) (1,4-beta-cellobiohydrolase) ; cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei) ; cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride) ; (M16190) cellobiohydrolase II [Trichoderma reesei] ; cellobiohydrolase II [Trichoderma reesei]"
20113	ENU03907	ANI61C1113	50-71	1763-1782	NAP		g543928	697	162	6.00E-59	38	87	Adenylyl cyclase-associated protein (CAP) ; adenylyl cyclase-associated protein cap - fission yeast (Schizosaccharomyces pombe) ; (L16577) adenylyl cyclase-associated protein [Schizosaccharomyces pombe] formyltetrahydrofolate D-formylase (formyl-FH(4) hydrolase) ; formyltetrahydrofolate deformylase (EC 3.5.1.10) - Corynebacterium sp. ; (U23955) 10-formyltetrahydrofolate hydrolase [Corynebacterium sp.] (AF067947) contains similarity to NADH oxidase [Caenorhabditis elegans]
20114	ENU03908	ANI61C9049:	33-52	1743-1767	NAP		g2500006	708	289	4.00E-77	52	56	(Z50108) esterase [Streptomyces lividans] hypothetical 75.2 KD protein in ACS1-GCV3 intergenic region ; probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae) ; (U12980) Ya1048cp [Saccharomyces cerevisiae] (AL034433) hypothetical protein [Schizosaccharomyces pombe] (AF103949) cytochrome P450 alkane hydroxylase [Debaromyces hanseii] probable membrane protein YLR004c - yeast (Saccharomyces cerevisiae) ; (Z73176) ORF YLR004c [Saccharomyces cerevisiae]
20115	ENU03909	ANI61C1144	71-91	1781-1805	NAP		g3193204	256	65	0.000000	36	19	
20116	ENU03910	ANI61C203:2	46-74	1756-1780	NAP		g908888	95	55	0.000002	31	27	
20117	ENU03911	ANI61C352:2	45-64	1759-1780	NAP		g731284	1337	475	e-133	47	80	
20118	ENU03912	ANI61C2376:	44-71	1755-1781	NAP		g4007753	513	166	2.00E-53	33	81	
20119	ENU03913	ANI61C6098:	72-95	1790-1811	NAP		g4557164	805	233	5.00E-83	45	74	
20120	ENU03914	ANI61C1044	44-64	1749-1784	NAP		g2132659	404	94	4.00E-29	32	77	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20121	ENU03915	AN161C1119:	69-88	1793-1812	NAP	g2342601	2120	161	1.00E-38	36	5		(X89442) peptidase synthetase [Metarhizium anisopliae]
20122	ENU03916	4762..2977 AN161C9379:	27-47	1751-1770	NAP	g2851586	1085	300	2.00E-84	48	94		repressible alkaline phosphatase precursor ; alkaline phosphatase (EC 3.1.3.1) - yeast (Saccharomyces cerevisiae) ; (U33050) Pho8p: repressible alkaline phosphatase; CAI: 0.16 [Saccharomyces cerevisiae]
20123	ENU03917	2659..867 AN161C8749:	70-89	1788-1819	NAP	g131768		118	1.00E-53				quinic acid permease (quinic acid transporter) ; quinic acid permease - Emericella nidulans ; (X13525) quinic acid permease [Emericella nidulans] (AC000133) ORF [Emericella nidulans]
20124	ENU03918	6201..4408 AN161C1159:	35-68	1751-1786	NAP	g1870209	2185	195	2.00E-77	84	61		hypothetical 45.2 KD GTP-binding protein in TRX1-RTA1 intergenic region ; probable membrane protein YGR210c - yeast (Saccharomyces cerevisiae) ; (Z49133) unknown [Saccharomyces cerevisiae] ; (U40843) ORF57: Method: conceptual translation supplied by author. [Saccharomyces cerevisiae] ; (Z72995) ORF YGR210c [Saccharomyces cerevisiae]
20125	ENU03919	815..2612 AN161C1488:	24-43	1744-1779	NAP	g1176059	1059	157	e-105				fatty acid amide hydrolase ; (U82535) fatty acid amide hydrolase [Homo sapiens] ; (AF098019) fatty acid amide hydrolase [Homo sapiens] (AL035216) component of chaperonin-containing T-complex (zeta subunit) [Schizosaccharomyces pombe]
20126	ENU03920	2420..623 AN161C8242:	27-52	1763-1782	NAP	g4557575	453	105	2.00E-33	36	87		SEL-10 protein ; (Z79757) Similarity to Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cDNA EST EMBL:D27698 comes from this gene; cDNA EST EMBL:D32793 comes from this gene; cDNA EST EMBL:D33271 comes from this gene;
20127	ENU03921	2678..878 AN161C6145:	58-81	1797-1816	NAP	g4160347	1694	549	e-180	69	95		...
20128	ENU03922	35..1841 AN161C8452:	56-75	1790-1820	NAP	g3915881	467	210	2.00E-53	38	30		...

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20129	ENU03923	ANI61C1699:	22-47	1771-1790	NAP	g2983324	578	201	9.00E-51	43	52		(AE000705) hypothetical protein [Aquifex aeolicus]
20130	ENU03924	ANI61C1046	23-49	1777-1796	NAP	g1084975	522	130	6.00E-68	38	76		"endo-beta-1,6-glucanase - fungus (Trichoderma harzianum) ; (X79197)
20131	ENU03925	ANI61C7744:	60-79	1807-1834	NAP	g2995342	890	206	3.00E-94	52	69		[Trichoderma harzianum]" (AL022244) hypothetical protein [Schizosaccharomyces pombe]
20132	ENU03926	ANI61C9735:	61-90	1804-1835	NAP	g2495263	2565	473	e-177	75	43		3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase) ; (X94307) HMG-CoA-reductase [Gibberella fujikuroi]
20133	ENU03927	ANI61C8580:	22-41	1790-1809	NAP	g2956763	936	300	4.00E-87	46	71		(AL022104) kinase-binding protein 1. [Schizosaccharomyces pombe]
20134	ENU03928	ANI61C3143:	28-47	1798-1817	NAP	g127562	437	152	7.00E-36	43	56		hydroxymethylglutaryl-CoA lyase (HMG-CoA lyase) (HL) (3-hydroxy-3-methylglutarate-CoA lyase) ; hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) - Pseudomonas sp ; (M31807) HMG-CoA-lyase (mvab) [Pseudomonas mevalonii] ; (M24016) HMG-CoA lyase (EC 4.1.3.4) [Pseudomonas mevalonii]
20135	ENU03929	ANI61C7424:	52-71	1822-1842	NAP	g2981103		75	8.00E-25				(AF052688) putative transmembrane transporter Lzl1p [Schizosaccharomyces pombe] ; [Schizosaccharomyces pombe] (AL023706) transmembrane transporter Lzl1p [Schizosaccharomyces pombe]
20136	ENU03930	ANI61C7315:	22-47	1793-1812	NAP	g2388904	144	65	2.00E-12	36	14		[Schizosaccharomyces pombe] (Z98974) hypothetical protein [Schizosaccharomyces pombe]
20137	ENU03931	ANI61C4353:	68-90	1838-1861	NAP	g2330711	737	282	7.00E-75	43	65		(Z98597) hypothetical protein [Schizosaccharomyces pombe]
20138	ENU03932	ANI61C9080:	37-56	1804-1833	NAP	g2258125	399	87	2.00E-33	26	99		[Schizosaccharomyces pombe] (Z83828) ArnMst-1 [Amanita muscaria]
20139	ENU03933	ANI61C8981:	37-56	1812-1833	NAP	g1711565	2232	493	0	64	78		Oligosaccharyl transferase STT3 subunit ; STT3 protein - yeast (Saccharomyces cerevisiae) ; (Z72544) ORF YGL022w [Saccharomyces cerevisiae]

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20140	ENU03934	ANI61C1122:	32-67	1802-1828	NAP	g730721	751	182	9.00E-45	40	99		SCD2 protein ; (U12539) scd2 [Schizosaccharomyces pombe] ; (Z69730) mating and morphogenesis protein [Schizosaccharomyces pombe] (AJ223327) rAsp f9 [Aspergillus fumigatus]
20141	ENU03935	ANI61C3398:	22-49	1794-1818	NAP	g2879890	665	276	3.00E-73	49	97		hypothetical 34.4 KD protein in IDS2-MP12 intergenic region ; hypothetical protein YJL145w - yeast (Saccharomyces cerevisiae) ; (X87371) ORF10 [Saccharomyces cerevisiae] ; (Z49420) ORF YJL145w [Saccharomyces cerevisiae]
20142	ENU03936	ANI61C4813:	25-46	1804-1823	NAP	g1353018	177	103	3.00E-21	33	29		Acetamidase ; amdS protein - Emericella nidulans ; (M16371) acetamidase enzyme [Emericella nidulans] (U84350) hypothetical hydroxylase a [Amycolatopsis orientalis] (AL035259) conserved hypothetical protein [Schizosaccharomyces pombe] "(D14846) endo alpha-1,4 polygalactosaminidase precursor [Pseudomonas sp.]" (AL031786) putative atp dependent ma helicase [Schizosaccharomyces pombe] hypothetical 64.5 KD protein in COX4-GT1 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae) ; (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae] ; (Z72708) ORF YGL186c [Saccharomyces cerevisiae] hypothetical protein 1 - Pseudomonas cepacia ; (U19883) unknown [Burkholderia cepacia]
20143	ENU03937	ANI61C1056	62-85	1839-1861	NAP	g113701	469	98	8.00E-26	40	68		
20144	ENU03938	ANI61C1054	41-60	1807-1842	NAP	g1872509	256	98	3.00E-19	31	67		
20145	ENU03939	ANI61C7623:	33-52	1809-1836	NAP	g4176557	522	132	2.00E-44	30	73		
20146	ENU03940	ANI61C6128	69-91	1854-1876	NAP	g286165	397	191	1.00E-47	41	41		
20147	ENU03941	ANI61C7855:	40-59	1833-1858	NAP	g3687476	907	161	6.00E-65	42	91		
20148	ENU03942	ANI61C7388:	46-64	1845-1865	NAP	g1723945	480	144	4.00E-37	32	87		
20149	ENU03943	ANI61C6750:	22-50	1824-1843	NAP	g2120652		126	5.00E-28	45	42		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
20150	ENU03944	ANI61C5845:	53-72	1853-1879	NAP	g731893	815	286	3.00E-76	38	97		putative transporter YIL166C; probable membrane protein YIL166c-yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces cerevisiae]
20151	ENU03945	ANI61C1049	22-55	1833-1852	NAP	g1709915	2011	695	0	72	95		phosphoribosylaminoimidazolecarboxamide formyltransferase 2 (AICAR transformylase) / IMP cyclohydrolase (inosinase) (IMP synthetase) (ATIC); hypothetical protein YMR120c - yeast (Saccharomyces cerevisiae); (Z49273) unknown [Saccharomyces cerevisiae]
20152	ENU03946	ANI61C9731:	32-52	1843-1864	NAP	g2145376	505	218	1.00E-55	47	33		"(Y09476) Yisk [Bacillus subtilis]; (Z99109) similar to 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase [Bacillus subtilis]" (AL031534) Major facilitator superfamily protein
20153	ENU03947	ANI61C916:2	64-82	1866-1899	NAP	g3560142	669	131	9.00E-60	32	95		[Schizosaccharomyces pombe] (AL034490) putative PHD-type zinc finger [Schizosaccharomyces pombe] (Z98602) hypothetical WW domain-containing protein
20154	ENU03948	ANI61C1096	41-63	1858-1878	NAP	g4008555	305	104	4.00E-32	28	95		[Schizosaccharomyces pombe] (AL034490) putative PHD-type zinc finger [Schizosaccharomyces pombe] (Z98602) hypothetical WW domain-containing protein
20155	ENU03949	ANI61C8717:	49-70	1865-1887	NAP	g2330816	792	205	3.00E-75	35	64		[Schizosaccharomyces pombe] (AL023860) short chain dehydrogenase [Schizosaccharomyces pombe] hypothetical 65.3 KD protein in MAD1-SCY1 intergenic region; probable membrane protein YGL084c-yeast (Saccharomyces cerevisiae); (Z72606) ORF YGL084c [Saccharomyces cerevisiae]
20156	ENU03950	ANI61C532:4	32-62	1852-1872	NAP	g3218393	261	125	1.00E-27	35	32		[Schizosaccharomyces pombe] (AL023860) short chain dehydrogenase [Schizosaccharomyces pombe] hypothetical 65.3 KD protein in MAD1-SCY1 intergenic region; probable membrane protein YGL084c-yeast (Saccharomyces cerevisiae); (Z72606) ORF YGL084c [Saccharomyces cerevisiae]
20157	ENU03951	ANI61C9167:	22-51	1838-1867	NAP	g1723878	1097	374	e-111	47	92		quinate permease (quinate transporter); quinate transport protein - Emericella nidulans; (X13525) quinate permease [Emericella nidulans]
20158	ENU03952	ANI61C8749:	22-49	1848-1869	NAP	g131768		118	1.00E-53				

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20159	ENU03953	ANI61C7362:	44-63	1877-1897	NAP		g140371	516	206	2.00E-56	32	95	"hypothetical 58.8 KD protein in GLK1-SRO9 intergenic region ; hypothetical protein YCL038c - Yeast (Saccharomyces cerevisiae) ; (X59720) YCL038c, len:528 [Saccharomyces cerevisiae] "
20160	ENU03954	ANI61C1642:	22-48	1848-1877	NAP		g2822399	320	84	1.00E-33	43	37	(AF016485) ORF H1434 [Halobacterium sp. NRC-1]
20161	ENU03955	ANI61C1137	40-61	1878-1897	NAP		g464876	363	82	4.00E-31			transcription factor TAU 131 KD subunit (TFIIC 131 KD subunit) ; transcription factor IIIC chain TFC4 - yeast (Saccharomyces cerevisiae) ; (L12722) transcription factor IIIB 131kDa subunit [Saccharomyces cerevisiae] ; (Z72832) ORF YGR047c [Saccharomyces cerevisiae]
20162	ENU03956	ANI61C888:2	24-52	1866-1885	NAP		g731640	1216	392	e-134	58	49	putative prolyl-TRNA synthetase YHR020W (proline--TRNA ligase) (PRORS) ; multifunctional amino acid--tRNA ligase homolog - yeast (Saccharomyces cerevisiae) ; (U10399) Yhr020wp [Saccharomyces cerevisiae] (X05204) arom polypeptide [Emericella nidulans]
20163	ENU03957	ANI61C4369:	24-45	1866-1888	NAP		g3834343	3235	888	0	99	38	homolog Oxi [Corynebacterium glutamicum]
20164	ENU03958	ANI61C4856:	45-66	1885-1909	NAP		g4583402	259	55	1.00E-19	32	55	DNA replication licensing factor MCM6 (P105MCM) ; (D84557) HsMcm6 [Homo sapiens]
20165	ENU03959	ANI61C8873:	23-51	1869-1888	NAP		g2497824	1471	324	e-127	47	72	NEMPA protein precursor ; (U62332) NEMPA [Emericella nidulans]
20166	ENU03960	ANI61C3272:	31-50	1873-1898	NAP		g2499479	2644	481	e-135	97	96	(Z99163) very hypothetical protein [Schizosaccharomyces pombe]
20167	ENU03961	ANI61C1676:	48-67	1898-1917	NAP		g4584706	300	53	4.00E-10	36	25	(AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]
20168	ENU03962	ANI61C2883:	22-45	1874-1893	NAP		g3738200	918	207	4.00E-96	35	65	(AL023518) hypothetical protein [Schizosaccharomyces pombe]
20169	ENU03963	ANI61C5338:	69-88	1922-1941	NAP		g3130053	967	277	7.00E-97	45	80	[Schizosaccharomyces pombe]

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20170	ENU03964	ANI61C1051	54-79	1908-1927	NAP		g3879809	172	85	1.00E-15			(Z47356) similar to protein kinase C substrate; cDNA EST EMBL:M75788 comes from this gene; cDNA EST EMBL:D71530 comes from this gene; cDNA EST EMBL:C08471 comes from this gene; cDNA EST yk427a3.3 comes from this gene; cDNA EST ...; (Z47358) similar to protein kinase C substrate; cDNA EST EMBL:M75788 comes from this gene; cDNA EST EMBL:D71530 comes from this gene; cDNA EST EMBL:C08471 comes from this gene; cDNA EST yk427a3.3 comes from this gene; cDNA EST ... comes from this gene; cDNA EST ... "(AL035085) t-complex protein 1, alpha subunit homolog; chaperonin family [Schizosaccharomyces pombe] (D45893) acr-2 [Neurospora crassa]
20171	ENU03965	ANI61C8625	63-82	1919-1938	NAP		g4107478	1900	541	0	73	98	tubulin alpha-2 chain; tubulin alpha-2 chain - Emericella nidulans (AL035259) putative utp--glucose-1-phosphate uridylyltransferase [Schizosaccharomyces pombe] (AL009146) alternatively spliced form [Drosophila melanogaster] (AL031786) hypothetical protein [Schizosaccharomyces pombe] L-aminic acid oxidase precursor (LAO) ; L-aminic acid oxidase (EC 1.4.3.2) precursor - Neurospora crassa hypothetical protein YDR425w - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr425wp; CAI: 0.15 [Saccharomyces cerevisiae]
20172	ENU03966	ANI61C1025	58-78	1910-1940	NAP		g1754596	129	92	1.00E-17	25	72	Retrovirus-related pol polyprotein from transposon TNT 1-94 [contains: protease; reverse transcriptase; endonuclease] ; hypothetical protein - common tobacco ; (X13777) ORF [Nicotiana tabacum]
20173	ENU03967	ANI61C3731	62-81	1927-1946	NAP		g133407	1617	592	e-168	97	67	
20174	ENU03968	ANI61C7229	50-69	1912-1934	NAP		g4176544	1741	691	0	68	81	
20175	ENU03969	ANI61C1097	22-45	1878-1908	NAP		g2827482		41	0.027			
20176	ENU03970	ANI61C9827	22-44	1890-1909	NAP		g3687484	193	79	9.00E-14	38	22	
20177	ENU03971	ANI61C1125	29-48	1902-1921	NAP		g129307	885	126	5.00E-55	52	22	
20178	ENU03972	ANI61C8860	68-87	1947-1966	NAP		g2131481	271	116	5.00E-25	34	43	
20179	ENU03973	ANI61C3512	55-90	1926-1955	NAP		g130582		77	4.00E-13			



Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvtg	Description
20180	ENU03974	ANI61C9440: 37-58	1908-1938		NAP	g2257503	484	195	1.00E-53	42	52		(AB004535) BEM46 protein [Schizosaccharomyces pombe]
20181	ENU03975	ANI61C4271: 38-57	1919-1939		NAP	g2896767	656	157	8.00E-78	42	51		(AL021899) hypothetical protein Rv2030c [Mycobacterium tuberculosis]
20182	ENU03976	ANI61C8421: 68-90	1942-1969		NAP	g2492615	280	68	2.00E-10	35	26		acetate kinase (acetokinase) ; (X89084) acetate kinase [Corynebacterium glutamicum]
20183	ENU03977	ANI61C3682: 22-45	1900-1926		NAP	g1408257	222	88	2.00E-16	32	16		(U60989) putative transposase [Magnaporthe grisea]
20184	ENU03978	ANI61C4018: 22-51	1896-1926		NAP	g231361	332	167	2.00E-40	38	62		l-aminocyclopropane-1-carboxylate deaminase (ACC deaminase) ; (M73488) l-aminocyclopropane-1-carboxylate deaminase [Pseudomonas sp.]
20185	ENU03979	ANI61C7081: 22-48	1903-1928		NAP	g2622063	272	99	2.00E-28	32	48		(AE000870) conserved protein [Methanobacterium thermoautotrophicum]
20186	ENU03980	ANI61C1105 9:2142..1967	1906-1935		NAP	g1542908		96	1.00E-18				(Z80108) lipI [Mycobacterium tuberculosis]
20187	ENU03981	ANI61C9507: 54-73	1948-1970		NAP	g586354	353	136	4.00E-31	28	88		putative 60.3 KD transcriptional regulatory protein in PRP5-THI2 intergenic region ; probable regulatory protein - yeast (Saccharomyces cerevisiae) ; (Z36108) ORF YBR239c [Saccharomyces cerevisiae]
20188	ENU03982	ANI61C7071: 56-77	1954-1973		NAP	g3281851	707	94	2.00E-18	43	26		(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]
20189	ENU03983	ANI61C1040 5:785..2755	1979-1999		NAP	g3075511	968	385	e-106	47	82		(AF059534) severin kinase [Dictyostelium discoideum]
20190	ENU03984	ANI61C9829: 35-67	1946-1967		NAP	g4249357	275	92	2.00E-28	31	40		(U22463) T-2 toxin biosynthesis protein; TRI7 [Fusarium sporotrichioides]
20191	ENU03985	ANI61C7972: 40-62	1955-1974		NAP	g2116732	277	68	2.00E-10	34	55		(D85129) bphC [Pseudomonas stutzeri]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20192	ENU03986	AN161C6593: 42-61		1956-1980	NAP		g117619	500	230	2.00E-59	28	67	chooline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
		5081..3101											chooline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20193	ENU03987	AN161C6331: 53-82		1981-2001	NAP		g3130051	1240	311	e-132	52	86	(AL023518) conserved hypothetical protein [Schizosaccharomyces pombe]
20194	ENU03988	AN161C8122: 45-65		1979-1998	NAP		g2132851	303	122	1.00E-26	29	52	probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae]
20195	ENU03989	AN161C4157: 70-89		1996-2026	NAP		g1723584	698	234	1.00E-60	48	60	hypothetical 41.3 KD protein C26F1.12C in chromosome I ; (Z73100) unknown [Schizosaccharomyces pombe]
20196	ENU03990	AN161C6693: 58-77		2001-2020	NAP		g913016	651	188	1.00E-46	31	19	"(S76267) Sng2 homolog=bf1 [Schizosaccharomyces pombe=fission yeast, Peptide, 1530 aa]
20197	ENU03991	AN161C7484: 42-61		1989-2008	NAP		g1709060	437	157	3.00E-37	39	46	[Schizosaccharomyces pombe] "mitochondrial outer membrane protein MIM1 ; mitochondrial outer membrane protein MIM1 - yeast (Saccharomyces cerevisiae) ; (Z73111) ORF YLL006w [Saccharomyces cerevisiae] ; (X91488) L1357/MMM1 protein [Saccharomyces cerevisiae] (AL034567) putative protein [Arabidopsis thaliana] (AL023704) weak similarity to B.subtilis spore outgrowth factor B [Schizosaccharomyces pombe] (AL049609) hypothetical protein [Schizosaccharomyces pombe] (Z97204) hypothetical protein [Schizosaccharomyces pombe]
20198	ENU03992	AN161C1217: 22-45		1981-2003	NAP		g4049341	402	74	2.00E-37	38	53	
20199	ENU03993	AN161C314: 22-47		1983-2004	NAP		g3169059	1605	207	e-140	57	75	
20200	ENU03994	AN161C6921: 24-43		1988-2007	NAP		g4584703	569	214	1.00E-54	29	63	
20201	ENU03995	AN161C1070: 30-49		1996-2015	NAP		g2226422	2075	744	0	58	97	
		0:2196..4224											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20202	ENU03996	AN161C9941: 22-51	2745..704	2021	NAP		g401441	1673	263	0	50	85	dolichyl-phosphate-mannose--protein mannosyltransferase 2 ; hypothetical protein YAL023 - yeast (Saccharomyces cerevisiae) ; (L05146)
20203	ENU03997	AN161C1146	48-68	2027-2047	NAP		g4007778	284	166	5.00E-40	30	38	Pmt2p: protein O-D-mannosyltransferase [Saccharomyces cerevisiae] ; (L05027) ORF YAL23 [Saccharomyces cerevisiae] (Z69730) similar to RanBP7-importin-beta-Cse1p superfamily
20204	ENU03998	AN161C6137: 45-68	2940..896	2021-2046	NAP		g3766370	698	129	1.00E-67	39	88	[Schizosaccharomyces pombe] (AL031907) lysyl-trna synthetase [Schizosaccharomyces pombe]
20205	ENU03999	AN161C3240: 32-52	2321..270	2009-2041	NAP		g2507312	402	141	7.00E-39	56	35	60S ribosomal protein L23A (L25) ; (U44800) ribosomal protein L23a [Puccinia graminis f. sp. avenae] (U89924) protein phosphatase 1 binding protein PTG [Mus musculus] (AL031534) Major facilitator superfamily protein
20206	ENU04000	AN161C1068	22-54	2016-2036	NAP		g1888566		73	5.00E-12		78	[Schizosaccharomyces pombe] (AF015771) putative transcriptional regulator [Magnaporthe grisea] (X97657) serine/threonine kinase [Neurospora crassa]
20207	ENU04001	AN161C6812: 70-89	2231..4290	2052-2087	NAP		g3560142	479	90	1.00E-37	31	78	hypothetical 143.6 KD protein C26A3.09C in chromosome I ; (Z69240) hypothetical protein [Schizosaccharomyces pombe]
20208	ENU04002	AN150C8879	60-79	2066-2085	NAP		g2367591		136	5.00E-31	45	71	"hypothetical zinc metalloproteinase YIL108W" ; probable membrane protein YIL108w - yeast (Saccharomyces cerevisiae) ; (Z38125) orf, len: 696, CAl: 0.15 [Saccharomyces cerevisiae]
20209	ENU04003	AN161C7903: 36-55	1959..4027	2041-2062	NAP		g1870019	1576	254	e-176	57	97	(U68040) polyketide synthase [Cochliobolus heterostrophus] (AL034490) putative ATP-dependent DNA helicase [Schizosaccharomyces pombe]
20210	ENU04004	AN161C6374: 39-64	1829..3908	2056-2076	NAP		g1723237	319	103	2.00E-34	38	13	
20211	ENU04005	AN161C6284: 29-55	4146..6226	2047-2067	NAP		g731856	820	348	9.00E-95	37	92	
20212	ENU04006	AN161C195:2	67-87	2080-2106	NAP		g1546072	364	96	2.00E-28	33	14	
20213	ENU04007	AN161C8249: 28-50	1665..3749	2049-2069	NAP		g4008550	656	154	2.00E-36	34	97	

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20214	ENJU04008	ANI61C1046	22-52	2044-	NAP		g2648250	73	7.00E-12				(AE000946) 3-hydroxyacyl-CoA dehydrogenase (hbd-10)
		7:3670..1587		2063									[Archaeoglobus fulgidus]
20215	ENJU04009	ANI61C8491:	40-59	2062-	NAP		g1872502	184	83	5.00E-15	35	29	(U84349) hypothetical hydroxylase a [Amycolatopsis orientalis]
		55..2138		2081									"probable taurine catabolism
20216	ENJU04010	ANI61C7424:	56-75	2078-	NAP		g2506921	322	66	1.00E-29	42	51	dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613)
		1403..3487		2098									dioxygenase [Escherichia coli] ; (U73857) dioxygenase [Escherichia coli] ; (AE000143) taurine
													dioxygenase, 2-oxoglutarate-dependent [Escherichia coli] "
20217	ENJU04011	ANI61C1159:	23-44	2036-	NAP		g1870209	2185	353	e-124	84	87	(AC000133) ORF [Emeritella nidulans]
		4526..4419		2071									(AF091042) putative cercosporin transporter [Cercospora kikuchii]
20218	ENJU04012	ANI61C378:6	66-85	2098-	NAP		g3885836	769	258	1.00E-67	33	91	hypothetical 49.7 KD protein in GIN2-STE3 intergenic region ; hypothetical protein YKL172w - yeast
		832..8934		2126									(Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28172) ORF YKL172w
20219	ENJU04013	ANI61C5355:	32-52	2077-	NAP		g549736	485	154	2.00E-36	37	52	[Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
		3871..5977		2096									Phosphatidylinositol 4-kinase STT4 (P14-kinase) (PTDINS-4-kinase) ; probable 1-phosphatidylinositol 4-kinase (EC 2.7.1.67) - yeast
20220	ENJU04014	ANI61C257:4	29-50	2073-	NAP		g586048	1636	431	e-148	54	31	(Saccharomyces cerevisiae) ; (D13717) homologous protein to P13-kinase (STT4) [Saccharomyces cerevisiae] ; (U17247) Stt4p: Phosphatidylinositol-4-kinase [Saccharomyces cerevisiae]
		869..2761		2095									alpha-adaplin homolog ; (Y11104) melanogaster]
20221	ENJU04015	ANI61C8788:	22-55	2067-	NAP		g3912968	1229	362	e-128	41	72	(AF094516) E1-1I-like protein [Homo sapiens]
		65..2177		2092									
20222	ENJU04016	ANI61C6107:	22-48	2067-	NAP		g3820614	949	231	e-106	43	84	
		2158..45		2093									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20223	ENU04017	ANI61C9256:	72-94	2119-2143	NAP		g401172		65	0.000000			Tetracycline resistance protein (transposon TN4351 / TN4400); NADP-requiring oxidoreductase - Bacteroides fragilis; (M37699) tetracycline resistance protein [Transposon Tn4351]
20224	ENU04018	ANI61C6644:	45-64	2096-2117	NAP		g481285	3041	1143	0	85	98	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger; (Z26938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger]; NADPH cytochrome P450 reductase [Aspergillus niger] (AL023777) hypothetical protein [Schizosaccharomyces pombe] (AF094516) E1-like protein [Homo sapiens]
20225	ENU04019	ANI61C1430:	40-62	2086-2114	NAP		g3184096	1012	263	e-115	40	98	phenylalanine ammonia-lyase; phenylalanine ammonia-lyase (EC 4.3.1.5) - fungus (Rhodosporidium toruloides) (strain CBS14); (X51513) phenylalanine ammonia-lyase [Rhodosporidium toruloides]; (X12702) L-phenylalanine ammonia-lyase [Rhodosporidium toruloides]
20226	ENU04020	ANI61C6107:	30-59	2079-2105	NAP		g3820614	949	231	e-106	43	84	A-agglutinin attachment subunit precursor; a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae); (M60590) a-agglutinin core subunit [Saccharomyces cerevisiae]; (Z71659) ORF YNR044w [Saccharomyces cerevisiae]
20227	ENU04021	ANI61C467:	4 62-81	2135-2154	NAP		g129593	1039	270	e-115	43	79	pisatin demethylase (cytochrome P450 57A2); pisatin demethylase - fungus (Nectria haematococca); (X73145) pisatin demethylase [Nectria haematococca]
20228	ENU04022	ANI61C6214:	43-62	2113-2137	NAP		g416592		40	0.052			
20229	ENU04023	ANI61C4312:	24-55	2086-2118	NAP		g585695	208	120	4.00E-26	29	54	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20230	ENU04024	AN161C1100	22-45	2096-	NAP		g731771	453	148	1.00E-47	31	82	"hypothetical 59.7 KD protein in BET1-PAN1 intergenic region ; probable membrane protein YIL001w - yeast (Saccharomyces cerevisiae) ; (Z38062) orf, len: 513, CAL: 0.12 [Saccharomyces cerevisiae]"
20231	ENU04025	AN161C5348:	29-48	2115-	NAP		g2501339	2759	813	0	80	99	Copper amine oxidase 1 ; (U31869) copper amine oxidase [Aspergillus niger]
20232	ENU04026	AN161C9151:	37-59	2129-	NAP		g2959373	297	137	2.00E-32	34	62	(AL022117) hypothetical protein [Schizosaccharomyces pombe]
20233	ENU04027	AN161C9700:	70-89	2161-	NAP		g2435522	619	164	9.00E-73	38	72	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]
20234	ENU04028	AN161C9533:	54-75	2153-	NAP		g2130244	120	46	0.001	39	31	hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
20235	ENU04029	AN161C1143	58-77	2159-	NAP		g4033481	304	148	1.00E-34	33	33	putative tartrate transporter ; (U32375) membrane protein [Agrobacterium vitis]
20236	ENU04030	AN161C1020	29-52	2127-	NAP		g4007795	1053	407	e-115	34	55	(AL034463) putative nuclear envelope pore membrane protein [Schizosaccharomyces pombe]
20237	ENU04031	AN161C8814:	22-57	2130-	NAP		g2226427	1130	318	e-120	44	91	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
20238	ENU04032	AN161C5857:	23-43	2139-	NAP		g3334847	392	180	2.00E-44	41	30	(AJ007840) Clr4 protein [Schizosaccharomyces pombe] ; (AL034382) mating-type locus and centromeric silencing protein Clr4p [Schizosaccharomyces pombe]
20239	ENU04033	AN161C466:4	28-47	2142-	NAP		g2501570	395	137	1.00E-36	35	70	hypothetical 51.4 KD protein in RAR1-SCJ1 intergenic region ; hypothetical protein YMR210w - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae]
20240	ENU04034	AN161C5683:	23-45	2141-	NAP		g729091	1165	418	e-130	48	83	cell division control protein 5 ; probable transcription factor cdc5 - fission yeast (Schizosaccharomyces pombe) ; (L19525) Cdc5 [Schizosaccharomyces pombe]

# Sequence Definition

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20241	ENU04035	ANI61C5347:	23-58	2164-2183	NAP		g3646451	391	158	1.00E-37	41	44	[AL031603] mRNA cap methyltransferase
20242	ENU04036	ANI61C1073	32-51	2174-2200	NAP		g4291	167	87	6.00E-16	41	22	[Schizosaccharomyces pombe] (X00528) URF c-ras (sc-2)
20243	ENU04037	ANI61C9737:	61-80	2212-2231	NAP		g3184082	1297	494	e-139	39	95	[Saccharomyces cerevisiae] (AL023781) N-terminal acetyltransferase 1
20244	ENU04038	ANI61C4134:	57-76	2209-2230	NAP		g1709439	951	262	e-102	53	69	[Schizosaccharomyces pombe] 2-oxoisovalerate dehydrogenase alpha subunit precursor (branched-chain alpha-keto acid dehydrogenase component alpha chain (E1)) (BCKDH E1-alpha) ; (L47335) branched chain alpha ketoacid decarboxylase E1a subunit [Mus musculus]
20245	ENU04039	ANI61C4107:	42-61	2202-2219	NAP		g1703215	400	147	2.00E-34	28	54	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c
20246	ENU04040	ANI61C1092	29-52	2185-2211	NAP		g131761		59	4.00E-28			[Saccharomyces cerevisiae] quinate permease (quate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
20247	ENU04041	ANI61C1113	64-83	2256-2275	NAP		g416866	1065	273	1.00E-92	65	53	Cyanide hydratase (formamide hydrolyase) ; cyanide hydratase (EC 4.2.1.66) - imperfect fungus (Gloeocercospora sorghi) ; (M99044) cyanide hydratase [Gloeocercospora sorghi]
20248	ENU04042	ANI61C1109	22-51	2227-2246	NAP		g2276360	848	330	3.00E-89	36	98	(Z97992) N'-acetylglucosaminyl-phosphatidylinositol biosynthetic protein [Schizosaccharomyces pombe]
20249	ENU04043	ANI61C1047	41-63	2247-2266	NAP		g3929362	396	113	2.00E-30	32	80	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mp VI]

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer 2247-	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20250	ENU04044	AN161C5969:	32-51	2247-	2266	NAP		g731746	119	52	0.000000	30	38	hypothetical 42.4 KD protein in ENO2-STB5 intergenic region ; hypothetical protein YHR176w - yeast
		3987..1712									003			(Saccharomyces cerevisiae) ; (U00027) Yhr176wp [Saccharomyces cerevisiae]
20251	ENU04045	AN161C6532:	46-65	2260-	2281	NAP		g136287	3886	1273	0	99	98	Anthraniolate synthase component II (contains: glutamine amidotransferase; indole-3-glycerol phosphate synthase (IGPS); N-(5'-phosphoribosyl)anthranilate isomerase (PRAII) ; anthranilate synthase multifunctional protein - Emericella nidulans
		3329..1053												(U62935) multidrug resistance protein 2 [Aspergillus fumigatus] ; (U62936) multidrug resistance protein 2 [Aspergillus fumigatus]
20252	ENU04046	AN161C2678:	42-62	2261-	2280	NAP		g2673955	755	192	8.00E-48	67	13	hypothetical 104.5 KD protein C26A3.10 in chromosome I ; (Z69240) putative zinc finger protein [Schizosaccharomyces pombe]
		273..2553												D-lactate dehydrogenase (cytochrome) precursor (D-lactate ferricytochrome C oxidoreductase) (D-LCR) ; D-lactate dehydrogenase (cytochrome) (EC 1.1.2.4) - yeast (Saccharomyces cerevisiae) ; (Z67750) D-lactate dehydrogenase [Saccharomyces cerevisiae] ; (Z74222) ORF YDL174c [Saccharomyces cerevisiae]
20253	ENU04047	AN161C2605:	63-89	2282-	2308	NAP		g1723238	578	193	4.00E-48	31	72	(AF059202) ACAT related gene product 1 [Homo sapiens]
		2520..233												(U68040) polyketide synthase [(Cochliobolus heterostrophus)]
20254	ENU04048	AN161C9553:	23-51	2243-	2268	NAP		g2506961	640	139	7.00E-50	41	75	fatty acid amide hydrolase ; (U82535) fatty acid amide hydrolase [Homo sapiens] ; (AF098019) fatty acid amide hydrolase [Homo sapiens]
		2365..4652												
20255	ENU04049	AN161C1074:	65-84	2297-	2318	NAP		g3746533	379	175	1.00E-42	34	46	
		7:1744..4039												
20256	ENU04050	AN161C6708:	58-88	2298-	2317	NAP		g1546072	1290	169	9.00E-41	35	10	
		2595..4897												
20257	ENU04051	AN161C8242:	24-55	2272-	2291	NAP		g4557575	453	105	3.00E-33	35	71	
		2932..623												



# Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat ncbi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
20258	ENU04052	AN161C153:2	39-61	2285-2308	NAP	g1168266	1199	316	3.00E-85	45	96		alpha-L-arabinofuranosidase A precursor (arabinosidase A) (ABF A) ; (L29005) alpha-L-arabinofuranosidase [Aspergillus niger]
20259	ENU04053	AN161C6248: 8568..6252	35-57	2280-2309	NAP	g3023956	1360	344	1.00E-93	38	42		Vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]
20260	ENU04054	AN150C2773 4_1:2361..39	46-66	2308-2326	NAP	g548630		349	e-128	46	92		peptide transporter PTR2 (peptide permease PTR2) ; peptide transport protein PTR2 - yeast (Saccharomyces cerevisiae) ; (X73541) ORF YKR413 [Saccharomyces cerevisiae] ; (Z28318) ORF YKR093w [Saccharomyces cerevisiae]
20261	ENU04055	AN161C8136: 285..2616	61-83	2331-2350	NAP	g3123199	953	354	e-102	40	94		CUT9 protein ; anaphase control protein cut9 - fission yeast (Schizosaccharomyces pombe) ; (Z98533) cut9 protein; possible anaphase control [Schizosaccharomyces pombe] ; cut9 gene [Schizosaccharomyces pombe] "hypothetical protein WP6 - Chlamydomonas eugametos ; (L29028) amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .. 109, 128 .. 130, 132 .. 134, 158 .. 160, 163 .. 165; amino acid feature: Rod protein domain, aa 169 .. 340; amino acid feature: globular pro...
20262	ENU04056	AN161C1097 6:4140..3035	38-61	2314-2337	NAP	g1076205	86	45	0.003	26	26		Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20263	ENU04057	AN161C498:3 824..5910	35-55	2313-2334	NAP	g3915154	868	115	1.00E-24	43	16		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20264	ENNU04058	ANI61C9423:	64-84	2343-2368	NAP		g4506957	412	152	1.00E-35	57	30	unknown ; clathrin coat assembly protein AP19 (clathrin coat associated protein AP19) (GOLGI adaptor AP-1 19 KD adaptin) (HA1 19 KD subunit) (clathrin assembly protein complex 1 small chain) ; (AB015320) sigma1B subunit of AP-1 clathrin adaptor complex [Homo sapiens]
20265	ENNU04059	ANI61C3730:	34-53	2306-2341	NAP		g2498971	725	173	3.00E-65	39	75	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans]
20266	ENNU04060	ANI61C753:4	22-51	2313-2332	NAP		g1352945	188	63	2.00E-19	28	49	hypothetical 39.0 KD protein in DAL5-TH111 intergenic region ; hypothetical protein YJRI154w - yeast (Saccharomyces cerevisiae) ; (Z49654) ORF YJRI154w [Saccharomyces cerevisiae]
20267	ENNU04061	ANI61C9176:	27-53	2320-2340	NAP		g1711561	261	62	7.00E-22	29	67	SUGAR transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter, CAI: 0.19 [Saccharomyces cerevisiae]
20268	ENNU04062	ANI61C5315:	70-89	2370-2390	NAP		g1351637	581	168	5.00E-57	39	74	"hypothetical 58.5 KD protein C12G12.14 in chromosome I ; hypothetical protein SPAC12G12.14 - fission yeast (Schizosaccharomyces pombe) ; (Z66568) SPAC12G12.14, unknown, len: 510, some similarity to PIR:A24907 hypothetical protein 1 (chromosome 4 centromere) - yeast [Schizosaccharomyces pombe] " (D73369) pyranose oxidase [Coriolus versicolor]
20269	ENNU04063	ANI61C9185:	24-49	2323-2348	NAP		g1845549	555	192	8.00E-48	38	57	"(AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda] "
20270	ENNU04064	ANI61C1046	63-81	2365-2391	NAP		g2245570	437	89	2.00E-36	33	43	hypothetical 38.5 KD protein C3H8.04 in chromosome I ; (Z69086) unknown [Schizosaccharomyces pombe]
20271	ENNU04065	ANI61C1113	22-57	2333-2352	NAP		g1723215	162	94	4.00E-18	36	24	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20272	ENU04066	AN161C9607:	22-50	2345-3318..5702	NAP		g3915154	334	156	5.00E-37	26	75	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (U96968) alcohol oxidase [Pichia pastoris] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] (AF092565) splicing factor Ptp8 [Homo sapiens]
20273	ENU04067	AN161C4610:	47-66	2366-2569..4956	NAP		g2104963	2260	330	e-177	68	98	probable serine/threonine-protein kinase YJL057C ; probable membrane protein YJL057c - yeast (Saccharomyces cerevisiae) ; (Z49332) ORF YJL057c [Saccharomyces cerevisiae]
20274	ENU04068	AN161C1053	49-84	2377-2625..3014	NAP		g3549879	649	256	5.00E-67	46	27	(AF091342) neurofilament-M subunit [Bos taurus]
20275	ENU04069	AN161C1031	42-62	2362-8:8701..11091	NAP		g3661610	9138	1158	0	73	33	putative ATP-dependent RNA helicase C12C2.06 ; (Z54140) probable ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20276	ENU04070	AN161C7390:	28-49	2356-2167..4558	NAP		g1346384	293	166	6.00E-40	30	32	Nucleoporin NUP100/NSP100 (nuclear pore protein NUP100/NSP100) ; nuclear pore complex protein NUP100 - yeast (Saccharomyces cerevisiae) ; (Z15035) nuclear pore complex protein NUP100 [Saccharomyces cerevisiae] ; (X75780) B959 [Saccharomyces cerevisiae] ; (Z28068) ORF YKL068w [Saccharomyces cerevisiae] ; nuclear pore complex protein NUP100 [Saccharomyces cerevisiae]
20277	ENU04071	AN161C1117	36-55	2384-9:1892..4301	NAP		g3641350	132	63	0.000000			
20278	ENU04072	AN161C8270:	22-47	2372-819..3231	NAP		g1175426	889	150	2.00E-66	56	39	
20279	ENU04073	AN161C6479:	22-56	2413-1..2453	NAP		g400320	296	85	2.00E-15			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20280	ENU04074	AN161C6479:	22-56	2413-2432	NAP		g400320	296	85	2.00E-15			Nucleoporin NUP100/NSP100 (nuclear pore protein NUP100/NSP100); nuclear pore complex protein NUP100 - yeast (Saccharomyces cerevisiae); (Z15035) nuclear pore complex protein NUP100 [Saccharomyces cerevisiae]; (X75780) B959 [Saccharomyces cerevisiae]; (Z28068) ORF YKL068w [Saccharomyces cerevisiae]; nuclear pore complex protein NUP100 [Saccharomyces cerevisiae] probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae); (Z75214) ORF YOR306c [Saccharomyces cerevisiae] (U51927) Spilr [Salmonella typhimurium] Sugar transporter STL1; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae] hypothetical 61.8 K D protein in KGD1-SIM1 intergenic region; probable membrane protein YIL120w - yeast (Saccharomyces cerevisiae); (Z46833) unknown [Saccharomyces cerevisiae]
20281	ENU04075	AN161C1047	22-54	2426-2445	NAP		g2132942	206	122	5.00E-27	25	50	
20282	ENU04076	AN161C1016	26-45	2434-2453	NAP		g1498305	233	96	8.00E-19	26	43	
20283	ENU04077	AN161C9107:	72-95	2486-2509	NAP		g1711561	718	180	8.00E-54	38	46	
20284	ENU04078	AN161C9639:	27-52	2438-2469	NAP		g731864	383	176	4.00E-43	25	67	
20285	ENU04079	AN161C3499:	22-43	2464-2483	NAP		g1166378	271	132	1.00E-29	36	15	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" hypothetical 90.6 K D protein C1D4.10 in chromosome I; (Z69239) unknown [Schizosaccharomyces pombe] (Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe] pisatin demethylase (cytochrome P450 57A1); pisatin demethylase - fungus (Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpv]
20286	ENU04080	AN161C8896:	44-63	2515-2534	NAP		g1723232	404	89	2.00E-16	27	86	
20287	ENU04081	AN161C6543:	38-59	2508-2530	NAP		g2414650	346	95	2.00E-31	66	34	
20288	ENU04082	AN161C1047	32-51	2503-2531	NAP		g3929362	396	113	2.00E-30	31	75	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20289	ENU04083	AN161C6741:	22-50	2532-2948..5519	NAP		g115642	412	134	1.00E-36	37	85	acid protease precursor ; acid proteinase (EC 3.4.23.-) PEP1 precursor - yeast (Saccharomycopsis fibuligera) ; (D00313) open reading frame of PEP1 (putative secretable acid protease) [Saccharomycopsis fibuligera] ; acid protease PEP1 [Saccharomycopsis fibuligera]
20290	ENU04084	AN161C7542:	72-93	2580-3960..1378	NAP		g2293233		159	6.00E-38			(AF008220) YtcJ [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
20291	ENU04085	AN150C1102	52-71	2566-5_1:441..3023	NAP		g1175420		386	e-106	43	64	hypothetical 63.9 KD protein C12C2.03C in chromosome II ; (Z54140) putative oxidoreductase [Schizosaccharomyces pombe]
20292	ENU04086	AN161C1043	67-86	2576-9:2596..13	NAP		g2388966	188	105	1.00E-21	32	15	(Z98979) putative phosphatidylserine decarboxylase proenzyme [Schizosaccharomyces pombe]
20293	ENU04087	AN161C9480:	23-49	2550-57..2646	NAP		g3915964	1332	319	e-145	37	84	hypothetical 112.2 KD protein in T1F35-NPL3 intergenic region (ORF1) ; hypothetical protein YDR430c - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr430cp; CAI: 0.15 [Saccharomyces cerevisiae]
20294	ENU04088	AN161C9498:	22-47	2554-3043..442	NAP		g117619	371	90	5.00E-33	27	81	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20295	ENU04089	AN161C9516:	23-42	2571-3271..656	NAP		g2330659	2225	816	0	53	67	(Z98595) putative snf2 family helicase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20296	ENU04090	AN161C5840:	26-48	2618-2637	NAP		g115208	2843	555	0			"C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) (methy)ENETetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase ; methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) - yeast (Saccharomyces cerevisiae) ; (M12878) C-1-tetrahydrofolate synthase [Saccharomyces cerevisiae] ; (Z49133) C-1-tetrahydrofolate synthase [Saccharomyces cerevisiae] ; (Z72989) ORF YGR204w [Saccharomyces cerevisiae] "
20297	ENU04091	AN161C8143:	23-43	2617-2643	NAP		g125935	553	138	1.00E-60	33	54	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactic) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactic] DHP1 protein ; dhp1 protein - fission yeast (Schizosaccharomyces pombe) ; (D17752) Dhp1 protein [Schizosaccharomyces pombe] ; (Z69240) dna exoribonuclease [Schizosaccharomyces pombe] mitotic control protein DIS3 ; mitotic control protein DIS3 ; mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe) ; (M74094) mitotic control protein [Schizosaccharomyces pombe] ; (AL031743) mitotic control protein dis3 . [Schizosaccharomyces pombe]
20299	ENU04093	AN161C1106	70-93	2684-2715	NAP		g585053	2427	562	0	56	86	Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae] (U58946) transposase [Aspergillus awamori]
20300	ENU04094	AN161C9176:	40-58	2680-2699	NAP		g1711561	261	62	9.00E-22	29	58	
20301	ENU04095	AN161C9979:	24-45	2671-2695	NAP		g1805251	367	188	1.00E-46	30	60	

# Genomic Database

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
20302	ENU04096	ANI61C6593:	41-62	2708-3013..2451	NAP	g117619	500	230	3.00E-59	26	75		choleline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20303	ENU04097	ANI61C3011:	22-55	2744-670..3453	NAP	g131761	449	163	5.00E-49	28	71		quinate permease (quinate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
20304	ENU04098	ANI61C1560:	31-53	2751-2550..5335	NAP	g1168802	578	275	1.00E-72	37	56		Carboxypeptidase S precursor (YSCS) (GLY-X carboxypeptidase) ; Gly-X carboxypeptidase (EC 3.4.17.4) precursor - yeast (Saccharomyces cerevisiae) ; (X63068) carboxypeptidase yscS [Saccharomyces cerevisiae] ; (Z49447) ORF YJL172w [Saccharomyces cerevisiae] (AC004793) Strong similarity to g13600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb AF080119 and is a member of the reverse transcriptase family PF100078.
20305	ENU04099	ANI61C3679:	29-50	2749-5645..2857	NAP	g4512618	665	252	2.00E-93	28	63		Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae] (D83125) secretory component [Sarcophaga peregrina] "Ca2+-transporting ATPase (EC 3.6.1.38), fast skeletal muscle - edible frog; (X63009) fast skeletal muscle Ca-ATPase [Rana esculenta] ; Ca ATPase [Rana esculenta] " hypothetical protein C56F8.17C in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe]
20306	ENU04100	ANI61C1146	71-91	2802-4:4675..1884	NAP	g1711561	592	282	8.00E-75	37	57		
20307	ENU04101	ANI61C9791:	32-58	2776-10551..7746	NAP	g1402634	288	155	1.00E-36	32	29		
20308	ENU04102	ANI61C8214:	56-77	2824-2948..121	NAP	g104311	2172	541	0	54	87		
20309	ENU04103	ANI61C241:	3	67-85	NAP	g1723448	37	0.0003					

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20310	ENU04104	AN161C230:1	39-58	2815-2834	NAP	g1166378	924	442	e-123	33	84	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
20311	ENU04105	34..2683 AN161C7266: 46-65	2830-2855	2830-2855	NAP	g422615	277	125	1.00E-27	21	26	"myosin heavy chain form B, nonmuscle - African clawed frog ; (L09740) nonmuscle myosin heavy chain b [Xenopus laevis]"
20312	ENU04106	383..520 AN161C716:3	68-97	2867-2888	NAP	g4580007	3063	1016	0	61	91	(D87259) poly(A)+ RNA transport protein Ptt3p [Schizosaccharomyces pombe]
20313	ENU04107	1942..4824 AN161C8701: 22-52	2834-2862	2834-2862	NAP	g3150139	720	131	6.00E-78	36	57	(AL023594) amino-acid permease [Schizosaccharomyces pombe]
20314	ENU04108	1455..4387 AN161C7618: 22-45	2882-2911	2882-2911	NAP	g1710803	714	145	2.00E-33	42	21	Retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRE588; EMBL:SCRTG2X:M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae] ; (M97691) Rtg2p [Saccharomyces cerevisiae] ; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]
20315	ENU04109	4..2959 AN161C9:204	45-65	2919-2938	NAP	g125935	459	108	8.00E-43	30	45	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis]"
20316	ENU04110	394..3332 AN161C8661: 72-91	2947-2968	2947-2968	NAP	g4263786	850	225	1.00E-99	37	74	"(AC006068) putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana]"
20317	ENU04111	2948..9 AN161C1760: 69-89	2948-2966	2948-2966	NAP	g2808634	1017	211	3.00E-60	45	49	(AJ001909) transcriptional activator [Aspergillus niger]
20318	ENU04112	795..3765 AN161C8623: 41-60	2949-2968	2949-2968	NAP	g3913798	1430	348	e-115	59	41	"Exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellobiohydrolase I) (beta-glucanocellobiohydrolase I) ; (AB002821) cellobiohydrolase I [Aspergillus aculeatus]"
20319	ENU04113	3947..974 AN161C7699: 22-45	2923-2953	2923-2953	NAP	g1723974	1511	564	e-160	50	74	"hypothetical 75.4 KD protein in HAP2-ADE5,6 intergenic region ; hypothetical protein YGL236c - yeast (Saccharomyces cerevisiae) ; (Z72758) ORF YGL236c [Saccharomyces cerevisiae]"



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20320	ENU04114	ANI61C4655:	38-57	2952-3399..423	NAP		g730723	1444	604	e-171	67	38	CAMP-dependent protein kinase SCH9 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (U00029) Sch9p: CAMP-dependent protein kinase [Saccharomyces cerevisiae]
20321	ENU04115	ANI61C9768:	28-61	2936-3378..6362	NAP		g118901	2303	426	0	45	63	DNA polymerase zeta catalytic subunit ; DNA-directed DNA polymerase (EC 2.7.7.) REV3 - yeast (Saccharomyces cerevisiae) ; (M29683) DNA polymerase (pot.) ; putative [Saccharomyces cerevisiae] ; (Z73523) ORF YPL167c [Saccharomyces cerevisiae] ; (X96770) P2535 protein [Saccharomyces cerevisiae]
20322	ENU04116	ANI61C8537:	45-64	2973-5851..8841	NAP		g549755	360	89	2.00E-26	27	50	"Carboxylic acid transporter protein homolog ; hypothetical protein YKL217w - yeast (Saccharomyces cerevisiae) ; (X75951) ORF3, A616 [Saccharomyces cerevisiae] ; (Z28217) ORF YKL217w [Saccharomyces cerevisiae] ; (U24155) carboxylic acid transporter protein homolog [Saccharomyces cerevisiae]"
20323	ENU04117	ANI61C6226:	33-64	2970-4891..7889	NAP		g728850		43	0.009			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, sta1, len: 1367, CAI: 0.3, AMYH_yeast P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus]"
20324	ENU04118	ANI61C7076:	62-81	944-963	NAP		g2132846	495	156	2.00E-37	29	58	probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20325	ENU04119	AN161C1070	63-86	944-965	NAP		g120777	1144	373	e-103	57	64	"Succinate-semialdehyde dehydrogenase (NADP+) (SSDH); (M88334) succinic semialdehyde dehydrogenase [Escherichia coli]; (AE000351) succinate-semialdehyde dehydrogenase, NADP-dependent activity [Escherichia coli]"
		5:1016..72											
20326	ENU04120	AN161C4798:	41-62	924-944	NAP		g2388907	606	65	6.00E-10	29	22	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
		1015..1960											
20327	ENU04121	AN161C1948:	25-46	908-928	NAP		g4127832	475	171	6.00E-42	37	57	(Y17243) cytochrome P450 [Gibberella fujikuroi]
		2166..3111											
20328	ENU04122	AN161C681:2	58-80	946-965	NAP		g119216	1224	322	3.00E-87	65	63	"Elongation factor TU, mitochondrial precursor; translation elongation factor Tu precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (Z75095) ORF YOR187w [Saccharomyces cerevisiae]"
		529..1579											
20329	ENU04123	AN161C6816:	48-70	938-957	NAP		g4079649	162	63	7.00E-18	32	21	(U78168) cAMP-regulated guanine nucleotide exchange factor I [Homo sapiens]
		1106..155											
20330	ENU04124	AN161C1101	66-85	957-979	NAP		g1351683	341	139	2.00E-32	35	55	hypothetical 53.9 KD protein C1F5.08C in chromosome I; (Z68136) unknown [Schizosaccharomyces pombe]
		6:2127..1172											
20331	ENU04125	AN161C1047:	38-57	934-954	NAP		g3122248	669	233	1.00E-60	40	67	D-hydantoïnase (dihydropyrimidinase) (DHPASE); (X91070) D-hydantoïnase [Agrobacterium radiobacter]
		1301..343											
20332	ENU04126	AN161C6326:	22-49	917-943	NAP		g3647336	439	102	3.00E-44	52	46	(AL031644) hypothetical protein [Schizosaccharomyces pombe]
		1017..54											
20333	ENU04127	AN161C1037	36-66	938-957	NAP		g1352875	801	66	1.00E-22	33	19	hypothetical 154.9 KD protein in CPR7-PET191 intergenic region; hypothetical protein YJR033c - yeast (Saccharomyces cerevisiae); (Z49533) ORF YJR033c [Saccharomyces cerevisiae]
		9:6723..5760											
20334	ENU04128	AN161C9715:	42-61	946-965	NAP		g1794292	1171	353	1.00E-96	55	65	(U77983) WD-domain protein [Schizosaccharomyces pombe]
		101..1066											
20335	ENU04129	AN161C627:4	69-93	981-1001	NAP		g2133298	552	233	1.00E-60	49	82	"chitinase, 33k, precursor - fungus (Trichoderma harzianum); (X80006) chitinase [Trichoderma harzianum]"
		53..1427											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20336	ENU04130	AN161C9947:	43-62	942-977	NAP		g3915154	647	154	1.00E-36	34	57	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichoides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichoides]
20337	ENU04131	AN161C942:4	22-40	942-964	NAP		g2228233	336	130	1.00E-29	40	27	(U24215) p-cumic aldehyde dehydrogenase [Pseudomonas putida]
20338	ENU04132	AN161C7124:	56-74	980-1001	NAP		g2497154	337	133	2.00E-30	35	73	hypothetical 42.9 KD protein in IL V2-ADE17 intergenic region ; hypothetical protein YMR114c - yeast (Saccharomyces cerevisiae) ; (Z49702) unknown [Saccharomyces cerevisiae] (Y16399) multidrug resistance protein [Candida albicans] (Y16399) multidrug resistance protein [Candida albicans]
20339	ENU04133	AN161C8753:	72-94	997-1020	NAP		g3378550		84	1.00E-15			Proline iminopeptidase (prolyl aminopeptidase) ; prolyl aminopeptidase (EC 3.4.11.5) - Aeromonas sobria ; (D30714) prolyl aminopeptidase [Aeromonas sobria] (AC006570) putative polypeptide [Arabidopsis thaliana]
20340	ENU04134	AN161C8753:	72-94	997-1020	NAP		g3378550		84	1.00E-15			"Exopolysaccharuronase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) ; (L48982) exo-alpha 1,4-polygalacturonase [Cochliobolus carbonum] "
20341	ENU04135	AN161C1583:	42-61	974-999	NAP		g1730576	316	90	3.00E-17	35	58	(AL021841) amiB [Mycobacterium tuberculosis]
20342	ENU04136	AN161C8605:	63-90	997-1023	NAP		g4432807	477	89	5.00E-36	32	20	(AL031739) beta transducin [Schizosaccharomyces pombe]
20343	ENU04137	AN161C1048	50-69	989-1012	NAP		g2499717	430	86	3.00E-16	34	25	hypothetical 58.0 KD protein C2C6.08 in chromosome I ; (AL031324) hypothetical protein [Schizosaccharomyces pombe]
20344	ENU04138	AN161C7225:	28-47	976-996	NAP		g2894215	427	139	4.00E-34	37	71	(AL031154) putative transmembrane transporter [Schizosaccharomyces pombe]
20345	ENU04139	AN161C3186:	23-43	961-992	NAP		g3650407	435	115	7.00E-25	43	59	
20346	ENU04140	AN161C5164:	41-59	989-1010	NAP		g3183406	846	274	6.00E-73	49	57	
20347	ENU04141	AN161C9636:	22-50	971-993	NAP		g3367790	723	100	1.00E-31	49	60	

Seq num	Seq id	Contig Source	5 pos	Primer 3 pos	Primer Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20348	ENU04142	ANI61C9116:	45-67	997-1017	NAP		g1293655	778	109	4.00E-46	40	47	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
20349	ENU04143	ANI61C6687:	24-46	977-996	NAP		g2226429	826	260	2.00E-78	47	53	(Z97204) putative vacuolar protein sorting-associated protein. [Schizosaccharomyces pombe]
20350	ENU04144	ANI61S2225:	56-75	1010-1029	NAP		g3810866		108	6.00E-30	50	94	(AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
20351	ENU04145	ANI61C9501:	34-53	987-1009	NAP		g2132474	1332	518	e-146	74	55	probable membrane protein YDR091c - yeast (Saccharomyces cerevisiae) ; (Z50111) unknown [Saccharomyces cerevisiae]
20352	ENU04146	ANI61C164:3	42-64	998-1018	NAP		g114971	1677	276	2.00E-73	45	37	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucosylhydrolase) ; beta-glucosidase (EC 3.2.1.21) precursor - yeast (Kluyveromyces marxianus var. marxianus) ; (X05918) beta-glucosidase (AA 1 - 845)
20353	ENU04147	ANI61C9646:	30-50	990-1011	NAP		g4538856	247	111	6.00E-24	35	49	[Kluyveromyces marxianus] (AJ223758) 54 kDa vacuolar H(+)-ATPase subunit [Sus scrofa]
20354	ENU04148	ANI61C8673:	23-47	980-1011	NAP		g3183238	529	181	7.00E-54	36	46	hypothetical 81.2 KD protein C3D6.13C in chromosome II ; (Z95620) putative thioredoxin [Schizosaccharomyces pombe]
20355	ENU04149	ANI61C8886:	71-90	1037-1060	NAP		g1084944	742	319	3.00E-86	59	32	hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20356	ENU04150	ANI61C7428:	62-81	1030-1051	NAP		g125401	163	94	2.00E-18			choiline kinase ; choline kinase (EC 2.7.1.32) - yeast (Saccharomyces cerevisiae) ; (J04454) choline kinase [Saccharomyces cerevisiae] ; (X91258) choline kinase [Saccharomyces cerevisiae] ; (U53881) Cki1p: choline kinase [Saccharomyces cerevisiae] ; (Z73305) ORF YLR133w [Saccharomyces cerevisiae]
20357	ENU04151	ANI61C1035	47-67	1016-1041	NAP		g3334221	1166	203	3.00E-90	60	74	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) ; (AF038152) 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]
20358	ENU04152	ANI61C3101:	22-54	999-1018	NAP		g3023999	1801	210	e-108	85	55	"Isocitrate dehydrogenase (NADP), mitochondrial precursor (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) ; (AB000261) NADP-dependent isocitrate dehydrogenase precursor [Aspergillus niger] ; (AB000262) NADP-dependent isocitrate dehydrogenase precursor [Aspergillus niger]"
20359	ENU04153	ANI61C7048:	70-89	1055-1076	NAP		g3378447	462	153	6.00E-48	39	73	(AF079317) unknown [Sphingomonas aromaticivorans]
20360	ENU04154	ANI61C299:1	40-59	1020-1046	NAP		g2408044	108	56	0.000000	22	43	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
20361	ENU04155	ANI61C1017	22-50	1014-1035	NAP		g2673947	994	346	1.00E-98	67	23	(U62931) multidrug resistance protein 1 [Aspergillus flavus] ; (U62932) multidrug resistance protein 1 [Aspergillus flavus]
20362	ENU04156	ANI61C9779:	70-97	1062-1086	NAP		g465668	930	235	3.00E-61	42	22	"ubiquitin fusion degradation protein 4 (UB fusion protein 4) ; hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae) ; (S53418) orf YKL162 [Saccharomyces cerevisiae=yeast, Peptide, 1483 aa] [Saccharomyces cerevisiae] ; (Z28010) ORF YKL010c [Saccharomyces cerevisiae]"

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20363	ENU04157	AN161C4566: 1873..809	33-58	1034-1054	NAP	g3041656	717	110	1.00E-43	43	62		NADPH:adrenodoxin oxidoreductase precursor (adrenodoxin reductase) (ferredoxin-NADP(+) reductase) ; (J03826) adrenodoxin reductase precursor species 1 [Homo sapiens]
20364	ENU04158	AN161C269:9 58..2023	22-47	1017-1045	NAP	g113600	99	41	0.000000	29	89		alcohol dehydrogenase (NADP(+)) (aldehyde reductase) ; alcohol dehydrogenase (NADP(+)) (EC 1.1.1.2) - human ; (J04794) aldehyde reductase (EC 1.1.1.2) [Homo sapiens] ; (AF036683) aldehyde reductase [Homo sapiens]
20365	ENU04159	AN161C7606: 2390..1323	60-79	1065-1084	NAP	g3411013	450	175	6.00E-43	33	35		(AF000232) protein mannosyltransferase 1 [Candida albicans]
20366	ENU04160	AN161C1879: 1257..2325	29-54	1037-1055	NAP	g3702635	532	184	1.00E-45	35	79		(AL031825) hypothetical protein [Schizosaccharomyces pombe]
20367	ENU04161	AN161C4366: 1466..396	23-44	1032-1051	NAP	g3434965	1013	316	2.00E-85	54	66		(AB002530) mus-23 [Neurospora crassa]
20368	ENU04162	AN161C1061 3:3032..1957	71-90	1083-1102	NAP	g3850152	564	184	3.00E-54	36	76		(AL033396) hypothetical protein [Candida albicans]
20369	ENU04163	AN161C7489: 2110..1036	22-46	1035-1054	NAP	g1363755	931	244	7.00E-64	50	26		hypothetical protein YLR410w - yeast (Saccharomyces cerevisiae) ; (U20162) Ylr410wp [Saccharomyces cerevisiae]
20370	ENU04164	AN161C2606: 2026..951	31-50	1042-1063	NAP	g2599117	1269	189	e-125	80	93		(AF028783) proteasome regulatory subunit 12 [Hypocrea jecorina]
20371	ENU04165	AN161C8172: 1317..243	64-83	1077-1096	NAP	g3947854	481	148	2.00E-38	50	76		(AL034381) conserved hypothetical PFAM UPP0031 containing protein [Schizosaccharomyces pombe]
20372	ENU04166	AN161C4401: 135..1211	67-86	1081-1101	NAP	g3336839	290	81	3.00E-28	30	57		(Y16834) hexose transporter [Candida albicans]
20373	ENU04167	AN161C2761: 1270..194	54-73	1067-1088	NAP	g3549891	364	102	7.00E-42	32	61		(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi]
20374	ENU04168	AN161C1042 5:576..1655	22-51	1040-1059	NAP	g4502369	324	156	3.00E-37	30	89		gamma-Butyrobetaine Hydroxylase ; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]

# Sequence Annotation

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20375	ENU04169	ANI61C7010:	42-61	1052-1080	NAP		g1176483	500	129	2.00E-33	45	45	hypothetical 70.2 KD protein in GSH1-CHS6 intergenic region ; hypothetical protein YJL100w - yeast
		21..1103											(Saccharomyces cerevisiae) ; (X85021) orf 12 [Saccharomyces cerevisiae] ; (Z49375) ORF YJL100w
													[Saccharomyces cerevisiae]
20376	ENU04170	ANI61C1082	25-48	1033-1063	NAP		g4539596	179	102	2.00E-22	28	44	(AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces pombe]
		7:471..1551											
20377	ENU04171	ANI61C5138:	25-43	1041-1063	NAP		g21332490	228	100	3.00E-24	41	29	probable membrane protein YDR282c - yeast (Saccharomyces cerevisiae) ; (U51030) Ydr282cp [Saccharomyces cerevisiae]
		172..1252											(AL033389) aminotransferase [Schizosaccharomyces pombe]
20378	ENU04172	ANI61C22:30	69-92	1096-1115	NAP		g3850081	987	294	7.00E-79	50	67	"Exopolysaccharuronase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) ; (X99795) exopolysaccharuronase [Aspergillus tubingensis] "
		60..4145											probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c
20379	ENU04173	ANI61C9101:	60-78	1090-1109	NAP		g2499716	564	97	2.00E-52	38	68	[Saccharomyces cerevisiae]
		1688..597											(AL023554) dna topoisomerase iii. [Schizosaccharomyces pombe]
20380	ENU04174	ANI61C5379:	22-49	1051-1071	NAP		g21332942	348	145	7.00E-34	29	66	(Y12819) putative RNA helicase (DEAD box) [Danio rerio]
		58..1149											
20381	ENU04175	ANI61C2460:	25-51	1053-1077	NAP		g4388617	1412	259	7.00E-80	49	52	
		2020..3114											
20382	ENU04176	ANI61C1138	59-83	1103-1122	NAP		g2558533	596	94	2.00E-29	39	42	
		2:1354..2459											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20383	ENU04177	ANT61C9581:	61-80	1106-1125	NAP		g3876562	194	88	1.00E-16	28	37	(Z81074) Similarity to Soybean 3-methylcrotonyl-CoA carboxylase (TR:Q42777); cDNA EST EMBL:M75819 comes from this gene; cDNA EST EMBL:M89099 comes from this gene; cDNA EST EMBL:D32763 ... (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
20384	ENU04178	ANT61C9305:	47-68	1089-1112	NAP		g1020413	363	59	0.000000	22	68	(AL031854) hypothetical protein [Schizosaccharomyces pombe]
20385	ENU04179	ANT61C5766:	65-88	1108-1130	NAP		g3738180	216	52	0.000000	002	46	hypothetical 70.5 KD protein in AGP3-DAK3 intergenic region ; probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL054C [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae]
20386	ENU04180	ANT61C5933:	71-90	1111-1137	NAP		g1175958	445	194	1.00E-48	35	46	"(AC001229) ESTs gb 145673.gb N37512 come from this gene. [Arabidopsis thaliana] " mitochondrial processing peptidase alpha subunit precursor (alpha-MPP) ; mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - Neurospora crassa
20387	ENU04181	ANT61C2930:	43-62	1080-1110	NAP		g2190550	420	182	3.00E-51	42	95	(U26160) 43 kDa secreted glycoprotein precursor [Paracoccidioides brasiliensis] ; glycoprotein gp43 [Paracoccidioides brasiliensis] (AL022070) yeast m1c1 homolog [Schizosaccharomyces pombe]
20388	ENU04182	ANT61C1100	53-78	1108-1127	NAP		g127286	1673	316	4.00E-93	62	63	"(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe] "
20389	ENU04183	ANT61C1104	48-68	1099-1123	NAP		g1050956	1043	273	e-104	52	84	
20390	ENU04184	ANT61C9293:	41-61	1100-1119	NAP		g2950486	249	111	7.00E-24	30	33	
20391	ENU04185	ANT61C1010	35-54	1095-1114	NAP		g1749480	332	96	4.00E-19	35	77	



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20392	ENU04186	ANI61C1135	22-57	1086-	NAP		g4008554		53	0.000003			(AL034490) putative tyrosine kinase [Schizosaccharomyces pombe]
20393	ENU04187	ANI61C5254:	59-78	1127-	NAP		g731688	641	107	2.00E-35	32	37	hypothetical 104.0 KD protein in HXT5-NRK1 intergenic region; hypothetical protein YHR098c - yeast (Saccharomyces cerevisiae); (U00060) Yhr098cp [Saccharomyces cerevisiae]; (AJ009784) Sfb3 [Saccharomyces cerevisiae]
20394	ENU04188	ANI61C2574:	23-42	1091-	NAP		g2894293	380	93	3.00E-18	32	62	(AL021837) hypothetical protein [Schizosaccharomyces pombe]
20395	ENU04189	ANI61C7640:	37-56	1109-	NAP		g1711561	495	165	3.00E-47	34	57	sugar transporter STL1; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stilp: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20396	ENU04190	ANI61C1134:	63-82	1131-	NAP		g3256111		38	0.13			(AL024456) 1-evidence=predicted by motif; 1-match_accession=PROSITE:PS00017; 1-match_description=ATP/GTP-binding site motif A (P-loop); 1-method=ppsearch;; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS...
20397	ENU04191	ANI61C8073:	46-74	1122-	NAP		g2842688	558	77	2.00E-13	26	21	hypothetical 70.6 KD protein C1F8.03C in chromosome 1; (Z81312) unknown [Schizosaccharomyces pombe]
20398	ENU04192	ANI61C6332:	29-56	1102-	NAP		g549755	690	156	2.00E-37	39	27	"carboxylic acid transporter protein homolog; hypothetical protein YKL217w - yeast (Saccharomyces cerevisiae); (X75951) ORF3, A616 [Saccharomyces cerevisiae]; (Z28217) ORF YKL217w [Saccharomyces cerevisiae]; (U24155) carboxylic acid transporter protein homolog [Saccharomyces cerevisiae]"

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20399	ENU04193	ANT61C4155:	22-42	1104-1123	NAP		g2497126	96	64	0.000000	26	54	actin-like protein ARP9 ; probable membrane protein YMR033w - yeast (Saccharomyces cerevisiae) ; (Z49213) unknown [Saccharomyces cerevisiae] "GNS1 protein ; probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae) ; (X56909) YCR521 [Saccharomyces cerevisiae] ; (S78624) YCR521 [Saccharomyces cerevisiae=yeast, Peptide, 347 aa] [Saccharomyces cerevisiae] ; (X59720) YCR034w, len:347 [Saccharomyces cerevisiae] ; (AF012655) v-snare bypass mutant [Saccharomyces cerevisiae] "
20400	ENU04194	ANT61C2929:	27-47	1110-1129	NAP		g140489	735	142	2.00E-68			(AL023634) protein kinase dsk1 [Schizosaccharomyces pombe] sexual differentiation process protein ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe) ; (D14064) ORF [Schizosaccharomyces pombe]
20401	ENU04195	ANT61C7783:	22-52	1105-1126	NAP		g3150261		85	1.00E-15			potassium-activated aldehyde dehydrogenase precursor ; probable aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) YOR374w - yeast (Saccharomyces cerevisiae) ; (Z75282) ORF YOR374w [Saccharomyces cerevisiae]
20402	ENU04196	ANT61C6885:	72-91	1154-1181	NAP		g729862	157	72	4.00E-16	32	32	(AL033391) COO3 homologue [Candida albicans] (AL022071) fructosyl amine [Schizosaccharomyces pombe] hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]
20403	ENU04197	ANT61C4087:	25-44	1099-1134	NAP		g2506349	449	109	8.00E-46	33	67	
20404	ENU04198	ANT50C1851	46-65	1128-1155	NAP		g3850128		120	2.00E-26	34	76	
20405	ENU04199	ANT61C1123	25-44	1110-1134	NAP		g2950465	216	85	7.00E-16			
20406	ENU04200	ANT61C1724:	39-60	1136-1155	NAP		g3183342	350	109	2.00E-41	33	83	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20407	ENU04201	ANI61C5929:	56-75	1153-	NAP		g3929399	2005	438	0	99	67	proline-specific permease (proline transport protein) ; (X79797) proline permease [Emmericella nidulans] (AB011173) KIAA0601 protein [Homo sapiens]
		1346..188		1172									
20408	ENU04202	ANI61C9268:	22-52	1124-	NAP		g3043726	505	176	2.00E-43	45	22	(AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces pombe]
		4133..2971		1142									
20409	ENU04203	ANI61C6430:	22-43	1115-	NAP		g3560143	77	55	0.000000	35	10	(AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces pombe]
		8426..7264		1142					7				
20410	ENU04204	ANI61C9220:	22-49	1123-	NAP		g2500937	1219	221	5.00E-96	48	62	probable glucose transporter RCO-3 ; (U54768) RCO3 [Neurospora crassa]
		2429..1263		1146									
20411	ENU04205	ANI61C9825:	44-63	1139-	NAP		g3367585	164	90	3.00E-17	33	44	(AL031135) putative polygalacturonase [Arabidopsis thaliana]
		23..1190		1169									
20412	ENU04206	ANI61C3276:	28-47	1141-	NAP		g3687231	208	114	1.00E-24	31	51	(AC005169) hypothetical protein [Arabidopsis thaliana]
		3347..2173		1160									
20413	ENU04207	ANI61C2648:	54-73	1166-	NAP		g1077378	522	179	2.00E-44	35	39	probable membrane protein YLR222c - yeast (Saccharomyces cerevisiae) ; (U19027) YH222cp [Saccharomyces cerevisiae]
		1339..165		1186									(U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes]
20414	ENU04208	ANI61C5015:	24-43	1124-	NAP		g517205	261	134	1.00E-30	31	59	(AL021411) putative oxidoreductase [Streptomyces coelicolor]
		1300..122		1159									
20415	ENU04209	ANI61C7035:	59-78	1167-	NAP		g2808776	242	125	6.00E-28	33	62	(AL031515) putative secreted cellulase [Streptomyces coelicolor]
		40..1217		1194									
20416	ENU04210	ANI61C5367:	22-47	1131-	NAP		g3560020	520	210	1.00E-53	38	40	putative sterigmatocystin biosynthesis peroxidase STCC ; (U34740) putative peroxidase [Emmericella nidulans]
		1331..151		1160									
20417	ENU04211	ANI61C3671:	55-74	1177-	NAP		g2498968	112	50	0.000000	30	57	thiamin pyrophosphokinase (TPK) (thiamin kinase) ; thiamin pyrophosphokinase (EC 2.7.6.2) - fission yeast (Schizosaccharomyces pombe) ; (X84417) thiamin pyrophosphokinase [Schizosaccharomyces pombe] ; (Z98533) thiamin pyrophosphokinase [Schizosaccharomyces pombe]
		1222..34		1200					03				
20418	ENU04212	ANI61C1123	47-67	1173-	NAP		g1174727	199	52	7.00E-14	38	37	
		2:1473..284		1193									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20419	ENU04213	ANT61C1041	22-48	1141-	NAP	g2384693	91	48	5.00E-10	28	51	51	(AF013216) unknown [Myxococcus xanthus]
20420	ENU04214	ANT61C3678:	22-43	1165-	NAP	g3819705	726	187	6.00E-62	37	53	53	(AL032824) syntaxin binding protein 1; sec1 family secretor y protein [Schizosaccharomyces pombe]
20421	ENU04215	ANT61C2667:	54-76	1204-	NAP	g2289244		37	0.000005				(U97107) membrane glycoprotein CIG30 [Mus musculus]
20422	ENU04216	ANT61C1041	56-75	1201-	NAP	g4490992	312	122	4.00E-27	37	76	76	(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
20423	ENU04217	ANT61C1191:	22-54	1175-	NAP	g417358	260	113	5.00E-37	30	56	56	ADA3 protein (NGG1 protein) ; NGG1 protein - yeast (Saccharomyces cerevisiae) ; (L12137) NGG1 [Saccharomyces cerevisiae] ; (Z46727) Ngg1p [Saccharomyces cerevisiae] (L35487) mannanase [Aspergillus aculeatus]
20424	ENU04218	ANT61C1120	31-51	1185-	NAP	g558311	1277	332	e-121	66	93	93	probable calcium-transporting ATPase 6 ; hypothetical protein YEL031w - yeast (Saccharomyces cerevisiae) ; (U18530) P-type ATPase; YEL031W [Saccharomyces cerevisiae]
20425	ENU04219	ANT61C6026:	22-55	1181-	NAP	g731415	1049	317	7.00E-86	56	29	29	putative transporter YTL166C ; probable membrane protein YTL166c - yeast (Saccharomyces cerevisiae) ; (Z46921) unknown [Saccharomyces cerevisiae]
20426	ENU04220	ANT61C433:3	22-45	1174-	NAP	g731893	922	217	2.00E-62	39	67	67	(Z98981) hypothetical protein [Schizosaccharomyces pombe]
20427	ENU04221	ANT61C9916:	59-87	1211-	NAP	g2388995	159	66	7.00E-13	27	30	30	hypothetical 50.5 KD protein in RNAI-RNT1 intergenic region ; probable membrane protein YMR238w - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae]
20428	ENU04222	ANT61C5847:	28-52	1207-	NAP	g2497199	514	152	5.00E-48	33	77	77	(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
20429	ENU04223	ANT61C8210:	22-40	1203-	NAP	g4104775		46	0.0005				(AJ001261) NIPSNAP2 protein [Mus musculus]
20430	ENU04224	ANT61C6527:	59-79	1240-	NAP	g2769258	367	53	3.00E-12	26	55	55	
		5092..6335		1260									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20431	ENU04225	ANI61C9146:	31-52	1219-	NAP		g4585875	169	48	0.000000	32	89	Unknown protein (AC005850)
		831..739		1238						2			[Arabidopsis thaliana]
20432	ENU04226	ANI61C8955:	33-52	1225-	NAP		g1175374	1122	433	e-120	57	75	hypothetical 57.8 KD protein C2F7.11 in chromosome I ; hypothetical protein SPAC2F7.11 - fission yeast
		198..1453		1246									(Schizosaccharomyces pombe) ; (Z50142) unknown
													[Schizosaccharomyces pombe] ; (AF079876) Nrd1p
													[Schizosaccharomyces pombe] (AF014950) chitinase A
20433	ENU04227	ANI61C5197:	22-50	1222-	NAP		g2429326	89	62	2.00E-15	30	36	[Stenotrophomonas maltophilia]
		4347..3086		1241									(AL031534) Major facilitator superfamily protein
20434	ENU04228	ANI61C1024	32-55	1225-	NAP		g3560142	716	173	2.00E-42	33	64	[Schizosaccharomyces pombe]
		3:2189..3452		1253									proline-specific permease (proline transport protein) ; (X79797) proline permease [Emmericella nidulans]
20435	ENU04229	ANI61C1120	61-80	1263-	NAP		g3929399	1125	380	e-104	48	76	(AL022244) hypothetical protein [Schizosaccharomyces pombe]
		3:1271..2534		1282									(M82963) hexose transporter [Saccharomyces cerevisiae]
20436	ENU04230	ANI61C9721:	42-61	1245-	NAP		g2995339	1134	337	e-109	56	46	hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) ; (U10400) Ysc84p [Saccharomyces cerevisiae]
		1288..21		1266									(AJ235272) SCO2 protein precursor (sco2) [Rickettsia prowazekii]
20437	ENU04231	ANI61C7513:	41-61	1248-	NAP		g171741	395	164	1.00E-39	25	74	"(AF031228) D-arabinono-1,4-lactone oxidase; L-galactono-gamma-lactone oxidase [Candida albicans]"
		2858..1583		1274									transcription factor btf3 homolog ; (U29488) similar to human
20438	ENU04232	ANI61C352:1	72-92	1290-	NAP		g626598	707	247	7.00E-72	43	83	cerevisiae GAL4 DNA-binding enhancer protein [Caenorhabditis elegans]
		358..78		1309									
20439	ENU04233	ANI61C1051	26-49	1248-	NAP		g3861132	225	97	3.00E-19	29	60	
		1:667..1942		1267									
20440	ENU04234	ANI61C6078:	23-47	1247-	NAP		g4090945	619	307	1.00E-82	38	76	
		3729..5017		1269									
20441	ENU04235	ANI61C3595:	60-79	1284-	NAP		g2493356	309	125	5.00E-28	47	39	
		1111..2400		1307									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
20442	ENU04236	ANT61C1023	23-48	1252-1273	NAP		g1352621	1338	303	e-115	64	83	dihydroliipoamide acetyltransferase component of pyruvate dehydrogenase complex precursor (E2) (PDC-E2) (MRP3) ; dihydroliipoamide acetyltransferase homolog - Neurospora crassa ; (J04432) ribosomal protein [Neurospora crassa]
20443	ENU04237	ANT61C5788: 4310..3016	22-46	1247-1274	NAP		g3581917	200	86	6.00E-16	40	65	(AL031545) hypothetical protein [Schizosaccharomyces pombe]
20444	ENU04238	ANT61C8008: 882..2188	22-48	1268-1286	NAP		g3885836	584	113	5.00E-62	37	62	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
20445	ENU04239	ANT61C132:1 038..1569	38-61	1284-1303	NAP		g2645229	430	163	3.00E-39	37	40	(U78597) kinesin light chain [Plectonema boryanum]
20446	ENU04240	ANT61C7007: 94..1402	23-52	1257-1289	NAP		g2213548	432	181	8.00E-45	33	70	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
20447	ENU04241	ANT61C7007: 94..1402	23-52	1257-1289	NAP		g2213548	432	181	8.00E-45	33	70	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
20448	ENU04242	ANT61C194:2 083..757	53-76	1317-1337	NAP		g1911486	269	81	1.00E-14	41	47	"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"
20449	ENU04243	ANT61C756:1 778..449	71-91	1336-1358	NAP		g544049	263	78	1.00E-13			"3',5'-cyclic-nucleotide phosphodiesterase (PDEASE) ; probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) pdel-fission yeast (Schizosaccharomyces pombe) ; (S64907) Dictyostelium discoideum phosphodiesterase homolog [Schizosaccharomyces pombe=fission yeast, Peptide, 346 aa] [Schizosaccharomyces pombe] ; (AL031545) 3',5'-cyclic-nucleotide phosphodiesterase [Schizosaccharomyces pombe] ; pde1 gene [Schizosaccharomyces pombe]"

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20450	ENJU04244	ANI61C2416:	22-45	1293-1312	NAP		g400276	531	142	2.00E-53			"mitochondrial peptide chain release factor 1 precursor (MRF-1) ; translation releasing factor RF-1, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X60381) mitochondrial release factor 1 [Saccharomyces cerevisiae] ; (Z72665) ORF YGL143c [Saccharomyces cerevisiae] ; (X99960) YGL143c [Saccharomyces cerevisiae] "
20451	ENJU04245	ANI61C1065	22-43	1290-1312	NAP		g1346290	339	87	2.00E-35	29	63	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces fragilis] hypothetical protein YER060w - yeast (Saccharomyces cerevisiae) (Z95397) unknown [Schizosaccharomyces pombe]
20452	ENJU04246	ANI61C5171:	68-90	1345-1364	NAP		g1072485	442	166	4.00E-40	31	79	cycloheximide resistance protein ; (M64932) cyclohexamide resistance protein [Candida maltosa]
20453	ENJU04247	ANI61C3347:	42-64	1326-1345	NAP		g2104457	666	244	1.00E-68	46	92	hypothetical 44.9 KD protein in ERG7-NMD2 intergenic region ; hypothetical protein YHR075c - yeast (Saccharomyces cerevisiae) ; (U10556) Yhr075cp [Saccharomyces cerevisiae]
20454	ENJU04248	ANI61C1024	72-96	1351-1375	NAP		g416864		103	3.00E-21			Peroxisomal targeting signal receptor (peroxisomal protein PAY32) (peroxin-5) (PTS1 receptor) ; (U28155) Pay32p [Yarrowia lipolytica] ; Pay32 gene [Yarrowia lipolytica]
20455	ENJU04249	ANI61C2921:	38-57	1321-1345	NAP		g731676	349	85	8.00E-16	38	84	Hypothetical 55.6 KD protein C13F4.15C in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (AL031322) putative diphthamide biosynthesis protein [Schizosaccharomyces pombe]
20456	ENJU04250	ANI61C6844:	68-89	1345-1378	NAP		g2501342	1085	409	e-113	54	68	
20457	ENJU04251	ANI61C2078:	44-63	1333-1356	NAP		g1723275	544	189	4.00E-47	35	80	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20458	ENU04252	ANI6IC2445:	48-71	1348-	NAP		g3915154	523	198	6.00E-50	34	76	trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
		1772..411		1367									(AL031532) putative acetylornithine aminotransferase precursor [Schizosaccharomyces pombe]
20459	ENU04253	ANI6IC6612:	56-73	1361-	NAP		g3560246	806	327	9.00E-89	45	90	urea active transporter ; urea transport protein - yeast (Saccharomyces cerevisiae) ; (U11582) No definition line found [Saccharomyces cerevisiae]
		1528..162		1380									hypothetical protein YOL057w - yeast (Saccharomyces cerevisiae) ; (Z74799) ORF YOL057w [Saccharomyces cerevisiae]
20460	ENU04254	ANI6IC6742:	22-47	1325-	NAP		g729376	787	201	1.00E-50	31	61	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
		685..2056		1351									hypothetical 123.7 KD protein C14C4.02 in chromosome I (AL031530) hypothetical protein [Schizosaccharomyces pombe]
20461	ENU04255	ANI6IC211:3	25-46	1336-	NAP		g2132005	271	59	4.00E-11	29	49	(AF014950) chitinase A [Stenotrophomonas maltophilia]
		451..2076		1357									(ACO05724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana] (Z29098) transposase (putative) [Drosophila hydei]
20462	ENU04256	ANI6IC1019	36-56	1347-	NAP		g2132942	525	189	4.00E-47	33	79	
		6:1027..2404		1371									
20463	ENU04257	ANI6IC3867:	24-44	1341-	NAP		g3287945	447	140	1.00E-34	36	22	
		3780..2398		1363									
20464	ENU04258	ANI6IC6734:	26-48	1348-	NAP		g3560227	558	158	2.00E-65	39	83	
		2085..3468		1367									
20465	ENU04259	ANI6IC5197:	22-50	1347-	NAP		g2429326	89	69	1.00E-17	31	38	
		4347..2961		1366									
20466	ENU04260	ANI6IC9460:	22-54	1347-	NAP		g4185142	795	314	9.00E-85	41	37	
		60..1448		1368									
20467	ENU04261	ANI6IC9182:	22-56	1337-	NAP		g436464	179	71	2.00E-11	24	89	
		704..2092		1368									



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20468	ENU04262	ANI61C1082	22-51	1356-1374	NAP		g1351640	1327	354	6.00E-97	55	78	hypothetical 62.7 KD protein C8A4.06 in chromosome I ; hypothetical protein SPAC8A4.06 - fission yeast (Schizosaccharomyces pombe) ; (Z66569) unknown [Schizosaccharomyces pombe] ; (AL032824) putative chromatin binding snw family nuclear pr otein. [Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori]
20469	ENU04263	ANI61C5930:	22-51	1356-1375	NAP		g1805251	1103	150	2.00E-35	40	29	"hypothetical 107.9 KD protein in POL4-SRD1 intergenic region ; probable membrane protein YCCR017c - yeast (Saccharomyces cerevisiae) ; (X59720) YCCR017c, len:953 [Saccharomyces cerevisiae] "
20470	ENU04264	ANI50C2449	48-68	1383-1411	NAP		g140464		195	2.00E-88	48	48	(U78597) kinesin light chain [Plectonema boryanum]
20471	ENU04265	ANI61C3644:	54-73	1396-1418	NAP		g2645229	494	153	2.00E-36	37	57	dynamitin-related protein DNM1 ; dynamitin-related protein DNM1 - yeast (Saccharomyces cerevisiae) ; (Z73106) ORF YLL001w [Saccharomyces cerevisiae] ; (X91488) L1381/DNM1 protein [Saccharomyces cerevisiae] (AF052515) eburicol 14alpha demethylase; CYP51; cytochrome P450 sterol 14-demethylase [Erysiphe graminis f. sp. hordei]
20472	ENU04266	ANI61C1085	68-91	1415-1437	NAP		g1706485	1827	277	1.00E-73	55	52	"putative leucyl--TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS) ; (Z73100) unknown [Schizosaccharomyces pombe] "
20473	ENU04267	ANI61C1059	22-43	1371-1396	NAP		g4049645	1538	484	e-136	64	82	
20474	ENU04268	ANI61C7107:	53-83	1408-1434	NAP		g1711638	1372	128	e-105	51	39	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20475	ENU04269	ANI61C8415:	72-91	1445-1464	NAP		g1211146	602	209	2.00E-67	48	59	geranylgeranyl pyrophosphate synthetase (GGP synthetase) (dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - Neurospora crassa ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]
20476	ENU04270	ANI61C2838:	44-64	1411-1439	NAP		g3182996	539	78	1.00E-30	42	92	translation initiation factor EIF-2B beta subunit (EIF-2B GDP-GTP exchange factor) (S20115) ; (U40756) S20115 [Fugu rubripes]
20477	ENU04271	ANI61C7391:	38-59	1416-1436	NAP		g448379	681	155	5.00E-52	41	82	lignostilbene dioxygenase [Sphingomonas paucimobilis]
20478	ENU04272	ANI61C1048:	44-63	1423-1446	NAP		g422215	825	290	8.00E-94	43	89	alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
20479	ENU04273	ANI61C1029:	52-71	1441-1460	NAP		g1351676	992	330	e-101	52	87	probable peptidyl-prolyl cis-trans isomerase C21E11.05C ; hypothetical protein SPAC21E11.05c - fission yeast (Schizosaccharomyces pombe) ; (Z67999) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
20480	ENU04274	ANI61C8002:	69-88	1463-1485	NAP		g3758890	2466	656	0	65	65	(Y14317) catalase/peroxidase [Streptomyces reticuli]
20481	ENU04275	ANI61C6047:	52-71	1447-1469	NAP		g1709501	414	181	1.00E-44	30	97	putative dolichyl-diphosphooligosaccharide--protein glycosyltransferase alpha subunit precursor (oligosaccharyl transferase alpha subunit) ; (Z69368) unknown [Schizosaccharomyces pombe]
20482	ENU04276	ANI61C1060:	23-42	1417-1441	NAP		g2879870		59	0.000000	06		(AL021816) hypothetical protein [Schizosaccharomyces pombe]
20483	ENU04277	ANI61C5186:	23-51	1420-1443	NAP		g3746666	281	101	3.00E-23	36	98	(AF076848) trihydroxytoluene oxygenase [Burkholderia cepacia]

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20484	ENU04278	ANI61C9834:	72-93	1480-1499	NAP		g2621739	892	308	6.00E-83	46	74	(AE000845) long-chain-fatty-acid-CoA ligase [Methanobacterium thermoautotrophicum]
20485	ENU04279	ANI61C5211:	65-85	1474-1493	NAP		g4007751	485	125	6.00E-28	36	62	(Z99126) putative chromatin assembly factor subunit [Schizosaccharomyces pombe]
20486	ENU04280	ANI61C8457:	48-68	1458-1485	NAP		g731422	724	110	4.00E-30	43	33	hypothetical 70.6 KD protein in HXT8-CAN1 intergenic region ; hypothetical protein YEL065w - yeast (Saccharomyces cerevisiae) ; (U18795) Yel065wp [Saccharomyces cerevisiae]
20487	ENU04281	ANI61C1136	22-41	1440-1459	NAP		g731864	438	154	1.00E-36	29	79	hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YTL120w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae]
20488	ENU04282	ANI61C1015	36-55	1455-1474	NAP		g118507	771	236	2.00E-79	41	96	"aldehyde dehydrogenase, dimeric nadp-prefering (class 3) (tumor-associated aldehyde dehydrogenase) (HTC-ALDH) ; aldehyde dehydrogenase (NADP+) (EC 1.2.1.4) 3, tumor-associated - rat ; (J03637) aldehyde dehydrogenase [Rattus norvegicus] "
20489	ENU04283	ANI61C6871:	22-47	1442-1462	NAP		g112800	524	130	3.00E-55	39	73	4-coumarate--CoA ligase 1 (4CL) ; 4-coumarate--CoA ligase (EC 6.2.1.12) (clone pc4CL-1) - parsley ; (X13324) 4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544) [Petroselinum crispum]
20490	ENU04284	ANI61C3461:	30-49	1442-1476	NAP		g2605934	2542	914	0	98	94	(AF029885) putative homoserine O-acetyltransferase [Emicella nidulans]
20491	ENU04285	ANI61C7333:	71-90	1500-1519	NAP		g493580	1781	287	e-111	58	57	(U09580) beta-D-glucoside glucosyltransferase [Trichoderma reesei]
20492	ENU04286	ANI50C7209	23-47	1453-1472	NAP		g2257513		147	4.00E-52	31	66	(AB004533) hypothetical 105.9 KD protein in AAC3-RFC5 intergenic region. [Schizosaccharomyces pombe]
20493	ENU04287	ANI50C7209	23-47	1453-1472	NAP		g2257513		147	4.00E-52	31	66	(AB004533) hypothetical 105.9 KD protein in AAC3-RFC5 intergenic region. [Schizosaccharomyces pombe]

# Sequence Selection

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20494	ENU04288	ANI61C1125	23-50	1456-1476	NAP		g730942	744	134	1.00E-47			probable thiamin biosynthetic bifunctional enzyme [contains: thiamin-phosphate pyrophosphorylase (TMP pyrophosphorylase) (TMP-PPASE); hydroxyethylthiazole kinase (4-methyl-5-beta-hydroxyethylthiazole kinase) (THZ kinase) ... ; thid4 protein - fission yeast (Schizosaccharomyces pombe) ; (X78824) thid4 [Schizosaccharomyces pombe] ; (Z98977) thiamin biosynthetic bifunctional enzyme [Schizosaccharomyces pombe] hypothetical 70.4 KD protein C4G9.04C in chromosome I ; (Z69727) hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]
20495	ENU04289	ANI61C1139:	22-44	1450-1480	NAP		g1723423	602	92	2.00E-33	27	70	hypothetical 70.4 KD protein C4G9.04C in chromosome I ; (Z69727) hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]
20496	ENU04290	ANI61C1055	27-46	1468-1487	NAP		g2924503	979	306	3.00E-82	44	84	hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]
20497	ENU04291	ANI61C5108:	36-56	1481-1500	NAP		g3417417	357	116	1.00E-34	36	59	hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]
20498	ENU04292	ANI61C901:4	22-41	1477-1496	NAP		g3915154	728	173	2.00E-73	39	84	hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]
20499	ENU04293	ANI61C9197:	25-46	1481-1501	NAP		g1549144		70	3.00E-11			hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]
20500	ENU04294	ANI61C1903:	60-79	1504-1538	NAP		g3929337	271	114	1.00E-24	25	44	hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]
20501	ENU04295	ANI61C8936:	43-63	1502-1522	NAP		g2127851	616	136	6.00E-44	34	82	hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]
20502	ENU04296	ANI61C1103	44-68	1508-1527	NAP		g171850	350	152	5.00E-36	31	65	hypothetical protein [Schizosaccharomyces pombe] [AL022019] glucosyltransferase [Schizosaccharomyces pombe] [AL031261] hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20503	ENU04297	ANI61C3982:	37-57	1500-1525	NAP		g544017	624	268	7.00E-71	35	90	protein kinase CHK1 (checkpoint kinase CHK1) ; protein kinase chk1 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe) ; (L13742) protein kinase [Schizosaccharomyces pombe] ; (U37421) protein kinase [Schizosaccharomyces pombe] ; (AL034564) protein kinase chk1 [Schizosaccharomyces pombe] (AF027687) GTPase activating protein homolog [Cochliobolus heterostrophus] (AL033389) aminotransferase [Schizosaccharomyces pombe] peroxisome biosynthesis protein PAS1 (peroxin-1) ; PAS1 protein - yeast (Pichia pastoris) ; (Z36987) PAS1 [Pichia pastoris]
20504	ENU04298	ANI61C8369:	48-67	1518-1544	NAP		g2598189	899	123	1.00E-39	47	60	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe] (AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe] "(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]" (AB018331) KIAA0788 protein [Homo sapiens] (AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens]
20505	ENU04299	ANI61C2578:	22-57	1507-1526	NAP		g3850081	962	293	6.00E-84	45	97	
20506	ENU04300	ANI61C1144	63-86	1551-1570	NAP		g1172019	1098	345	4.00E-94	50	37	
20507	ENU04301	ANI61C1100	59-77	1561-1580	NAP		g1346422	1720	624	e-178	62	84	
20508	ENU04302	ANI61C1042	64-87	1558-1588	NAP		g3169065	1046	181	e-108	52	44	
20509	ENU04303	ANI61C8276:	40-59	1554-1573	NAP		g1749480	431	154	1.00E-36	61	16	
20510	ENU04304	ANI61C4319:	63-82	1582-1601	NAP		g3882297	2494	460	e-128	48	37	
20511	ENU04305	ANI61C8432:	67-95	1577-1612	NAP		g2801701	575	134	2.00E-48	32	49	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20512	ENU04306	ANT61C3797:	31-54	1549-	NAP		g2132851	204	82	1.00E-14	24	87	probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae]
20513	ENU04307	ANT61C9558:	22-47	1555-	NAP		g1711561	506	199	5.00E-50	30	85	sugar transporter STL1 - yeast (Saccharomyces cerevisiae) ; (U33057) STL1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20514	ENU04308	ANT61C8986:	23-44	1556-	NAP		g4007794	111	69	1.00E-10	28	41	(AL034463) hypothetical protein [Schizosaccharomyces pombe]
20515	ENU04309	ANT61C5894:	26-46	1565-	NAP		g1351684	1064	314	e-109	43	13	hypothetical 420.8 KD protein C1F5.11C in chromosome I ; (Z68136) unknown [Schizosaccharomyces pombe]
20516	ENU04310	ANT61C1677:	40-59	1589-	NAP		g2506776	993	410	e-113	42	79	"translation initiation factor IF-2, mitochondrial precursor (IF-2MT) ; translation initiation factor IF-2, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z74765) ORF YOL023w [Saccharomyces cerevisiae]"
20517	ENU04311	ANT61C8887:	70-90	1642-	NAP		g1723769	177	61	0.000000	27	41	putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
20518	ENU04312	ANT61C1038:	26-45	1608-	NAP		g3560201	423	153	2.00E-36	34	45	(AL031528) pseudouridine synthase [Schizosaccharomyces pombe]
20519	ENU04313	ANT61C9601:	48-70	1642-	NAP		g2408051	1465	271	e-119	45	57	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
		4936..3281		1661									

# Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20520	ENU04314	ANI61C6953:	22-44	1625-1645	NAP		g1175369	331	126	4.00E-28	32	83	hypothetical DNA polymerase beta-like protein C2F7.06C ; hypothetical protein SPAC2F7.06c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown
		1015..2681											[Schizosaccharomyces pombe] (L25310) beta-mannase [Trichoderma reesei]
20521	ENU04315	ANI61C2457:	68-86	1669-1692	NAP		g506848	771	327	2.00E-88	47	66	"5-aminolevulinic acid synthase, mitochondrial precursor (delta-aminolevulinic synthase) (delta-Ala synthetase) ; 5-aminolevulinic synthase (EC 2.3.1.37) precursor - Emerticella nidulans ; (X64170) 5-aminolevulinic acid synthase [Emerticella nidulans]"
		611..2271											hypothetical 76.8 KD protein in chromosome II ; (AF064207) putative histone deacetylase
20522	ENU04316	ANI50C4730	33-52	1641-1660	NAP		g585244		1033	0	99	82	[Schizosaccharomyces pombe] (AL035065) putative urea active transporter [Schizosaccharomyces pombe]
		_1:12..1681											(AL021816) hypothetical protein [Schizosaccharomyces pombe] (AE000703) N-methylhydantoinase A [Aquifex aeolicus]
20523	ENU04317	ANI61C1190:	33-54	1645-1667	NAP		g3023933	1040	73	8.00E-31	42	55	(Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVII] (AF027979) carnitine acetyl transferase [Magnaporthe grisea]
		15284..13607											
20524	ENU04318	ANI61C8043:	70-93	1678-1708	NAP		g4106690	758	220	3.00E-56	41	48	
		4994..3314											
20525	ENU04319	ANI61C7218:	69-93	1699-1722	NAP		g2879870	1686	182	5.00E-45	35	48	
		6352..8047											
20526	ENU04320	ANI61C8090:	40-61	1670-1695	NAP		g2983296	794	309	4.00E-83	36	82	
		3206..1509											
20527	ENU04321	ANI61C1567:	39-70	1682-1701	NAP		g3549879	742	292	4.00E-78	39	91	
		99..1803											
20528	ENU04322	ANI61C3019:	22-55	1663-1688	NAP		g3929362	432	197	3.00E-49	32	72	
		4317..2609											
20529	ENU04323	ANI61C8724:	22-47	1677-1698	NAP		g2688966	537	139	2.00E-55	26	90	
		3953..5671											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20530	ENU04324	ANI61C379:2	38-57	1700-1721	NAP		g2497193	785	170	2.00E-60	36	69	hypothetical 56.2 KD protein in ERG8-UBP8 intergenic region ; probable membrane protein YMR221c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae]
20531	ENU04325	ANI61C1536: 15..1749	35-55	1708-1727	NAP		g3650401	278	137	2.00E-31	27	52	(AL031739) zinc finger protein [Schizosaccharomyces pombe]
20532	ENU04326	ANI61C8724: 22-51	3923..5671	1707-1728	NAP		g2688966	537	139	2.00E-55	26	90	(AF027979) carnitine acetyl transferase [Magnaporthe grisea]
20533	ENU04327	ANI61C1070: 63-83	530..2304	1776-1795	NAP		g4033486	274	82	5.00E-23	31	40	putative tartrate transporter ; (U25634) putative tartrate transporter; inducible by tartrate; Method: conceptual translation supplied by author. [Agrobacterium vitis] ; ttuB gene [Agrobacterium vitis]
20534	ENU04328	ANI61C8868: 22-52	6159..4379	1725-1756	NAP		g2144167	1713	362	e-143	55	71	beta-glucosidase (EC 3.2.1.21) - yeast (Candida molischiana) ; (U16259) beta-glucosidase [Pichia capsulata]
20535	ENU04329	ANI61C9692: 58-77	4164..2329	1836-1855	NAP		g3924850	252	109	8.00E-23	32	27	"(Z81586) predicted using GeneFinder; similar to Alcohol/other dehydrogenases, short chain type [Caenorhabditis elegans]" (U84894) 239AB [Homo sapiens]
20536	ENU04330	ANI61C7957: 67-87	4466..2619	1853-1872	NAP		g4502497	149	69	2.00E-19	32	59	regulatory protein GAL4 ; regulatory protein GAL4 - yeast (Saccharomyces cerevisiae) ; (K01486) GAL4 protein [Saccharomyces cerevisiae] ; (Z67751) GAL4 [Saccharomyces cerevisiae] ; (Z73604) ORF YPL248c [Saccharomyces cerevisiae]
20537	ENU04331	ANI61C791: 23-46	716..2576	1819-1841	NAP		g1169823		61	0.000000			(U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [Homo sapiens] ; (AF016708) E6-AP ubiquitin-protein ligase [Homo sapiens]
20538	ENU04332	ANI61C1004	70-92	1867-1889	NAP		g1872514	513	120	3.00E-26	37	33	



# Database Hit

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20539	ENU04333	ANI61C7032:	22-54	1823-	NAP		g466152	446	173	9.00E-48	35	44	hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEE5N66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
		1524..3386		1842									
20540	ENU04334	ANI61C7032:	22-54	1823-	NAP		g466152	446	173	9.00E-48	35	44	hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEE5N66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
		1524..3386		1842									
20541	ENU04335	ANI61C6610:	28-47	1847-	NAP		g3929362	555	147	2.00E-70	36	98	pisatin demethylase [cytochrome P450 57A1] ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mp VII]
		3603..3426		1880									
20542	ENU04336	ANI61C9614:	68-86	1915-	NAP		g3184088	392	160	8.00E-44	29	76	(AL023781) hypothetical protein [Schizosaccharomyces pombe]
		47..1956		1934									
20543	ENU04337	ANI61C7030:	22-48	1873-	NAP		g2626826		98	3.00E-19			"(D83967) Yfkn [Bacillus subtilis] ; (Z99108) similar to 2'-3'-cyclic-nucleotide 2'-phosphodiesterase [Bacillus subtilis] "
		3655..1743		1892									
20544	ENU04338	ANI61C7115:	71-90	1931-	NAP		g2133268	97	85	2.00E-15	25	52	DNA-binding protein amda - Emericella nidulans ; (L28810) regulatory protein [Emericella nidulans]
		130..2055		1954									
20545	ENU04339	ANI61C3433:	22-41	1890-	NAP		g3925758	182	84	3.00E-15	26	76	(AL034352) hypothetical C2H2-type zinc-finger protein
		1237..3168		1909									[Schizosaccharomyces pombe]
20546	ENU04340	ANI61C7725:	22-51	1900-	NAP		g2688313		59	0.000000			"(AE001146) sensory transduction histidine kinase, putative [Borrelia burgdorferi] "
		2046..107		1919									(AB023911) chitin synthase [Emericella nidulans]
20547	ENU04341	ANI61C6803:	43-70	1932-	NAP		g4519181	3365	1236	0	99	63	(U68040) polyketide synthase [Cochliobolus heterostrophus]
		6..1995		1960									
20548	ENU04342	ANI61C6259:	51-72	1955-	NAP		g1546072	1439	149	7.00E-35	30	22	
		5140..7105		1974									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20549	ENJU04343	ANI61C2341:	54-74	1979-	NAP		g2104457	246	104	8.00E-29	31	45	(Z95397) unknown
		2086..99		1999									[Schizosaccharomyces pombe]
20550	ENJU04344	ANI61C9697:	45-67	1967-	NAP		g399198	603	183	8.00E-73	38	35	cell division control protein 25 ; SKCDC25 protein - yeast (Saccharomyces kluyveri) (fragment) ; (M82964) CDC25 [Saccharomyces kluyveri]
		3156..1168		1991									trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (U78320) chitinase [Entamoeba invadens]
20551	ENJU04345	ANI61C4603:	24-44	1965-	NAP		g3915154	353	83	2.00E-24	33	91	(Z95620) n-acetylglucosaminyl-phosphatidylinositol [Schizosaccharomyces pombe]
		2740..737		1985									"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613) dioxygenase [Escherichia coli] ; (U73857) dioxygenase [Escherichia coli] ; (AE00143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli] "
20552	ENJU04346	ANI61C1932:	35-54	1983-	NAP		g1685364	337	113	1.00E-41	33	44	auxin-induced protein PCNT115 ; auxin-induced protein - common tobacco ; (X56267) auxin-induced protein [Nicotiana tabacum] (AL049628) putative exporter [Streptomyces coelicolor]
		1552..3563		2004									"ferric reductase transmembrane component 2 precursor - yeast (Saccharomyces cerevisiae) ; (X75950) ORF5, F711 [Saccharomyces cerevisiae] ; (Z28220) ORF YKL220c [Saccharomyces cerevisiae] ; ORF 5 [Saccharomyces cerevisiae] "
20553	ENJU04347	ANI61C9831:	41-60	2004-	NAP		g2117303	1418	346	e-155	66	90	
		2452..4478		2023									
20554	ENJU04348	ANI61C6656:	54-73	2018-	NAP		g2506921	161	55	0.000001	32	43	
		3133..1105		2040									
20555	ENJU04349	ANI61C5227:	22-52	1984-	NAP		g728744		53	0.000007			
		3425..3954		2009									
20556	ENJU04350	ANI61C1039	56-77	2022-	NAP		g4585598		65	2.00E-35			
		0:4698..2668		2043									
20557	ENJU04351	ANI61C1023	45-64	2036-	NAP		g549758	157	119	6.00E-26	28	36	
		4:2074..22		2055									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20558	ENU04352	ANI61C9133:	54-73	2053-2073	NAP		g3650375	586	254	2.00E-66	37	55	(AL031740) putative mitochondrial translation system component [Schizosaccharomyces pombe]
		393..2453											
20559	ENU04353	ANI61C2779:	68-89	2079-2099	NAP		g4528		360	0	58	88	(X54316) GTP-binding protein [Saccharomyces cerevisiae]
		2459..2351											
20560	ENU04354	ANI61C1106	40-59	2054-2073	NAP		g3182972	794	217	e-127	47	68	probable coatomer gamma subunit (gamma-coat protein) (gamma-COP) ; (Z95396) putative coatomer gamma subunit [Schizosaccharomyces pombe]
		7:3274..1719											
20561	ENU04355	ANI61C1103	26-49	2041-2063	NAP		g2645229	442	195	8.00E-49	36	39	(U78597) kinesin light chain [Plectonema boryanum]
		1:2700..5209											
20562	ENU04356	ANI61C9409:	23-45	2031-2060	NAP		g131782	956	239	9.00E-89	32	52	DNA repair protein RAD50 (153 KID protein) ; RAD50 protein - yeast (Saccharomyces cerevisiae) ; (X14814) 153 KID protein (AA 1 - 1312) [Saccharomyces cerevisiae] ; (X96722) ORF N0872 [Saccharomyces cerevisiae] ; (Z71526) ORF YNL250w [Saccharomyces cerevisiae] (Z83828) AmMst-1 [Amanita muscaria]
		480..2560											
20563	ENU04357	ANI61C439:5	70-89	2092-2112	NAP		g2258125	520	209	1.00E-59	33	95	(AL021746) phosphatidylserine decarboxylase [Schizosaccharomyces pombe]
		373..5887											
20564	ENU04358	ANI61C8264:	46-67	2074-2109	NAP		g2842521	730	322	6.00E-87	50	100	trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
		1449..3554											
20565	ENU04359	ANI61C4603:	26-61	2108-2128	NAP		g3915154	353	83	2.00E-24	33	87	(AL021816) hypothetical protein [Schizosaccharomyces pombe]
		2881..737											
20566	ENU04360	ANI61C1060:	23-42	2143-2162	NAP		g2879870		59	0.000000	09		SpoC1-C1C protein - Emericella nidulans ; (M83571) SpoC1-C1C [Emericella nidulans]
		2378..196											
20567	ENU04361	ANI61C9302:	68-92	2183-2212	NAP		g283343	304	80	1.00E-17	58	16	
		2590..1817											

# Database

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20568	ENU04362	ANI61C1076	61-80	2318-	NAP		g1174987	1186	166	3.00E-61	45	20	vacuolar protein sorting-associated protein VPS35 ; vacuolar protein-sorting protein VPS35 - yeast (Saccharomyces cerevisiae) ; (Z49429)
		9:1972..4306		2350									ORF YJL154c [Saccharomyces cerevisiae]
20569	ENU04363	ANI61C216:3	35-55	2322-	NAP		g1352937	48	45	0.002	25	28	hypothetical 39.9 KD protein in HOM6-PMT4 intergenic region ; probable membrane protein YJIR141w - yeast (Saccharomyces cerevisiae) ; (Z49641) ORF YJIR141w [Saccharomyces cerevisiae]
		135..785		2343									(AL031579) conserved hypothetical protein [Schizosaccharomyces pombe]
20570	ENU04364	ANI61C5788:	49-68	2330-	NAP		g3618207	721	320	3.00E-86	33	88	DNA repair protein RAD9 ; rad9 protein - fission yeast (Schizosaccharomyces pombe) ; rad9 protein - fission yeast (Schizosaccharomyces pombe) ; rad9 protein - fission yeast (Schizosaccharomyces pombe) ; (X58231) rad9 protein [Schizosaccharomyces pombe] ; (X64648) rad9 [Schizosaccharomyces pombe] ; (X77276) rad9 [Schizosaccharomyces pombe]
		2376..22		2361									
20571	ENU04365	ANI61C1001	66-87	2359-	NAP		g131816	189	64	6.00E-16			
		4:243..2606		2385									
20572	ENU04366	ANI61C9256:	60-80	2362-	NAP		g3915154		75	2.00E-31			
		4444..4770		2381									
20573	ENU04367	ANI61C4216:	58-77	2391-	NAP		g3024061	3393	545	0	85	97	6-phosphofructokinase (phosphofructokinase) (phosphohexokinase) ; (Z79690) phosphofructokinase [Aspergillus niger]
		3367..970		2410									
20574	ENU04368	ANI61C1048	47-72	2372-	NAP		g1175379	541	111	2.00E-44	44	27	hypothetical 88.2 KD protein C2F7.18C in chromosome I (U13644) F56D2.5 gene product [Caenorhabditis elegans]
		2:4278..4010		2403									
20575	ENU04369	ANI61C3090:	22-48	2413-	NAP		g1945502	98	82	2.00E-14	34	6	
		650..3116		2445									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20576	ENU04370	ANI61C9380:	70-89	2490-2510	NAP		g1175371	138	80	5.00E-14	31	22	hypothetical 71.9 KD protein C2F7.08C in chromosome I; hypothetical protein SPAC2F7.08c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe]
20577	ENU04371	ANI61C9639:	44-75	2490-2516	NAP		g731864	383	176	4.00E-43	25	65	hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YTL120w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae]
20578	ENU04372	ANI61C3273:	34-53	2497-2517	NAP		g2465152	240	95	2.00E-18	40	13	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
20579	ENU04373	ANI61C450:2	43-64	2552-2571	NAP		g3930517	1333	455	e-127	40	86	(AF059906) ubiquitin fusion degradation protein-2 [Schizosaccharomyces pombe]
20580	ENU04374	ANI61C9792:	24-45	2547-2566	NAP		g730221	3335	788	0	67	81	[Schizosaccharomyces pombe] 2-oxoglutarate dehydrogenase E1 component precursor (alpha-ketoglutarate dehydrogenase) ; oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) precursor - yeast (Saccharomyces cerevisiae) ; (Z46833) 2-oxoglutarate dehydrogenase E1 component [Saccharomyces cerevisiae]
20581	ENU04375	ANI61C1144	64-85	2639-2658	NAP		g549038	133	71	1.00E-13			"transcription initiation factor III, alpha subunit (TFIIIE-alpha) (transcription factor A large subunit) (factor A 66 KD subunit) ; transcription initiation factor III chain TFA1 - yeast (Saccharomyces cerevisiae) ; (Z28028) ORF YKL028w [Saccharomyces cerevisiae] ; (U12825) transcription factor TFIIIE, large subunit [Saccharomyces cerevisiae] " (AB018297) KIAA0754 protein [Homo sapiens]
20582	ENU04376	ANI61C8159:	70-89	2659-2682	NAP		g3882229	85	46	0.001	26	21	

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20583	ENU04377	ANI61C4130:	22-41	2608-	NAP		g3005592	548	166	7.00E-40	34	27	(AF051911) telomerase reverse transcriptase; mTERT [Mus musculus]
		3177..520		2637									; (AF073311) telomerase catalytic subunit [Mus musculus]
20584	ENU04378	ANI61C9698:	56-75	2651-	NAP		g1723845	377	171	3.00E-41	34	45	putative ATP-dependent RNA helicase YGL064C ; hypothetical protein YGL064c - yeast (Saccharomyces cerevisiae) ; (Z72586) ORF YGL064c [Saccharomyces cerevisiae]
		3605..2478		2671									(AL023592) putative helicase [Schizosaccharomyces pombe]
20585	ENU04379	ANI61C1132:	72-94	2676-	NAP		g3136048	2024	362	5.00E-99	50	64	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 ; HIP116 protein - human ; (L34673) ATPase [Homo sapiens] "
		155..2820		2695									"(AC006068) putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana] "
20586	ENU04380	ANI61C8590:	22-55	2689-	NAP		g4507071	509	229	5.00E-59	33	43	"chloride channel 3 ; chloride channel protein 3, long form - human ; (X78520) chloride channel 3 [Homo sapiens] "
		1848..4579		2711									(AL023290) putative ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20587	ENU04381	ANI61C8661:	71-90	2828-	NAP		g4263786	850	225	e-100	37	86	(U65488) fumocumarin-inducible cytochrome P450 [Papilio polyxenes]
		50..2869		2848									(X94399) cAMP-dependent protein kinase catalytic subunit [Aspergillus niger]
20588	ENU04382	ANI61C919:	51-70	2813-	NAP		g4502869	1191	176	e-105	43	64	(L42454) EF-hand protein [Schizosaccharomyces pombe]
		554..3384		2839									(AL023328) hypothetical protein [Schizosaccharomyces pombe]
20589	ENU04383	ANI61C9577:	38-57	2971-	NAP		g3116148	1166	196	e-133	37	62	gamma-adaplin - smut fungus (Ustilago maydis) [Ustilago maydis]
		3062..68		2990									(Z95334) putative helicase [Schizosaccharomyces pombe]
20590	ENU04384	ANI61C3260:	26-46	631-655	NAP		g1513174	66	87	9.00E-17	22	43	
		1407..2082											
20591	ENU04385	ANI61C1511:			NAP		g2113796	807	196	1.00E-57	59	54	
		378..1307											
20592	ENU04386	ANI61C6899:	222-240	531-552	NAP		g832882	351	116	1.00E-25	57	100	
		134..706											
20593	ENU04387	ANI61C9048:			NAP		g3116134	882	219	2.00E-56	42	10	
		1..1497											
20594	ENU04388	ANI61C2436:	35-54	632-651	NAP		g1078673	545	83	3.00E-34	60	22	
		942..1651											
20595	ENU04389	ANI61C4421:	34-60	539-561	NAP		g2094863	306	171	3.00E-42	43	19	
		583..1											

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20596	ENU04390	ANI61C291:7	42-61	578-603	NAP		g2501165	134	79	2.00E-14	32	28	hypothetical 59.6 KD protein in DSK2-CAT8 intergenic region [Saccharomyces cerevisiae]
		480..6857											sterninatocystin 7-O-methyltransferase precursor [Aspergillus parasiticus]
20597	ENU04391	ANI61C1032	70-88	516-536	NAP		g2498702	86	70	1.00E-11	37	31	(Z83319) similar to ABC transporters; cDNA EST EMBL:D67223 comes from this gene; cDNA EST EMBL:ID67486 comes from this gene; cDNA EST yk385d1.5 comes from this gene; cDNA EST yk398a5.5 comes from this gene; cDNA EST yk398a5.3 co...
		0:4040..4598											[Schizosaccharomyces pombe]
20598	ENU04392	ANI61C1073:	71-90	579-598	NAP		g3879319	431	177	5.00E-44	44	29	aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) [Saccharomyces cerevisiae]"
		1..662											[Saccharomyces cerevisiae]"
20599	ENU04393	ANI61C5507:	122-139	442-461	NAP		g2408049	136	46	0.0001	29	8	elongation factor 1-alpha (EF-1-alpha) (elongation factor TU) (EF-TU) [Sulfolobus solfataricus]
		3945..3369											(AL023288) hypothetical dolichyl-phosphate beta-glucosyltransferase protein [Schizosaccharomyces pombe]
20600	ENU04394	ANI61C3342:	114-133	372-391	NAP		g731024	295	145	2.00E-34	46	38	hypothetical 23.9 KD protein in THI5-AGP3 intergenic region [Saccharomyces cerevisiae]
		1..470											(U30376) Lipomyces kononenkoae subsp. spenceriartinsiae alpha-amyrase [Lipomyces kononenkoae]
20601	ENU04395	ANI61C8781:	23-43	728-747	NAP		g729397	616	260	8.00E-69	41	64	hypothetical 85.4 KD protein C14C4.11 in chromosome I [Schizosaccharomyces pombe]
		1035..1											[Schizosaccharomyces pombe]
20602	ENU04396	ANI61C5009:	114-133	331-358	NAP		g3116140	276	124	2.00E-28	48	38	(L41834) nuclear protein [Ensis minor]
		1..392											hypothetical 54.9 KD protein in CBR5-NOT3 intergenic region [Saccharomyces cerevisiae]
20603	ENU04397	ANI61S1051:	22-44	261-280	NAP		g1175960	223	97	9.00E-20	53	43	
		298..604											
20604	ENU04398	ANI61C8380:	22-47	394-414	NAP		g1173537	285	140	5.00E-33	42	28	
		2017..1526											
20605	ENU04399	ANI61C5287:	59-86	454-479	NAP		g3183344	276	105	2.00E-22	37	22	
		84..543											
20606	ENU04400	ANI61S1675:			NAP		g786117	180	51	0.00001	24	55	
		1..835											
20607	ENU04401	ANI61C6597:	52-71	805-829	NAP		g731799	405	129	2.00E-29	38	48	
		10548..9385											

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20608	ENU04402	ANT61C9383:	97-116	709-730	NAP		g586521	303	143	2.00E-33	36	29	hypothetical 86.4 KD protein in PHOS-VPS15 intergenic region
		6240..7174											[Saccharomyces cerevisiae]
20609	ENU04403	ANT61C1091	24-51	801-828	NAP		g3261632	498	116	3.00E-28	46	42	(Z79700) accD2 [Mycobacterium tuberculosis]
		2:1357..1											"phosphoenolpyruvate synthase (pyruvate,water dikinase) (PEP synthase) [Synecocystis sp.]"
20610	ENU04404	ANT61C4623:	27-46	660-679	NAP		g2499460	1545	267	9.00E-76	54	33	(AB014886) typeII DNA topoisomerase [Emericella nidulans]
		1815..1											sodium transport ATPase 5 [Saccharomyces cerevisiae]
20611	ENU04405	ANT61C1654:	25-52	726-744	NAP		g3172113	1585	522	e-148	97	16	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]
		1010..1											(AL008967) hypothetical protein Rv2750 [Mycobacterium tuberculosis]
20612	ENU04406	ANT61C1070	35-54	790-811	NAP		g3121791	701	162	2.00E-63	53	23	cutinase transcription factor 1 beta [Fusarium solani f. sp. pisi]
20613	ENU04407	ANT61S1450:			NAP		g3037018	302			36	97	(AL031907) putative cystine-rich transcriptional regulator
		850..174											[Schizosaccharomyces pombe]
20614	ENU04408	ANT61C5938:			NAP		g2624272	56	69	3.00E-11	27	89	salivary proline-rich protein PO (allele M) (contains: peptide P-D) [Homo sapiens]
		264..1155											"neutral trehalase (alpha,alpha-trehalase) (alpha,alpha-trehalose glucosylhydrolase) [Emericella nidulans]"
20615	ENU04409	ANT61C1002	22-48	808-829	NAP		g1706177	754	111	6.00E-24	29	27	abaA protein - Emericella nidulans [Emericella nidulans]
20616	ENU04410	ANT61C3739:	29-48	756-781	NAP		g3766365	756	155	3.00E-37	39	23	hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
		1..1223											(AF036707) RAD6 [Candida albicans]
20617	ENU04411	ANT61S974:9			NAP		g1709793	151	60	0.000000	29	69	hypothetical 58.1 KD protein in PET117-CEM1 intergenic region [Saccharomyces cerevisiae]
		2..551											41-2 protein antigen precursor [Plasmodium falciparum]
20618	ENU04412	ANT61C8633:	25-52	802-829	NAP		g3929388	3438	221	e-140	99	35	
		1..2156											
20619	ENU04413	ANT61C7207:			NAP		g482275	661	266	5.00E-71	79	21	
		2146..1628											
20620	ENU04414	ANT61C3378:	28-49	723-749	NAP		g731689	578	164	7.00E-40	30	7	
		1304..1											
20621	ENU04415	ANT61C1036	39-58	390-413	NAP		g3273562	425	145	3.00E-34	81	59	
		0:514..1											
20622	ENU04416	ANT61C7198:			NAP		g1723597	318	136	1.00E-31	42	32	
		1588..1082											
20623	ENU04417	ANT61C7472:	26-53	310-329	NAP		g112925	127	71	7.00E-12	30	88	
		1962..1577											



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20624	ENU04418	ANI61S4602:	90-108	530-547	NAP		g465511	359	136	2.00E-31	41	33	hypothetical 73.8 KD protein in SAS3-SEC17 intergenic region [Saccharomyces cerevisiae]
		665..1											allantoinease [Saccharomyces cerevisiae]
20625	ENU04419	ANI61C3410:	110-137	804-827	NAP		g728828	496	219	3.00E-56	52	49	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
		2232..1354					g2408036	291	117	7.00E-26	35	50	carboxylesterase (EC 3.1.1.1) - Pseudomonas sp. (strain KWI-56)
20626	ENU04420	ANI61C2027:	171-190	347-366	NAP		g423793	75	58	0.000000	35	45	[Pseudomonas sp.]
		1..578								05			(X97346) FCYX [Saccharomyces cerevisiae]
20627	ENU04421	ANI61C7678:	22-47	429-448	NAP		g1321944	224	54	0.000001	26	47	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
		7628..7174					g4218005	263	46	0.0002	27	36	"(AC004849) similar to several hypothetical proteins: U70849 (PID:g1572765), U00043 (PID:g470341), Z50070 (PID:g899462), AL033127 (PID:g3821335), and P40034 (PID:g731464) [Homo sapiens]" (AL034490) similar to yeast ngg1-interacting factor 3 [Schizosaccharomyces pombe]
20628	ENU04422	ANI61C5312:	22-48	804-823	NAP		g3980554	227	110	6.00E-24	34	63	glucosaminyl transferase 2) [Emeticella nidulans]
		1..1093											NADH-cytochrome B5 reductase precursor (P34/P32) [Saccharomyces cerevisiae]
20629	ENU04423	ANI61S2268:			NAP								(AF056182) G-protein beta subunit [Emeticella nidulans]
		1..784											rad4+/cut5+ product - fission yeast (Schizosaccharomyces pombe) []
20630	ENU04424	ANI61S3044:	98-117	412-435	NAP								hypothetical protein YDL087c - yeast (Saccharomyces cerevisiae)
		1..528											[Saccharomyces cerevisiae]
20631	ENU04425	ANI61C3082:	22-46	459-477	NAP		g4008560	215	88	5.00E-17	57	45	
		366..833					g1705828	2423	530	e-150	99	26	
20632	ENU04426	ANI61C5001:	90-109	717-736	NAP								
		1459..1					g549725	520	189	2.00E-47			
20633	ENU04427	ANI61C8508:	23-50	804-829	NAP								
		1020..2041					g3493539	1740	431	e-120	99	69	
20634	ENU04428	ANI61C1064	22-41	805-829	NAP		g476807	365	87	8.00E-34	38	51	
		4:1..1254					g2131329	388	87	8.00E-35	32	98	
20635	ENU04429	ANI61C7169:	43-62	626-653	NAP								
		755..1											
20636	ENU04430	ANI61C7108:	29-56	806-828	NAP								
		2551..3462											

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20637	ENU04431	ANT6IC1554: 1480..1			NAP		g1351183	806	136	2.00E-44	43	38	"tyrosyl-TRNA synthetase, mitochondrial precursor (tyrosine--TRNA ligase) (TYRRS) [Neurospora crassa]"
20638	ENU04432	ANT6IC9626: 22-41 2931..4989		792-814	NAP		g3702631	2007	406	e-113	68	36	(AL031824) protein transport protein sec23 homolog [Schizosaccharomyces pombe]
20639	ENU04433	ANT6IS953:6 14..1	182-204	567-593	NAP		g3647341	556	237	6.00E-62	58	21	(AL031644) RAD16 nucleotide excision repair protein homolog [Schizosaccharomyces pombe]
20640	ENU04434	ANT6IC2676: 22-47 1204..1	712-739		NAP		g2654106	1074	201	4.00E-51	74	39	(AF034260) protein kinase NRC-2 [Neurospora crassa]
20641	ENU04435	ANT6IC4833: 1060..1			NAP		g4027860	1541	242	e-125	92	38	(U47540) Tama [Emeticella nidulans]
20642	ENU04436	ANT6IC5942: 38-57 1632..399	778-797		NAP		g3183172	874	124	2.00E-52	41	56	"probable threonyl-TRNA synthetase, mitochondrial precursor (threonine--TRNA ligase) (THRRS) [Schizosaccharomyces pombe]"
20643	ENU04437	ANT6IC528:6 22-49 252..8036	809-828		NAP		g2131739	572	107	1.00E-22	38	36	hypothetical protein YLR002c - yeast [Saccharomyces cerevisiae]
20644	ENU04438	ANT6IC7264: 22-43 2976..1666	802-829		NAP		g3318897	725	158	4.00E-38	39	36	[Saccharomyces cerevisiae]
20645	ENU04439	ANT6IC1397: 80-100 901..1	719-738		NAP		g3834343	1429	468	e-131	95	17	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ["] (X05204) atom polypeptide [Emeticella nidulans]
20646	ENU04440	ANT6IC5143: 44-70 718..166	513-532		NAP		g1620896	620	251	2.00E-66	76	59	(D87956) protein involved in sexual development [Schizosaccharomyces pombe]
20647	ENU04441	ANT6IC3620: 144-164 1549..1228	280-301		NAP		g4507229	238	104	2.00E-22	44	20	Succinic semialdehyde dehydrogenase [Homo sapiens]
20648	ENU04442	ANT6IC6334: 22-44 4081..4982	722-749		NAP		g448109	216	101	7.00E-21	34	51	6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
20649	ENU04443	ANT6IC3534: 27-46 3454..1931	799-826		NAP		g3722	498	69	3.00E-19	31	39	(X52633) GAP1 protein (AA 1-601) [Saccharomyces cerevisiae]
20650	ENU04444	ANT6IC9310: 22-47 1086..2744	726-749		NAP		g114988	2453	480	e-135	95	22	kinesin-like protein BIMC [Emeticella nidulans]
20651	ENU04445	ANT6IC5922: 1467..1			NAP		g3183348	408	136	2.00E-31	35	52	hypothetical 60.1 KD protein C23C11.06C in chromosome I [Schizosaccharomyces pombe]

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20652	ENU04446	AN161C6611:	121-140	409-428	NAP		g3451071	247	80	2.00E-16	45	20	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]
20653	ENU04447	AN161C6297:	26-49	711-730	NAP		g3451463	344	113	2.00E-32	34	57	(AL031349) hypothetical protein [Schizosaccharomyces pombe]
20654	ENU04448	AN161C1107	185-204	617-641	NAP		g3914212	470	188	5.00E-47	49	19	5-oxoprolinase (5-oxo-L-prolinase) (pyroglutaminase) (5-opase) [Rattus norvegicus]
20655	ENU04449	AN161C181:2	22-49	705-730	NAP		g1805251	198	104	1.00E-21	27	41	(U58946) transposase [Aspergillus awamori]
20656	ENU04450	AN161C5884:			NAP		g340613	183	38	0.092	27	78	(L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]
20657	ENU04451	AN161C4283:	27-54	450-469	NAP		g2330797	199	71	1.00E-17	37	62	(Z98601) zinc finger protein [Schizosaccharomyces pombe]
20658	ENU04452	AN161C1138:	22-49	804-829	NAP		g3882339	82	139	2.00E-32	33	18	(AB018352) KIAA0809 protein [Homo sapiens]
20659	ENU04453	AN161S3751:	36-59	467-486	NAP		g4454043	916	333	7.00E-91	97	28	(AL035394) putative receptor kinase [Arabidopsis thaliana]
20660	ENU04454	AN161C2071:	106-127	671-690	NAP		g731805	463	192	2.00E-48	45	26	SYG1 protein [Saccharomyces cerevisiae]
20661	ENU04455	AN161C2856:	118-138	628-655	NAP		g1806628	488	115	1.00E-51	49	50	(U79250) glycerol-3-phosphate dehydrogenase [Homo sapiens]
20662	ENU04456	AN161C6770:	102-122	392-413	NAP		g1708835	188	71	3.00E-12	40	48	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilis]"
20663	ENU04457	AN161C2510:	43-62	416-437	NAP		g2313520	165	85	5.00E-16	30	45	(AE000557) cyclopropane fatty acid synthase (cfa) [Helicobacter pylori 26695]
20664	ENU04458	AN161C910:2			NAP		g2330815	137	73	7.00E-13	41	36	(Z98602) purine nucleotide binding protein fe5 [Schizosaccharomyces pombe]
20665	ENU04459	AN161C8051:	44-63	803-826	NAP		g586312	641	80	3.00E-21	33	43	hypothetical 63.4 KD protein in SMY2-RPS101 intergenic region [Saccharomyces cerevisiae]

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20666	ENU04460	ANI61C2836: 653..1378			NAP		g1175939	331	86	1.00E-32	40	58	hypothetical 41.9 KD protein in HAC1-CAK1 intergenic region [Saccharomyces cerevisiae]
20667	ENU04461	ANI61C2759: 1..716			NAP		g2492763	395	141	8.00E-38	48	67	hypothetical oxidoreductase in MRP144-MTF1 intergenic region [Saccharomyces cerevisiae]
20668	ENU04462	ANI61C1083 5:3653..3984	30-49	282-301	NAP		g1483145	93	36	0.002	29	97	(D64008) Cytochrome b5 [Ascaris suum]
20669	ENU04463	ANI61C1020 8:1..3278	29-56	804-829	NAP		g1723687	754	129	2.00E-29			hypothetical 140.5 KD protein in CTT1-PRP31 intergenic region [Saccharomyces cerevisiae]
20670	ENU04464	ANI61C4296: 1465..856	203-222	465-484	NAP		g3242972	416	109	1.00E-23	54	25	(AF069523) heat shock protein Hsp88 [Neurospora crassa]
20671	ENU04465	ANI61C6540: 1520..2718	45-64	778-797	NAP		g3218400	425	145	2.00E-40	38	75	(AL023860) ser-thr protein kinase [Schizosaccharomyces pombe]
20672	ENU04466	ANI61C4932: 720..3626	22-46	801-828	NAP		g731882	293	101	9.00E-21			hypothetical 195.1 KD protein in DNA43-UBI1 intergenic region [Saccharomyces cerevisiae]
20673	ENU04467	ANI61C1926: 1987..1581	105-132	366-386	NAP		g3687497	168	66	2.00E-12	44	67	(AL031788) putative mitochondrial inner membrane protease subunit 2 [Schizosaccharomyces pombe]
20674	ENU04468	ANI61C8052: 755..2503	22-48	720-744	NAP		g4502323	585	168	6.00E-41	40	17	"ATPase, Cu++ transporting, beta polypeptide (Wilson disease) [Homo sapiens]"
20675	ENU04469	ANI61S1734: 1..854			NAP		g100687	405	37	0.16	41	74	hydroxyproline-rich glycoprotein - rice [Oryza sativa]
20676	ENU04470	ANI61C724:2 882..1	22-45	807-826	NAP		g2493965	2089	317	5.00E-86	58	20	xanthine dehydrogenase (purine hydroxylase J) [Emicella nidulans]
20677	ENU04471	ANI61C1117 1:1..795	110-129	683-706	NAP		g2668553	311	89	5.00E-26	33	18	(U62929) multidrug resistance protein 1 [Filobasidiella neoformans]
20678	ENU04472	ANI61C1823: 1..1738	22-48	748-767	NAP		g2342601	738	137	9.00E-32	29	5	(X89442) peptide synthetase [Metarhizium anisopliae]
20679	ENU04473	ANI61C5324: 1589..1	43-62	722-741	NAP		g3043376	1653	240	e-100	75	42	(AJ005258) amyR [Aspergillus oryzae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20680	ENJU04474	ANI61C6771: 1090..1	24-44	675-697	NAP		g3879362	341	116	1.00E-25	33	52	"(Z81113) similar to DnaI, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from this gene; cDNA EST yk447h4.5 comes from this gene; cDNA EST yk474e4.5 c... ["]
20681	ENJU04475	ANI61C1089 9:586..1	215-234	464-484	NAP		g3139137	800	308	7.00E-85	84	22	(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
20682	ENJU04476	ANI61S4441: 554..1			NAP		g4835793	148	77	8.00E-14			"(AC007296) Similar to gb U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF00076 RNA recognition motif domains. ESTs gb T44278, gb K65195, gb N65904, gb H37499, gb R90487, gb N95952, gb T4427... ["]
20683	ENJU04477	ANI61C9025: 1337..1	37-56	792-812	NAP		g3540219	1169	130	6.00E-59	49	22	(D87686) KIAA0017 protein [Homo sapiens]
20684	ENJU04478	ANI61S1996: 1..775			NAP		g2135765	221	44	0.00002	35	8	"mucin 2 precursor, intestinal - human (fragments) ["]
20685	ENJU04479	ANI61C2726: 601..1	102-121	466-486	NAP		g1711467	277	122	2.00E-27	34	43	dibenzothioephene desulfurization enzyme A [Rhodococcus sp.] (U97002) similar to acyl-CoA
20686	ENJU04480	ANI61S2694: 450..1	38-65	403-429	NAP		g1938424	285	122	1.00E-27	51	13	dehydrogenases and epoxide hydrolases [Caenorhabditis elegans] (AL008967) lrp1 [Mycobacterium tuberculosis]
20687	ENJU04481	ANI61C7219: 2951..2457			NAP		g2624312	413	105	1.00E-40	53	40	(AF131877) amino-deoxyarabinheptulosonate-7-phosphate synthase [Streptomyces collinus]
20688	ENJU04482	ANI61S4608: 431..1	209-228	362-386	NAP		g4884833	322	103	7.00E-27			UDP-glucose dehydrogenase [Homo sapiens]
20689	ENJU04483	ANI61C9107: 8199..9462	22-45	807-829	NAP		g4507813	185	82	7.00E-15			probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
20690	ENJU04484	ANI61C4377: 1961..1330	30-51	583-610	NAP		g2132651	309	84	2.00E-26	32	35	(U01849) ORF2 [Trypanosoma brucei]
20691	ENJU04485	ANI61S591:3 41..767			NAP		g501027	147	31	4.6	33	99	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20692	ENU04486	ANI61C7389:	22-45	636-663	NAP		g2133317	1829	407	e-113	67	38	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 78K chain precursor - Neurospora crassa [Neurospora crassa] (AL021925) hypothetical protein Rv2263 [Mycobacterium tuberculosis] serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) [Schizosaccharomyces pombe]
20693	ENU04487	ANI61C2578:	26-45	809-829	NAP		g2909569	118	40	0.000003			
20694	ENU04488	ANI61C8776:	26-45	795-815	NAP		g1346422	1459	317	8.00E-86	60	46	
20695	ENU04489	ANI61C510:	24-46	777-796	NAP		g1730738	805	85	2.00E-19	38	35	actin-like protein ARP5 [Saccharomyces cerevisiae]
20696	ENU04490	ANI61C1122			NAP		g2239223	347	77	2.00E-13	40	98	(Z97210) hypothetical protein [Schizosaccharomyces pombe]
20697	ENU04491	ANI61C3235:	33-52	755-780	NAP		g114971	983	96	1.00E-36	34	32	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Kluyveromyces marxianus]
20698	ENU04492	ANI61C415:	22-49	615-642	NAP		g1706177	186	62	1.00E-13	34	21	cutinase transcription factor 1 beta [Fusarium solani f. sp. pisi] (Z99112) chromosome segregation SMC protein homolog [Bacillus subtilis]
20699	ENU04493	ANI61S851:	7		NAP		g2633966	304	102	3.00E-21	35	20	hypothetical 81.8 KD protein in YPT52-DBP7 intergenic region [Saccharomyces cerevisiae]
20700	ENU04494	ANI61C3482:	22-45	648-669	NAP		g549770	377	79	3.00E-22			translation initiation factor EIF-2B alpha subunit (EIF-2B GDP-GTP exchange factor) (guanine nucleotide exchange factor subunit GCN3) (GCD complex subunit GCN3) (transcriptional activator GCN3) [Saccharomyces cerevisiae]
20701	ENU04495	ANI61C7378:	54-73	804-829	NAP		g121065	548	196	2.00E-49			(AJ007564) Slx2 [Yarrowia lipolytica]
20702	ENU04496	ANI61C8363:	41-61	712-735	NAP		g3820457	817	214	7.00E-55	47	27	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
20703	ENU04497	ANI61S1437:	47-66	307-326	NAP		g3885836	265	96	2.00E-19	39	28	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ["] (AC000133) ORF [Emmericella nidulans]
20704	ENU04498	ANI61C4370:	37-56	655-679	NAP		g3318897	362	138	7.00E-32	44	31	
20705	ENU04499	ANI61C1120	25-51	510-529	NAP		g1870215	1027	291	2.00E-78	95	53	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20706	ENU04500	ANI61C1014	37-56	718-739	NAP		g2342601	827	286	2.00E-76	53	5	(X89442) peptide synthetase [Metarhizium anisopliae]
20707	ENU04501	ANI61C443:1	26-50	567-586	NAP		g3834343	1013	394	e-109	98	13	(X05204) arom polypeptide [Emericella nidulans]
20708	ENU04502	ANI61C5958: 651	59-78	457-479	NAP		g1293655	410	178	3.00E-44	55	25	(U51327) versicolorin B synthase [Aspergillus parasiticus]
20709	ENU04503	ANI61C7613: 1814..2650	32-51	706-725	NAP		g730506	101	95	7.00E-19	22	63	nuclear division RFT1 protein [Kluyveromyces lactis]
20710	ENU04504	ANI61C1839: 13..658	24-47	592-612	NAP		g3608397	83	68	5.00E-11	32	52	(AF071085) putative dTDP-4-keto-L-rhamnose reductase [Enterococcus faecalis]
20711	ENU04505	ANI61C5791: 587..1	58-84	531-550	NAP		g1293655	292	125	3.00E-28	41	29	(U51327) versicolorin B synthase [Aspergillus parasiticus]
20712	ENU04506	ANI61C262:4	54-73	798-820	NAP		g710551	282	76	6.00E-18	29	15	(L40632) ankyrin 3 [Mus musculus]
20713	ENU04507	ANI61C7276: 3527..4344			NAP		g1708836	255	136	2.00E-31	35	98	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilis]"
20714	ENU04508	ANI61C1144	61-80	514-538	NAP		g2811058	369	139	1.00E-32	42	51	hypothetical 39.5 KD protein in SIGZ-CSN intergenic region [Bacillus subtilis]
20715	ENU04509	ANI61C1164: 493..1695	22-45	803-829	NAP		g131769	1624	320	7.00E-87	97	70	QUTG protein []
20716	ENU04510	ANI61C1065	30-51	719-738	NAP		g3810843	2437	274	5.00E-73	65	25	"(AL032684) putative yeast cell division control protein 68 homolog, putative transcriptional activator [Schizosaccharomyces pombe]"
20717	ENU04511	ANI61S3760: 1..597	26-45	515-534	NAP		g3319372	547	133	1.00E-30	52	17	"(AF077409) similar to reverse transcriptases (PFam: rvt_hmm, score: 60.13) [Arabidopsis thaliana]"
20718	ENU04512	ANI61C7330: 1..2372	69-88	791-810	NAP		g114967	1244	227	7.00E-59	45	33	beta-glucosidase (gentibiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Agrobacterium tumefaciens]
20719	ENU04513	ANI61C8930: 1243..1956	26-45	483-502	NAP		g3395586	234	113	1.00E-24	42	29	(AL031179) similarity to phosphomannomutases [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20720	ENU04514	AN161C1385: 1258..1	22-42	704-731	NAP		g2467275	484	143	1.00E-33	32	56	(Z99759) serine/threonine-protein kinase [Schizosaccharomyces pombe] (AL033389) putative allantoate permease [Schizosaccharomyces pombe]
20721	ENU04515	AN161C1019: 9:2148..1067	25-52	792-816	NAP		g3850093	138	48	0.00006	30	42	
20722	ENU04516	AN161C1039: 7:1265..1	70-89	618-637	NAP		g1711561	582	126	2.00E-28	39	45	sugar transporter STL1 [Saccharomyces cerevisiae]
20723	ENU04517	AN161C7331: 4557..3583	24-43	764-783	NAP		g127568	298	124	9.00E-28	31	86	interferon-induced GTP-binding protein MX [Perca fluviatilis]
20724	ENU04518	AN161C8161: 4359..7310	22-46	721-740	NAP		g731689	1445	313	9.00E-85	51	7	hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae] (V00650) URF 1 [Emmericella nidulans]
20725	ENU04519	AN161C1040: 5:4687..4196			NAP		g12688	626	182	1.00E-58	89	46	
20726	ENU04520	AN161C9790: 1..3423	29-56	802-829	NAP		g731871	1132	153	1.00E-36	32	11	hypothetical 269.9 KD protein in FKH1-MET18 intergenic region [Saccharomyces cerevisiae] (AL031854) hypothetical protein [Schizosaccharomyces pombe] (X89442) peptide synthetase [Metarhizium anisopliae] (Z98974) putative cytochrome p450 [Schizosaccharomyces pombe] (AL022537) putative protein [Arabidopsis thaliana] (AL023706) hypothetical protein [Schizosaccharomyces pombe]
20727	ENU04521	AN161C1128: 5:1107..1	23-43	725-747	NAP		g3738194	664	153	1.00E-46	42	40	
20728	ENU04522	AN161C5443: 2914..1767	27-54	804-824	NAP		g2342601	618	206	2.00E-52	40	5	
20729	ENU04523	AN161C1558: 180..1075	22-48	805-829	NAP		g2388903	671	229	2.00E-59	53	49	
20730	ENU04524	AN161C6309: 1351..2378	52-71	770-788	NAP		g3063700	160	78	5.00E-15	32	15	
20731	ENU04525	AN161C5366: 147..1179	22-40	657-676	NAP		g3169096	785	204	6.00E-52	46	46	
20732	ENU04526	AN161C7102: 1002..1648	72-93	604-626	NAP		g1942383	154	82	3.00E-15	40	31	
20733	ENU04527	AN161S4490: 153..507	213-231	356-375	NAP		g1244642	89	51	0.000005	32	43	
20734	ENU04528	AN161C9993: 1511..3934	27-46	801-828	NAP		g1175408	612	34	0.033			
20735	ENU04529	AN161C4851: 1350..2018	59-78	602-626	NAP		g3550602	257	118	5.00E-26	36	22	

(Z99759) serine/threonine-protein kinase [Schizosaccharomyces pombe] (AL033389) putative allantoate permease [Schizosaccharomyces pombe]

sugar transporter STL1 [Saccharomyces cerevisiae]

interferon-induced GTP-binding protein MX [Perca fluviatilis]

hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae] (V00650) URF 1 [Emmericella nidulans]

hypothetical 269.9 KD protein in FKH1-MET18 intergenic region [Saccharomyces cerevisiae] (AL031854) hypothetical protein [Schizosaccharomyces pombe] (X89442) peptide synthetase [Metarhizium anisopliae] (Z98974) putative cytochrome p450 [Schizosaccharomyces pombe] (AL022537) putative protein [Arabidopsis thaliana] (AL023706) hypothetical protein [Schizosaccharomyces pombe]

[Schizosaccharomyces pombe]

Human 17-Beta-Hydroxysteroid-Dehydrogenase Type 1 Complexed With 17-Beta-Estradiol [ ] (U40374) aminoglycoside 3'-phosphotransferase [Cloning vector pMH30]

hypothetical 107.3 KD TRP-ASP repeats containing protein C31A2.14 in chromosome I [Schizosaccharomyces pombe] (AJ006710) phosphatidylinositol 3-kinase [Rattus norvegicus]



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20736	ENU04530	ANI61C3177:	23-48	770-789	NAP		g3914053	2015	426	e-119	76	30	DNA mismatch repair protein MSH2 [Neurospora crassa]
20737	ENU04531	1..1604 ANI61C1056:	35-55	531-558	NAP		g2501152	291	134	4.00E-31	48	33	threonine synthase [Schizosaccharomyces pombe]
20738	ENU04532	1..580 ANI61S4655:			NAP		g2131314	127	41	0.000000	37	37	hypothetical protein YD8142A.01 - yeast (Saccharomyces cerevisiae) (fragment) []
20739	ENU04533	830..314 ANI61C1355:	22-48	303-324	NAP		g1870215	851	342	9.00E-94	99	46	(AC000133) ORF [Emmericella nidulans]
20740	ENU04534	500..1 ANI61C5665:	22-48	805-824	NAP		g3150253	819	176	9.00E-52	42	24	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
20741	ENU04535	1..1756 ANI61C3240:	54-73	521-540	NAP		g120625	456	180	7.00E-45	60	100	G10 protein [Xenopus laevis]
20742	ENU04536	3384..3956 ANI61S3332:	47-67	198-223	NAP		g1706202	269	100	3.00E-21	54	47	cutinase precursor (L1) [Aspergillus oryzae]
20743	ENU04537	1..306 ANI61C9348:	122-143	333-359	NAP		g2911462	398	107	2.00E-37	73	17	(AF046923) serine/threonine protein kinase [Colletotrichum trifolii]
20744	ENU04538	1..380 ANI61C4409:	22-49	765-784	NAP		g4176523	341	104	6.00E-22	29	45	(AL035263) hypothetical protein [Schizosaccharomyces pombe]
20745	ENU04539	813..2276 ANI61C9831:	22-44	623-642	NAP		g3581903	480	124	9.00E-28	35	38	(AL031545) DEAD box ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20746	ENU04540	1646..1 ANI61C7608:	37-61	724-749	NAP		g4102980	121	42	0.005	20	49	(AF019082) virulent strain associated lipoprotein [Borrelia burgdorferi]
20747	ENU04541	884..1 ANI61C1617:	22-49	454-479	NAP		g464991	142	80	8.00E-15	40	43	ubiquitin carboxyl-terminal hydrolase YUHI (ubiquitin thioesterase) [Saccharomyces cerevisiae]
20748	ENU04542	1230..1561 ANI61C8017:	39-66	424-446	NAP		g4758430	256	93	1.00E-24			geranylgeranyl diphosphate synthase [Homo sapiens]
20749	ENU04543	547..1 ANI61C4194:	22-45	374-393	NAP		g1168953	76	54	0.000000	32	37	citrate lyase beta chain (citrate) (citryl-CoA lyase subunit) [Klebsiella pneumoniae]
20750	ENU04544	2114..2587 ANI61S2295:			NAP		g100753	167	46	0.000000	36	66	hydroxyproline-rich glycoprotein - sorghum [Sorghum bicolor]
20751	ENU04545	1..567 ANI61C7450:	23-44	807-829	NAP		g1256839	868	191	4.00E-73	63	52	(U53329) Ran1-like protein kinase [Fusarium solani f. sp. pisi]
20752	ENU04546	1431..2454 ANI61C3751:	68-87	416-435	NAP		g4902874	112	48	0.00004			"(AJ242575) oxide-reductase enzyme, putative [Sinorhizobium meliloti]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20753	ENU04547	AN161C1853: 1..459	25-52	411-438	NAP		g3914278	264	122	1.00E-27	55	34	pectate lyase B precursor [Glomerella cingulata]
20754	ENU04548	AN161C5321: 1554..2523	22-49	805-829	NAP		g3183173	591	187	6.00E-48	52	53	"seryl-TRNA synthetase, cytoplasmic (serine--TRNA ligase) (SERRS) [Schizosaccharomyces pombe]"
20755	ENU04549	AN161C1011: 6:1..710	24-47	481-499	NAP		g1834342	1043	248	e-106	92	15	(Z68905) ATP-binding cassette multidrug transporter [Emmericella nidulans]
20756	ENU04550	AN161C1045: 1:7120..8069			NAP		g3560208	274	95	7.00E-19	33	34	(AL031536) putative transcription factor of the GCS1-GLO3-SPS18 family [Schizosaccharomyces pombe]
20757	ENU04551	AN161C2588: 748..1	22-49	628-647	NAP		g130117	815	218	3.00E-79	69	39	phosphate-repressible phosphate permease [Neurospora crassa]
20758	ENU04552	AN161C5294: 996..455	22-46	498-521	NAP		g2501434	162	103	2.00E-22	30	92	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) [Schizosaccharomyces pombe]
20759	ENU04553	AN161C6129: 423..856	72-99	412-431	NAP		g730443	80	47	0.000000	34	70	quinone oxidoreductase (NADPH:quinone reductase) (zeta-crystallin homolog protein) []
20760	ENU04554	AN161C1614: 1643..72	56-75	777-796	NAP		g3646379	1450	199	8.00E-95	75	42	(AJ001540) phenylacetyl-CoA ligase [Penicillium chrysogenum]
20761	ENU04555	AN161C5779: 4080..7040	71-90	773-799	NAP		g2443355	723	108	4.00E-23			(AB003395) ent-Kaurene synthase [Phaeosphaeria sp. L487]
20762	ENU04556	AN161C1114: 1:866..1	23-42	788-815	NAP		g2625138	224	116	1.00E-25	34	14	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]
20763	ENU04557	AN161C7681: 1..2435	22-49	757-780	NAP		g1817584	917	117	8.00E-26	28	19	(Y08991) adaptor protein [Homo sapiens]
20764	ENU04558	AN161C1919: 860..1	221-240	765-784	NAP		g4165293	962	341	2.00E-99	71	28	(X58824) cdc21 protein [Schizosaccharomyces pombe]
20765	ENU04559	AN161C1065: 5:930..1	26-45	767-786	NAP		g1346521	1027	317	8.00E-86	78	62	S-adenosylmethionine synthetase (methionine adenosyltransferase) (ADOMET synthetase) [Neurospora crassa]
20766	ENU04560	AN161C2670: 1204..1	101-120	610-631	NAP		g604369	928	215	6.00E-70	53	34	(U17857) hMLH1 gene product [Homo sapiens]
20767	ENU04561	AN161C4238: 1645..2569	22-42	772-793	NAP		g3023682	998	332	9.00E-94	79	30	elongation factor 2 (EF-2) [Candida albicans]

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20768	ENU04562	ANI61S2955: 1..531			NAP		g4218005	140	43	0.002	25	25	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
20769	ENU04563	ANI61C1957: 422..1763	22-41	771-795	NAP		g461623	1173	92	2.00E-36	68	21	beta-galactosidase precursor (lactase) [Aspergillus niger]
20770	ENU04564	ANI61S3141: 666..1	182-209	612-631	NAP		g2062165	797	330	6.00E-90	87	38	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
20771	ENU04565	ANI61C3056: 3300..1880	33-60	801-820	NAP		g3850089	772	183	6.00E-61	52	62	(AL033389) putative yeast cell division cycle CDC50 homolog
20772	ENU04566	ANI61C8012: 5408..4491	22-45	810-829	NAP		g2842699	518	173	2.00E-42	54	43	[Schizosaccharomyces pombe] putative ubiquitin carboxyl-terminal hydrolase C6G9.08 (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
20773	ENU04567	ANI61S3854: 586..90	168-193	399-418	NAP		g3417425	202	53	5.00E-14	36	50	(AL031261) conserved hypothetical protein [Schizosaccharomyces pombe]
20774	ENU04568	ANI61C1100: 0:8321..9087	33-53	598-622	NAP		g643443	769	225	1.00E-78	72	39	(U08104) PHOG [Penicillium chrysogenum]
20775	ENU04569	ANI61C1131: 8:1..839	103-120	795-817	NAP		g1723773	335	144	7.00E-34	36	39	hypothetical 81.2 KD protein in MIES1-FOI2 intergenic region
20776	ENU04570	ANI61S2538: 671..1	220-247	585-605	NAP		g1723448	242	120	1.00E-26	43	31	[Saccharomyces cerevisiae] hypothetical protein C56F8.17C in chromosome I [Schizosaccharomyces pombe]
20777	ENU04571	ANI61C5097: 525..1	97-118	482-503	NAP		g2370479	146	71	7.00E-12	29	21	(Z98849) putative centromere protein [Schizosaccharomyces pombe]
20778	ENU04572	ANI61C2309: 1195..1	22-46	762-780	NAP		g544368	215	75	4.00E-14	29	51	galactose-proton symport (galactose transporter) [Escherichia coli]
20779	ENU04573	ANI61C9634: 642..1942	22-46	810-829	NAP		g2661622	640	145	4.00E-46	48	65	(AL009197) hypothetical protein phosphatase [Schizosaccharomyces pombe]
20780	ENU04574	ANI61C9830: 1643..363	33-52	683-702	NAP		g1729868	1503	367	e-101	72	53	"probable T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta) [Schizosaccharomyces pombe]"
20781	ENU04575	ANI61S3302: 567..1	180-207	443-470	NAP		g1397290	139	44	4.00E-11	47	67	(U61949) Similar to cytidine deaminase. [Caenorhabditis elegans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20782	ENU04576	ANI61C3245:	22-42	709-735	NAP		g2342601	1176	183	1.00E-45	35	5	(X89442) peptide synthetase [Metarhizium anisopliae]
20783	ENU04577	ANI61C7535:	2557..1		NAP		g4481947	211	65	4.00E-21	36	99	(AL035637) hypothetical protein. [Schizosaccharomyces pombe]
20784	ENU04578	ANI61C1091	33-52	784-803	NAP		g4454039	482	169	2.00E-41	47	31	(AL035394) putative Na <sup>+</sup> /H <sup>+</sup> -exchanging protein [Arabidopsis thaliana]
20785	ENU04579	ANI61C6944:	38-57	781-803	NAP		g3777495	1275	284	7.00E-76	65	27	(U92083) calcium transporting ATPase [Pichia angusta]
20786	ENU04580	ANI61C7384:	23-46	704-729	NAP		g128397	962	334	3.00E-91	99	100	nuclear movement protein NUDC [Emmericella nidulans]
20787	ENU04581	ANI61C7182:	3181..3930		NAP		g1870209	235	74	8.00E-13	46	30	(AC000133) ORF [Emmericella nidulans]
20788	ENU04582	ANI61C1122	27-54	761-780	NAP		g4836423	138	34	1.4			(AF119670) integral membrane protein [Magnaporthe grisea]
20789	ENU04583	ANI61C7682:	78-105	749-776	NAP		g4164428	473	205	5.00E-52	49	19	(AL035247) putative pre-mrna splicing factor ma helicase [Schizosaccharomyces pombe]
20790	ENU04584	ANI61C8016:	22-44	767-794	NAP		g3901117	970	135	2.00E-44	38	45	(AJ012752) maltose permease [Saccharomyces cerevisiae]
20791	ENU04585	ANI61C1556:	66-85	772-791	NAP		g1723187	505	80	3.00E-14	41	24	112.3 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]
20792	ENU04586	ANI61C5421:	118-137	528-546	NAP		g1805262	336	147	6.00E-35	35	10	"(U75347) fatty acid synthase, beta subunit [Emmericella nidulans]"
20793	ENU04587	ANI61C6728:	85-111	630-649	NAP		g418345	129	72	4.00E-12	39	46	probable methionyl-TRNA formyltransferase precursor [Saccharomyces cerevisiae]
20794	ENU04588	ANI61C5679:	22-47	723-742	NAP		g189036	121	71	1.00E-11	19	20	(M31013) nonmuscle myosin heavy chain (NMHC) [Homo sapiens]
20795	ENU04589	ANI61C2763:	55-74	307-331	NAP		g3264834	279	118	2.00E-26	44	33	(AF072541) xyliol dehydrogenase; XDH [Galactocandida mastotermittis]
20796	ENU04590	ANI61C7721:	23-44	803-829	NAP		g2673947	287	98	1.00E-22	31	20	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
20797	ENU04591	ANI61C1672:	23-50	430-449	NAP		g3859681	485	128	2.00E-49	50	60	(AL033503) transcription regulatory protein [Candida albicans]
20798	ENU04592	ANI61C9504:	49-72	480-504	NAP		g465847	336	83	4.00E-33			hypothetical 66.5 KD protein F02A9.5 in chromosome III []

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20799	ENU04593	ANI61C9338:	22-45	711-737	NAP		g2276359	1861	273	1.00E-72	38	11	(Z97992) putative phosphatidylinositol 3-kinase [Schizosaccharomyces pombe]
20800	ENU04594	ANI61C6660:	45-64	453-477	NAP		g42931	138	131	3.00E-30	31	100	(X56175) ORF 2 (AA 1 - 109) [Escherichia coli]
20801	ENU04595	ANI61C9395:	106-128	389-414	NAP		g1709760	271	87	1.00E-21	50	47	putative proteasome component PRE6 (macropain subunit) (multicatalytic endopeptidase complex subunit) [Schizosaccharomyces pombe]
20802	ENU04596	ANI61C6006:	22-43	709-736	NAP		g1255430	348	125	4.00E-28	37	71	(U53155) No definition line found [Caenorhabditis elegans]
20803	ENU04597	ANI61C7769:			NAP		g3873958	152	92	6.00E-18	26	79	(Z81458) similar to transposable element [Caenorhabditis elegans]
20804	ENU04598	ANI61C4415:	22-44	698-720	NAP		g4506221	665	60	2.00E-31	40	50	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 [Homo sapiens]"
20805	ENU04599	ANI61C5780:	23-47	518-545	NAP		g2501434	521	125	3.00E-53	63	100	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) [Schizosaccharomyces pombe]
20806	ENU04600	ANI61C7849:	30-57	712-731	NAP		g3947746	527	220	1.00E-56	56	29	(AJ009960) DNA photolyase [Trichoderma harzianum]
20807	ENU04601	ANI61C7563:	31-50	334-360	NAP		g3309657	372	159	1.00E-38	60	15	(AF074944) RRM3/PIF1 helicase homolog [Schizosaccharomyces pombe]
20808	ENU04602	ANI61C1080	25-44	774-794	NAP		g102827	63	72	4.00E-12			alpha-latrotoxin precursor - black widow spider [Latrodectus tredecimguttatus]
20809	ENU04603	ANI61C6782:	26-45	778-805	NAP		g731421	377	98	2.00E-34	38	47	hypothetical 53.3 KD protein in HXT8-CANI intergenic region [Saccharomyces cerevisiae]
20810	ENU04604	ANI61C4065:	218-238	385-406	NAP		g1723643	217	78	4.00E-20	41	33	hypothetical 44.9 KD protein in SEC9-MSB2 intergenic region [Saccharomyces cerevisiae]
20811	ENU04605	ANI61C5853:	22-45	807-826	NAP		g3738190	706	196	2.00E-49	43	82	(AL031854) putative ras related GTP-binding protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20812	ENU04606	ANI61C1054	39-56	724-746	NAP		g2956769	1614	169	9.00E-60	54	21	(AL022103) phosphatidylinositol phosphate phosphatase; synaptojanin-like [Schizosaccharomyces pombe]
20813	ENU04607	ANI61C7324: 4754..5464	50-69	670-690	NAP		g2408075	436	188	4.00E-47	41	98	(Z99167) hypothetical conserved protein [Schizosaccharomyces pombe]
20814	ENU04608	ANI61C2440: 1..643	186-213	589-608	NAP		g2132014	175	92	3.00E-18	37	39	hypothetical protein YOL124c - yeast [Saccharomyces cerevisiae]
20815	ENU04609	ANI61S1755: 1..588			NAP		g3413504	91	44	0.0007	22	4	[Saccharomyces cerevisiae] (Y16563) Bassoon [Rattus norvegicus]
20816	ENU04610	ANI61C4426: 844..1	41-64	717-743	NAP		g2147805	319	161	5.00E-39	36	33	NarB protein - Oscillatoria chalybea [Oscillatoria chalybea]
20817	ENU04611	ANI61C3356: 976..1	27-48	723-749	NAP		g1708850	222	93	3.00E-18	38	34	probable leukotriene A-4 hydrolase (LTA-4 hydrolase) [leukotriene A(4) hydrolase] [Saccharomyces cerevisiae]
20818	ENU04612	ANI61C4165: 3186..2199	28-47	774-793	NAP		g417318	589	185	3.00E-46	44	59	MSS51 protein [Saccharomyces cerevisiae]
20819	ENU04613	ANI61C1138 1:971..1478	27-46	398-416	NAP		g1172568	198	80	6.00E-17	48	73	low molecular weight phosphotyrosine protein phosphatase (low molecular weight cytosolic acid phosphatase) (PTPASE) (small tyrosine phosphatase) [Schizosaccharomyces pombe]
20820	ENU04614	ANI61C5427: 1940..1520	209-228	366-385	NAP		g1549231	121	38	0.000003	31	18	(D50497) chloride channel (ClC-5) [Rattus rattus]
20821	ENU04615	ANI61C1005 7:2999..584	23-47	800-822	NAP		g2132992	242	86	3.00E-16	27	25	probable membrane protein YPL183c - yeast [Saccharomyces cerevisiae]
20822	ENU04616	ANI61C1355: 2053..2529	203-222	459-478	NAP		g1870229	817	300	3.00E-81	97	100	[Saccharomyces cerevisiae] (AC000133) ORF [Emmericella nidulans]
20823	ENU04617	ANI61C5998: 7885..4728	22-42	802-821	NAP		g1166378	525	86	3.00E-16			"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" (U58946) transposase [Aspergillus awamori]
20824	ENU04618	ANI61C1102 6:1..629	107-127	506-527	NAP		g1805251	250	120	9.00E-27	35	37	(AJ001421) Rer1 protein [Homo sapiens]
20825	ENU04619	ANI61C7487: 243..1014	22-43	713-740	NAP		g2385369	466	146	9.00E-41	53	98	(U20323) ankyrin-like protein [Saccharomyces cerevisiae]
20826	ENU04620	ANI61C2085: 952..441	22-48	460-479	NAP		g665573	64	44	0.0006	31	98	emniatin synthetase - fungus (Fusarium scirpi) [Fusarium scirpi]
20827	ENU04621	ANI61C3624: 5678..1	35-54	630-649	NAP		g481866	2935	223	8.00E-62	44	8	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20828	ENU04622	ANT61C4110:	73-100	295-317	NAP		g2130022	117	66	1.00E-10	35	37	aldose reductase homolog - wild oat [Avena fatua]
20829	ENU04623	ANT61C3096:	23-43	777-800	NAP		g2132857	116	41	0.014			probable membrane protein YOL158c - yeast (Saccharomyces cerevisiae)
20830	ENU04624	ANT61C5542:	22-49	429-454	NAP		g137024	321	116	1.00E-25			[Saccharomyces cerevisiae] uridylylate kinase (UK) (uridine monophosphate kinase) (UMP kinase) [Saccharomyces cerevisiae]
20831	ENU04625	ANT61C3542:	42-61	803-829	NAP		g2499558	386	120	1.00E-26			hypothetical 84.2 KD protein SLR0473 [Synecocystis sp.]
20832	ENU04626	ANT61C2155:	27-46	722-741	NAP		g1084969	1548	399	e-129	97	42	sulfate adenylyltransferase (EC 2.7.7.4) - Emericella nidulans [Emericella nidulans]
20833	ENU04627	ANT61C5633:	102-129	586-612	NAP		g3929349	659	244	4.00E-64	54	47	C-14 sterol reductase (sterol C14-reductase) [Nectria haematococca]
20834	ENU04628	ANT61S4409:	29-56	272-295	NAP		g3549662	558	230	3.00E-60	96	23	(AL031394) hypothetical protein [Arabidopsis thaliana]
20835	ENU04629	ANT61C681:	6 22-45	525-552	NAP		g2132903	385	174	6.00E-43	55	23	probable membrane protein YOR165w - yeast (Saccharomyces cerevisiae)
20836	ENU04630	ANT61C6221:	41-62	407-434	NAP		g115689	306	132	2.00E-30	60	38	[Saccharomyces cerevisiae] nuclear protein SNF4 (regulatory protein CAT3) [Saccharomyces cerevisiae]
20837	ENU04631	ANT61C4344:	22-46	790-809	NAP		g2104447	961	169	2.00E-41	39	47	(Z95396) heat shock protein 70 homolog [Schizosaccharomyces pombe]
20838	ENU04632	ANT61C9952:	219-245	614-639	NAP		g2507475	595	242	3.00E-63	46	16	paired amphipathic helix protein [Saccharomyces cerevisiae] (U34998) Rad9 [Coprinus cinereus]
20839	ENU04633	ANT61C5160:	68-87	784-803	NAP		g13533390	167	68	1.00E-10			meiotic recombination protein REC14 [Schizosaccharomyces pombe]
20840	ENU04634	ANT61C4215:	22-45	807-829	NAP		g2498838	508	78	2.00E-42	47	72	hypothetical 20.9 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
20841	ENU04635	ANT61C6750:			NAP		g731690	152	87	9.00E-17	40	100	RAS suppressor protein 1 (RSU-1) (RSP-1 protein) (RSP-1) [Homo sapiens]
20842	ENU04636	ANT61C8558:	28-47	455-479	NAP		g2498866	84	58	0.000000	37	36	

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20843	ENU04637	AN161C9157:	26-45	537-556	NAP		g4027860	858	194	6.00E-49	98	24	(U47540) TamaA [Emericella nidulans]
20844	ENU04638	AN161C8418:			NAP		g122094	461	157	5.00E-38	92	83	histone H4.2 [Emericella nidulans]
		1549..1857											
20845	ENU04639	AN161C1129	96-119	725-749	NAP		g1546072	707	148	5.00E-35	35	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
		7:1..1664											
20846	ENU04640	AN161C1103	23-50	793-820	NAP		g3656	447	118	4.00E-26	28	53	(X55713) putative cytochrome P450 [Saccharomyces cerevisiae]
		4:3908..5575											
20847	ENU04641	AN161C1269:	22-46	804-829	NAP		g2196560	165	32	4			(AB004690) Mif6 [Schizosaccharomyces pombe]
		3063..1220											
20848	ENU04642	AN161C4393:	72-91	742-759	NAP		g120777	660	257	6.00E-68	50	53	succinate-semialdehyde dehydrogenase (NADP+) (SSDH) [Escherichia coli]
		1..785											
20849	ENU04643	AN161C3785:	24-51	724-749	NAP		g2226061	716	226	1.00E-58	46	51	(AF005040) folypolyglutamate synthetase: PPGS [Neurospora crassa]
		1270..1											
20850	ENU04644	AN161C8146:	102-124	454-479	NAP		g1749638	387	157	5.00E-38	62	53	"(D89215) similar to Saccharomyces cerevisiae transaldolase, SWISS-PROT Accession Number P15019 [Schizosaccharomyces pombe]"
		469..1											
20851	ENU04645	AN161C3784:	47-66	509-533	NAP		g2326237	60	66	1.00E-17	26	63	(AC004684) putative ribotoi dehydrogenase [Arabidopsis thaliana]
		637..1											
20852	ENU04646	AN161C8433:	24-43	332-356	NAP		g1172766	328	146	8.00E-35			adenylosuccinate synthetase (IMP--aspartate ligase) [Saccharomyces cerevisiae]
		1..377											
20853	ENU04647	AN161C8966:	44-63	711-730	NAP		g2132445	435	86	3.00E-16	40	27	probable membrane protein YDL148c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
		5392..6501											
20854	ENU04648	AN161C9765:	29-48	775-798	NAP		g1723249	2140	257	e-103	67	23	hypothetical 137.2 KD protein C27F1.09C in chromosome I [Schizosaccharomyces pombe]
		1..1767											
20855	ENU04649	AN161C5247:	40-59	667-686	NAP		g2499017	1022	173	7.00E-64	49	49	"alpha.alpha-trehalose-phosphate synthase (UDP-forming) 1 (trehalose-6-phosphate synthase) (UDP-glucose-glucosephosphate glucosyltransferase) [Aspergillus niger]"
		3740..5201											
20856	ENU04650	AN161C1061	22-48	725-751	NAP		g4154667	126	48	0.000000	29	71	(AE001454) fructose-BISphosphate aldolase [Helicobacter pylori j99]
		8:121..892								004			
20857	ENU04651	AN161C388:9	22-44	672-691	NAP		g757832	187	69	2.00E-16	30	44	(Z37980) hypothetical 4-hydroxyphenylacetate permease [Escherichia coli]
		35..1											



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20858	ENJU04652	ANI61S3598:			NAP		g3913423	356	95	4.00E-19	48	59	S-adenosylmethionine decarboxylase PROenzyme (ADOMETDC)
		1..644											(SAMDC) [Nicotiana tabacum]
20859	ENJU04653	ANI61C9728:	67-86	788-807	NAP		g135503	1230	438	e-122	93	58	tubulin gamma chain [Emmericella nidulans]
		1..897											putative sterigmatocystin biosynthesis polyketide synthase (PKS) [Emmericella nidulans]
20860	ENJU04654	ANI61C7518:	28-47	729-748	NAP		g2492661	2917	579	e-165	96	12	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
		373..2142											pyruvate decarboxylase [Emmericella nidulans]
20861	ENJU04655	ANI61S1593:			NAP		g283032	141	34	0.002	29	55	2-deoxy-D-glucuronate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) [Bacillus subtilis]
		1..606											"dynein heavy chain, cytosolic (DYHC) [Emmericella nidulans]"
20862	ENJU04656	ANI61S51:1..556			NAP		g2501326	555	212	6.00E-55	72	29	(AL031907) conserved hypothetical protein [Schizosaccharomyces pombe]
20863	ENJU04657	ANI61C1227:	22-49	806-827	NAP		g1730031	511	190	1.00E-47	50	98	[Methanobacterium thermoautotrophicum] "(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana]" (AC000133) ORF [Emmericella nidulans]
		1831..968											spem tail-specific protein mst101(2) - fruit fly (Drosophila hydei) []
20864	ENJU04658	ANI61C5694:	102-129	667-692	NAP		g1169440	1343	531	e-150	97	6	"hydroxyquinol 1,2-dioxygenase - Pseudomonas cepacia [Burkholderia cepacia]" (AL021838) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]
		1..808											
20865	ENJU04659	ANI61C5170:	51-71	710-732	NAP		g3766378	225	52	6.00E-10	42	100	
		1373..621											
20866	ENJU04660	ANI61C9574:	23-50	449-468	NAP		g2622925	91	66	2.00E-10	28	67	
		1187..1572											
20867	ENJU04661	ANI61C3829:	34-60	443-466	NAP		g4115913	129	82	1.00E-19	34	41	
		1..498											
20868	ENJU04662	ANI61C1010			NAP		g1870209	414	106	2.00E-22	33	50	
		5:1221..1											
20869	ENJU04663	ANI61S3791:			NAP		g2133632	118	48	0.00008	20	20	
		1..845											
20870	ENJU04664	ANI61C3055:	22-44	377-398	NAP		g2120651	244	100	1.00E-20	47	38	
		2351..2686											
20871	ENJU04665	ANI61C8620:	43-62	784-804	NAP		g2894281	872	257	5.00E-68	46	36	
		4660..6246											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20872	ENU04666	ANI61S1089:	1..536		NAP		g2117904	150	69	3.00E-11	34	48	ribose-phosphate pyrophosphokinase (EC 2.7.6.1) PRS1 - yeast ( <i>Candida albicans</i> ) []
20873	ENU04667	ANI61C7703:	22-47	797-821	NAP		g1063421	581	74	5.00E-18	33	43	(L48797) toxin pump [Cochliobolus carbonum]
20874	ENU04668	ANI61C1106	66-89	589-614	NAP		g729075	326	95	5.00E-19	52	99	cell division control protein 31 [Saccharomyces cerevisiae]
20875	ENU04669	ANI61C313:1	116-137	435-457	NAP		g1083855	133	79	2.00E-14	33	1	cyclosporin synthetase - <i>Tolypocladium inflatum</i> [Tolypocladium inflatum] (AF010263) tartarate dehydrogenase [Agrobacterium vitis]
20876	ENU04670	ANI61C6199:			NAP		g2305218	501	129	3.00E-50	54	59	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]
20877	ENU04671	ANI61C1123	22-49	700-727	NAP		g2673951	671	79	3.00E-16	31	18	hypothetical 23.1 KD protein in SHP1-PTC3 intergenic region
20878	ENU04672	ANI61C4534:	102-121	621-640	NAP		g465516	260	105	1.00E-25	48	74	[Saccharomyces cerevisiae] (AF078790) No definition line found [Caenorhabditis elegans]
20879	ENU04673	ANI61S2960:			NAP		g3329623	189	41	0.0003	24	53	probable membrane protein YOR271c - yeast (Saccharomyces cerevisiae)
20880	ENU04674	ANI61C3402:	115-134	615-634	NAP		g2132933	722	191	3.00E-60	60	72	[Saccharomyces cerevisiae] (AL034563) elongation factor g [Schizosaccharomyces pombe]
20881	ENU04675	ANI61S4333:	29-48	436-455	NAP		g542225	448	136	7.00E-32	66	42	probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)
20882	ENU04676	ANI61C1943:	102-124	360-381	NAP		g1705917	550	222	1.00E-57	57	11	ribosomal protein L4.e - fission yeast (Schizosaccharomyces pombe) []
20883	ENU04677	ANI61C9505:	71-98	540-567	NAP		g4049509	232	106	1.00E-22	31	24	probable clathrin heavy chain [Schizosaccharomyces pombe]
20884	ENU04678	ANI61C1094	41-60	626-643	NAP		g2132968	1222	135	4.00E-31	33	22	[Schizosaccharomyces pombe]
20885	ENU04679	ANI61C1049	112-131	805-829	NAP		g4107287	223	61	8.00E-15	32	45	probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)
20886	ENU04680	ANI61C9717:	27-46	785-812	NAP		g4098647	751	257	7.00E-68	51	56	[Saccharomyces cerevisiae] (AL035076) putative allantoin permease [Schizosaccharomyces pombe]
20887	ENU04681	ANI61C9944:	23-47	629-648	NAP		g4106673	796	171	3.00E-85	66	59	"(U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]" (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20888	ENU04682	ANI61C7199:	68-87	306-325	NAP		g730917	307	78	1.00E-18			"T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta) [Saccharomyces cerevisiae]"
20889	ENU04683	ANI61C1075	24-44	803-829	NAP		g1723251	417	70	3.00E-15	29	59	hypothetical 50.9 KD protein C3F10.06C in chromosome I [Schizosaccharomyces pombe]
20890	ENU04684	ANI61C2651:	22-49	785-805	NAP		g3123261	154	70	2.00E-11			meiotic recombination protein REC12 [Schizosaccharomyces pombe]
20891	ENU04685	ANI61C9331:	22-41	732-749	NAP		g1063421	519	108	1.00E-28	44	40	(L48797) toxin pump [Cochliobolus carbonum]
20892	ENU04686	ANI61S29:1..654			NAP		g2635181	553	213	7.00E-55	56	70	(Z99117) similar to protease [Bacillus subtilis]
20893	ENU04687	ANI61C9880:	22-41	808-829	NAP		g2498765	469	107	1.00E-28			peroxisomal membrane protein PEX16 (peroxin-16) [Yarrowia lipolytica]
20894	ENU04688	ANI61C891:1	51-69	457-481	NAP		g1805251	124	73	1.00E-16	30	29	(U58946) transposase [Aspergillus awamori]
20895	ENU04689	ANI61C3704:	69-89	805-823	NAP		g4586103	199	67	1.00E-22	33	76	(AL049638) putative protein [Arabidopsis thaliana]
20896	ENU04690	ANI61C758:3	22-48	714-741	NAP		g2497080	1119	125	5.00E-30	32	16	hypothetical 171.1 KD protein in YL16A-DAKI intergenic region [Saccharomyces cerevisiae]
20897	ENU04691	ANI61S2532:			NAP		g2119707	127	40	0.01	32	61	proline-rich protein precursor - rat [Hypodiplosis thaliana]
20898	ENU04692	ANI61C883:8	22-45	456-479	NAP		g1176053	156	90	1.00E-19	34	50	hypothetical 33.3 KD protein in ADE3-SER2 intergenic region [Saccharomyces cerevisiae]
20899	ENU04693	ANI61C2209:	22-42	719-738	NAP		g1077575	182	62	0.000000	27	41	hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
20900	ENU04694	ANI61C9811:	31-50	767-786	NAP		g120777	947	310	1.00E-83	56	58	[Saccharomyces cerevisiae] succinate-semialdehyde dehydrogenase (NADP+) (SSDH) [Escherichia coli]
20901	ENU04695	ANI61C8000:	41-60	727-749	NAP		g1703361	998	370	e-102			"ARG-6 protein precursor (contains: N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-... [Neurospora crassa])"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20902	ENU04696	ANI61C7553: 22-46	3582..4673	805-829	NAP		g3850084	370	87	2.00E-16	36	75	(AL033338) alcohol dehydrogenase [Schizosaccharomyces pombe]
20903	ENU04697	ANI61C6751: 120-147	294-316		NAP		g3150262	196	80	5.00E-15	38	32	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
20904	ENU04698	ANI61C6031: 30-54	647-673		NAP		g113314	1311	482	e-135	96	7	delta-(L-alpha-aminoadipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emmericella nidulans]
20905	ENU04699	ANI61C1084 51-70	714-733		NAP		g2132014	611	233	1.00E-60	45	61	hypothetical protein YOL124c - yeast (Saccharomyces cerevisiae)
20906	ENU04700	ANI61C201:1 94-113	308-335		NAP		g2131347	264	68	2.00E-11	52	19	hypothetical protein YDL153c - yeast (Saccharomyces cerevisiae)
20907	ENU04701	ANI61C4912: 49-72	600-627		NAP		g3122266	603	171	4.00E-60	65	56	[Saccharomyces cerevisiae] eukaryotic translation initiation factor 3 delta subunit (EIF-3 delta) [Schizosaccharomyces pombe]
20908	ENU04702	ANI61C7350: 199-218	594-617		NAP		g2507129	395	112	3.00E-24	40	36	transporter protein SMF1/ESP1 [Saccharomyces cerevisiae]
20909	ENU04703	ANI61C2646: 1..595			NAP		g4127832	306	140	8.00E-33	39	37	(Y17243) cytochrome P450 [Gibberella fujikuroi]
20910	ENU04704	ANI61C1132 23-43	703-729		NAP		g464369	221	78	8.00E-23	32	35	phenol 2-monooxygenase (phenol hydroxylase) [Trichosporon cutaneum]
20911	ENU04705	ANI61C7309: 71-92	460-483		NAP		g2956774	62	48	0.00003	27	72	(AL022103) hypothetical protein. [Schizosaccharomyces pombe]
20912	ENU04706	ANI61C332:1 81-99	421-438		NAP		g585251	318	134	4.00E-31	43	36	polyketide synthase HETM [Anabaena sp.]
20913	ENU04707	ANI61C101:1 22-46	801-828		NAP		g1870209	283	87	8.00E-24	32	50	(AC000133) ORF [Emmericella nidulans]
20914	ENU04708	ANI61C3232: 25-45	720-747		NAP		g2492658	3245	541	e-153	97	14	putative stergmatocystin biosynthesis fatty acid synthase beta subunit [Emmericella nidulans]
20915	ENU04709	ANI61C1335: 48-70	349-368		NAP		g585668	413	152	1.00E-36	62	34	polygalacturonase precursor (PG) (pectinase) [Gibberella fujikuroi]
20916	ENU04710	ANI61C1053 0:722..1			NAP		g2133039	447	198	5.00E-50	48	15	probable membrane protein YPR184w - yeast (Saccharomyces cerevisiae)
20917	ENU04711	ANI61C4364: 30-49	725-747		NAP		g2342601	814	123	2.00E-27	30	5	[Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae]

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20918	ENU04712	ANI6IS2752: 1..605			NAP		g4760549	77	53	0.000001			(AB019494) IDN3 [Homo sapiens]
20919	ENU04713	ANI6IC7196: 22-49		777-804	NAP		g3859775	415	111	2.00E-31	52	53	(Z54328) putative aminopeptidase p [Schizosaccharomyces pombe]
20920	ENU04714	ANI6IC9312: 22-46		802-829	NAP		g3915187	556	132	3.00E-30	33	14	probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N-recognin) [Schizosaccharomyces pombe]
20921	ENU04715	ANI6IC9006: 42-61		697-716	NAP		g83716	3301	404	e-141	95	32	regulatory protein alcR - Emericella nidulans [Emericella nidulans]
20922	ENU04716	ANI6IC1084: 22-44		623-643	NAP		g416965	658	50	3.00E-21	37	7	"erythronolide synthase, modules 1 and 2 (ORF 1) (6-deoxyerythronolide B synthase 1) (DEBS 1) [Schizosaccharomyces pombe]"
20923	ENU04717	ANI6IC6533: 22-48		727-749	NAP		g1175451	842	152	3.00E-36			hypothetical protein C22F3.14C in chromosome I [Schizosaccharomyces pombe]
20924	ENU04718	ANI6IC5137: 88-110		741-760	NAP		g3702632	592	137	3.00E-63	43	41	(AL031824) putative transcriptional regulator [Schizosaccharomyces pombe]
20925	ENU04719	ANI6IC419: 23-46		412-431	NAP		g1172542	388	168	3.00E-41	47	22	dolichyl-phosphate-mannose--protein mannosyltransferase 4 [Schizosaccharomyces cerevisiae]
20926	ENU04720	ANI6IC8353: 26-45		776-794	NAP		g122805	311	109	3.00E-23	30	53	6-hydroxy-D-nicotine oxidase (6-HDNO) [Arthrobacter oxidans]
20927	ENU04721	ANI6IC3877: 1384..1			NAP		g3122851	2113	284	e-134	89	41	sulfur metabolite repression control protein [Emericella nidulans]
20928	ENU04722	ANI6IC8873: 8184..7035			NAP		g1175441	458	83	3.00E-15	27	31	hypothetical 98.4 KD protein C24H6.13 in chromosome I [Schizosaccharomyces pombe]
20929	ENU04723	ANI6IC1126: 102-123		448-475	NAP		g4204352	396	166	1.00E-40	78	64	[Schizosaccharomyces pombe] (U07366) eIF-5A [Candida albicans]
20930	ENU04724	ANI6IC4166: 121-140		505-524	NAP		g1076211	227	45	0.0006	28	43	hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii]
20931	ENU04725	ANI6IC6980: 22-44		561-582	NAP		g2213560	369	164	4.00E-40	44	98	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
20932	ENU04726	ANI6IC9955: 22-49		760-783	NAP		g534844	501	184	7.00E-46	55	39	(U13672) beta-glucosidase [Candida wickerhamii]
20933	ENU04727	ANI6IC1013: 23-50		538-558	NAP		g2105430	316	145	4.00E-34	45	17	(U97079) U5-116KD [Mus musculus]

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20934	ENU04728	ANT61S4589: 1..553			NAP		g82698	177	47	0.00008	35	54	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
20935	ENU04729	ANT61C1053 45-64		792-819	NAP		g416643	231	65	7.00E-10	32	58	aristolochene synthase (sesquiterpene cyclase) (AS) [Penicillium roqueforti]
20936	ENU04730	5:2480..3612		467-490	NAP		g3128203	134	63	0.000000	36	75	(AC004521) unknown protein [Arabidopsis thaliana]
20937	ENU04731	3315..2805		652-671	NAP		g3915405	146	79	4.00E-14	37	96	hypothetical 17.5 KD protein in chromosome II [Schizosaccharomyces pombe]
20938	ENU04732	2535..1838											
20938	ENU04732	ANT61C1110 105-125		643-665	NAP		g3925752	276	68	1.00E-22	41	58	(AL034352) putative signal transduction protein [Schizosaccharomyces pombe]
20939	ENU04733	3:5478..4766											
20939	ENU04733	ANT61S3754: 31-56		371-390	NAP		g2911045	695	187	2.00E-73	95	51	(AL021961) putative protein [Arabidopsis thaliana]
20940	ENU04734	1..508											
20940	ENU04734	ANT61C9298: 818..1			NAP		g1401057	158	104	1.00E-21	25	14	(U40375) Supr16h [Mus musculus]
20941	ENU04735	1..565											
20941	ENU04735	ANT61S3133: 46-65		427-450	NAP		g4105798	164	99	2.00E-20	36	43	(AF049930) PGP237-11 [Petunia x hybrida]
20942	ENU04736	640..179											
20942	ENU04736	ANT61C7989: 71-89		418-441	NAP		g3880413	160	66	1.00E-10	33	46	(Z81137) Similarity to Yeast YTP1 protein (SW:P53039); cDNA EST EMBL:701608 comes from this gene; cDNA EST EMBL:C07393 comes from this gene; cDNA EST EMBL:C07550 comes from this gene; cDNA EST EMBL:C08746 comes from this gene; ... []
20943	ENU04737	ANT61C5949: 55-75		594-612	NAP		g2493011	323	151	5.00E-36	37	13	probable calcium-transporting ATPase 8 [Saccharomyces cerevisiae]
20944	ENU04738	1..816											
20944	ENU04738	ANT61C9477: 30-49		806-829	NAP		g4768831	418	38	0.12			(AF116827) unknown [Homo sapiens]
20945	ENU04739	1..1752											
20945	ENU04739	ANT61C1110 28-47		769-796	NAP		g4455787	886	195	4.00E-52	52	66	(AL035536) putative DNA polymerase accessory protein [Schizosaccharomyces pombe]
20946	ENU04740	7:9439..8176											
20946	ENU04740	ANT61C5813: 41-60		734-761	NAP		g1730621	585	223	1.00E-61	57	56	hypothetical 48.1 KD protein in TUB1-CPR3 intergenic region [Saccharomyces cerevisiae]
20947	ENU04741	272..1145											
20947	ENU04741	ANT61C6657: 33-52		422-445	NAP		g1706567	89	59	0.000000	25	40	putative enoyl-CoA hydratase [Mycobacterium leprae]
		1283..1644											

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20948	ENU04742	AN161C5440:	90-109	748-767	NAP		g728743	1212	322	e-103			"6-phosphogluconate dehydrogenase, decarboxylating 1 [Saccharomyces cerevisiae]"
20949	ENU04743	AN161C3035:	105-130	416-443	NAP		g4056553	133	86	1.00E-16	39	20	(AL034583) putative exonuclease [Schizosaccharomyces pombe]
20950	ENU04744	AN161C5064:	37-56	804-829	NAP		g231714	212	99	5.00E-20	36	24	CDC21 protein []
20951	ENU04745	AN161C7394:	107-126	401-420	NAP		g125155	283	127	4.00E-29	41	71	Adenylate kinase 2 (ATP-AMP transphosphorylase) [Saccharomyces cerevisiae]
20952	ENU04746	AN161C1243:	105-125	349-371	NAP		g114251	175	51	1.00E-12	41	40	L-asparaginase I (L-asparagine amidohydrolase I) [Escherichia coli]
20953	ENU04747	AN161C5328:	24-45	762-786	NAP		g3560207	361	89	3.00E-17	35	46	(AL031536) fnx1p. [Schizosaccharomyces pombe]
20954	ENU04748	AN161C8350:	22-44	766-788	NAP		g2791647	470	89	4.00E-17	31	42	(AL021287) hypothetical protein RV3049c [Mycobacterium tuberculosis]
20955	ENU04749	AN161S1354:			NAP		g1079170	137	52	0.000006	31	61	larval glue protein Lgp-3 precursor - fruit fly [Drosophila virilis]
20956	ENU04750	AN161C9637:	41-60	791-812	NAP		g4154817	480	107	1.00E-47	42	87	[Drosophila virilis] (AE001466) putative [Helicobacter pylori J99] (AB007770) translation elongation factor 1 alpha [Aspergillus oryzae]
20957	ENU04751	AN161C7698:	22-49	723-746	NAP		g4521247	1397	494	e-139	92	57	delta-(L-alpha-aminoacidipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emmericella nidulans]
20958	ENU04752	AN161C291:	1		NAP		g113314	1686	492	e-141	93	7	(Z99120) similar to Na+/nucleoside cotransporter [Bacillus subtilis] hypothetical hydrolase/peptidase Y4TM [Rhizobium sp. NGR234]
20959	ENU04753	AN161C1116:	22-48	763-783	NAP		g2635715	530	111	1.00E-35	41	63	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
20960	ENU04754	AN161C7546:	31-51	807-828	NAP		g2497952	221	98	1.00E-19			(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
20961	ENU04755	AN161S4137:			NAP		g283032	161	32	0.013	35	59	(U81165) MOD-E [Podospira anserina]
20962	ENU04756	AN161C936:	49-68	494-515	NAP		g3560228	423	157	6.00E-43	50	61	
20963	ENU04757	AN161C1316:	47-73	725-747	NAP		g2804612	1030	238	2.00E-89	83	37	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20964	ENU04758	ANI6IS4517: 1..440	24-47	373-393	NAP		g2330857	411	175	2.00E-43	60	10	phosphoribosylformylglycinamide synthase [Schizosaccharomyces pombe]
20965	ENU04759	ANI6IC3920: 22-46	723-746		NAP		g3650404	1579	148	4.00E-35	42	28	(AL031739) eukaryotic translation initiation factor 3 subunit [Schizosaccharomyces pombe]
20966	ENU04760	ANI6IC9383: 1..3966	24-51	807-826	NAP		g416765	1139	164	5.00E-40	27	13	general negative regulator of transcription subunit 1 [Saccharomyces cerevisiae]
20967	ENU04761	ANI6IC8310: 378..1	106-125	459-479	NAP		g1703347	311	85	8.00E-26	51	67	adenine phosphoribosyltransferase 1 (APRT 1) [Saccharomyces cerevisiae]
20968	ENU04762	ANI6IS2708: 1..750			NAP		g2493749	132	36	0.21	23	14	240 KD protein of rod photoreceptor CNG-channel [Bos taurus]
20969	ENU04763	ANI6IC3037: 575..1	23-45	519-546	NAP		g1352954	224	96	2.00E-19	35	25	hypothetical 77.7 KD protein in CCT3-CCT8 intergenic region [Saccharomyces cerevisiae]
20970	ENU04764	ANI6IC1117: 3:924..214	220-238	638-657	NAP		g136682	333	140	8.00E-33	39	99	ubiquitin carboxyl-terminal hydrolase isozyme L3 (UCH-L3) (ubiquitin thiolesterase L3) [Homo sapiens]
20971	ENU04765	ANI6IC6434: 2648..1866	23-44	712-731	NAP		g1076802	75	46	0.0003			extensin-like protein - maize [Zea mays]
20972	ENU04766	ANI6IC26:81 7..1	222-244	736-763	NAP		g1705828	1119	298	3.00E-85	95	23	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emicella nidulans]
20973	ENU04767	ANI6IC8888: 282..1609	25-52	713-737	NAP		g730755	837	129	2.00E-50	54	45	transporter protein SMF2 [Saccharomyces cerevisiae]
20974	ENU04768	ANI6IC4526: 1314..1	22-45	809-828	NAP		g3650406	754	199	1.00E-50	47	26	(AL031739) 26S proteasome regulatory subunit [Schizosaccharomyces pombe]
20975	ENU04769	ANI6IC1120: 11172..12742	22-44	714-731	NAP		g125727	701	141	1.00E-39			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase [Kluveromyces lactis])
20976	ENU04770	ANI6IC7885: 1238..835	102-122	334-353	NAP		g1711623	159	38	0.000000	41	11	"alanyl-TRNA synthetase, cytoplasmic (alanine--TRNA ligase) (ALARS) [Saccharomyces cerevisiae]"
20977	ENU04771	ANI6IC6793: 1..648	59-78	571-591	NAP		g3135013	755	302	1.00E-81	68	24	(AJ005963) 100 kDa protein [Ajiellomyces capsulatus]
20978	ENU04772	ANI6IC7746: 4718..4215	95-114	451-478	NAP		g1351714	190	73	1.00E-12	25	33	putative transporter C1D3.18C [Schizosaccharomyces pombe]



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20979	ENU04773	ANI61C1049:	48-69	588-615	NAP		g3288709	996	277	e-109	89	15	(AB010442) PMR1 [Penicillium digitatum]
20980	ENU04774	ANI61C8780:	48-65	799-826	NAP		g130333	554	154	6.00E-37	47	68	pectin lyase D precursor (PLD) (pectin lyase I) (PLI) [Aspergillus niger]
20981	ENU04775	ANI61C1252:	114-133	435-462	NAP		g400069	841	261	5.00E-87			insertion element IS1 protein INSB [Escherichia coli]
20982	ENU04776	ANI61C1269:	496..1		NAP		g2145993	125	69	4.00E-11	28	97	yfcA protein - Mycobacterium leprae [Mycobacterium leprae]
20983	ENU04777	ANI61C9834:	65-84	798-816	NAP		g3402279	702	156	1.00E-54	49	78	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]
20984	ENU04778	ANI61C3653:	121-140	342-361	NAP		g134920	101	47	0.00008	26	30	sulfated surface glycoprotein 185 (SSG 185) [Volvox carter]
20985	ENU04779	ANI61C6617:	23-42	576-595	NAP		g1079456	471	192	2.00E-49	60	62	"actin-capping protein beta chain, splice form 2 - chicken [Gallus gallus]"
20986	ENU04780	ANI61S1139:			NAP		g1572721	133	38	0.044	31	13	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
20987	ENU04781	ANI61C8129:	22-46	621-640	NAP		g730240	249	142	3.00E-33	34	54	osmotic growth protein 1 [Saccharomyces cerevisiae]
20988	ENU04782	ANI61C1094	186-204	729-748	NAP		g3560228	476	98	7.00E-31	43	77	(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
20989	ENU04783	ANI61C7234:			NAP		g2499716	1440	303	e-109	83	55	"exopolysaccharuronase precursor (exoPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
20990	ENU04784	ANI61C9604:	6879..6438		NAP		g729650	258	98	3.00E-20	44	30	"exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellobiohydrolase) [Penicillium janthinellum]"
20991	ENU04785	ANI61C6076:	22-45	496-515	NAP		g1197667	96	31	5.1	29	98	(U46857) vitellogenin [Anolis pulchellus]
20992	ENU04786	ANI61C5316:	68-87	362-381	NAP		g1174622	227	84	5.00E-16	52	19	"T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta) [Saccharomyces cerevisiae]"
20993	ENU04787	ANI61C9088:	111-130	532-555	NAP		g2826168	193	57	0.000000	36	42	(AB010714) salicylate hydroxylase [Pseudomonas putida]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20994	ENU04788	ANT61C5537: 22-43	456-479	NAP			g729763	198	101	4.00E-21	38	80	30 KD heat shock protein [Emericella nidulans]
20995	ENU04789	ANT61C753:7 22-49	702-721	NAP			g1083855	150	92	4.00E-18	26	1	cyclosporin synthetase - Tolypocladium inflatum [Tolypocladium inflatum]
20996	ENU04790	ANT61C1830: 107-129	802-821	NAP			g2501686	919	349	3.00E-95	59	16	hypothetical 187.1 KD protein in OGG1-CNA2 intergenic region [Saccharomyces cerevisiae]
20997	ENU04791	ANT61C8954: 93-112	556-579	NAP			g3978466	462	108	1.00E-47	45	29	(AF086822) dihydroxyacetone synthase [Candida boidinii]
20998	ENU04792	ANT61C1899: 35-54	805-829	NAP			g2501202	1767	272	e-108	75	51	protein disulfide isomerase precursor (PD) [Aspergillus niger]
20999	ENU04793	ANT61C3322: 164-183	454-479	NAP			g1722894	379	159	9.00E-39	52	42	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-l-arabinofuranosidase (arabinosidase) [Bacteroides ovatus]"
21000	ENU04794	ANT61C1684: 22-41	781-808	NAP			g2330829	557	170	1.00E-41	40	18	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
21001	ENU04795	ANT61C1574: 120-137	492-511	NAP			g2293194	99	57	0.000000	28	41	(AF008220) yreR [Bacillus subtilis]
21002	ENU04796	ANT61C1236: 22-45	766-792	NAP			g125462	1460	573	e-163			"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3)I) [Cloning vector pHIND2.2]"
21003	ENU04797	ANT61C5865: 108-127	724-750	NAP			g2492799	589	161	8.00E-58	44	72	putative sterigmatocystin biosynthesis dehydrogenase STCV [Emericella nidulans]
21004	ENU04798	ANT61C1994: 29-51	370-389	NAP			g4884104	110	57	0.000000			(AL050060) hypothetical protein [Homo sapiens]
21005	ENU04799	ANT61S1320: 1..590		NAP			g3874243	147	50	0.00002	20	50	(Z70204) similar to PHD-finger.; cDNA EST EMBL.T00556 comes from this gene; cDNA EST yk344f7.5 comes from this gene [Caenorhabditis elegans]
21006	ENU04800	ANT61C1743: 24-44	733-755	NAP			g3261605	699	185	3.00E-61	45	14	(Z74697) ppsA [Mycobacterium tuberculosis]
21007	ENU04801	ANT61C7911: 22-48	776-797	NAP			g2894293	507	105	6.00E-28	35	47	(AL021837) hypothetical protein [Schizosaccharomyces pombe]

# Database "Schizosaccharomyces pombe"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21008	ENU04802	ANT61C8612:	102-125	294-314	NAP		g2239205	198	90	5.00E-18	37	48	(Z97209) hypothetical protein [Schizosaccharomyces pombe]
21009	ENU04803	ANT61C8663:	28-49	806-828	NAP		g134854	269	92	4.00E-18	27	19	transcription initiation protein SPT6 [Saccharomyces cerevisiae]
21010	ENU04804	ANT61C1850:	25-52	720-747	NAP		g1805251	849	272	3.00E-72	54	50	(U58946) transposase [Aspergillus awamori]
21011	ENU04805	ANT61C5897:	33-52	590-617	NAP		g1870216	1136	416	e-116	100	100	(AC000133) f4p06 [Emericella nidulans]
21012	ENU04806	ANT61C9479:	22-44	792-818	NAP		g4056553	300	94	1.00E-18	39	34	(AL034583) putative exonuclease [Schizosaccharomyces pombe]
21013	ENU04807	ANT61C1226:	101-120	424-444	NAP		g1710045	274	106	2.00E-22	38	21	mitochondrial respiratory chain complexes assembly protein RCA1 (TAT-binding homolog 12) [Saccharomyces cerevisiae]
21014	ENU04808	ANT61C6000:	22-47	806-827	NAP		g2842516	484	88	7.00E-17			(AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe]
21015	ENU04809	ANT61C7282:	22-49	376-399	NAP		g3150141	504	128	2.00E-48	73	51	(AL023594) 40s ribosomal protein s4 type [Schizosaccharomyces pombe]
21016	ENU04810	ANT61C1158:	43-63	791-810	NAP		g1911743	1514	320	e-103	84	65	(S83229) beta-isopropylinalate dehydrogenase=isozyme [Aspergillus niger]
21017	ENU04811	ANT61C7741:	22-42	697-724	NAP		g1705679	2474	226	5.00E-99	78	31	cell division control protein 48 [Saccharomyces cerevisiae]
21018	ENU04812	ANT61C3249:	52-70	774-793	NAP		g1078072	247	85	8.00E-16	32	41	probable membrane protein YLR324w - yeast [Saccharomyces cerevisiae]
21019	ENU04813	ANT61C7670:	50-69	772-791	NAP		g3043376	261	60	0.000000			[Saccharomyces cerevisiae] (AJ005258) amyR [Aspergillus oryzae]
21020	ENU04814	ANT61C6680:	30-47	482-507	NAP		g4099032	892	176	8.00E-74	96	58	(U82084) unknown [bacteriophage SFX]
21021	ENU04815	ANT61S2301:	71-90	363-386	NAP		g1175364	183	82	2.00E-15	39	46	hypothetical 28.0 KD protein C13C5.04 in chromosome I [Schizosaccharomyces pombe]
21022	ENU04816	ANT61C9378:	23-45	775-802	NAP		g2132860	280	45	0.000000	42	91	probable membrane protein YOL162w - yeast [Saccharomyces cerevisiae]
		472..1418							6				[Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21023	ENU04817	ANI6IC9378: 1..456	22-48	407-434	NAP		g2132861	363	84	2.00E-29	51	75	probable membrane protein YOL163w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21024	ENU04818	ANI6IC1114: 4:516..1	32-51	398-415	NAP		g2222786	422	108	3.00E-23	63	69	(Z97185) hypothetical protein [Schizosaccharomyces pombe]
21025	ENU04819	ANI6IC2562: 1533..2108	51-70	449-468	NAP		g131768	569	211	3.00E-54	60	35	quinate permease (quinate transporter) [Emmericella nidulans]
21026	ENU04820	ANI6IC1106: 5:1224..1	30-49	670-691	NAP		g3183329	713	136	6.00E-53	57	52	hypothetical aminotransferase C6B12.04C [Schizosaccharomyces pombe]
21027	ENU04821	ANI6IC1024: 9:9831..9292	94-115	494-519	NAP		g1293655	113	70	1.00E-11	26	27	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21028	ENU04822	ANI6IS1471: 631..28			NAP		g418604	857	328	2.00E-93	89	64	hypothetical 35.6 KD protein in RPME-TDK intergenic region (ORFP) []
21029	ENU04823	ANI6IC8903: 1..1199	102-125	803-829	NAP		g232152	1231	421	e-132	97	51	G2/mitotic-specific cyclin B [Emmericella nidulans]
21030	ENU04824	ANI6IC7756: 1187..1	22-49	618-643	NAP		g3451467	569	212	4.00E-54	45	45	(AL031349) putative cystathionine gamma-synthase [Schizosaccharomyces pombe]
21031	ENU04825	ANI6IC4392: 822..1	22-43	697-715	NAP		g3947592	448	121	2.00E-46			"(AL034364) similar to homogenisate 1,2-dioxygenase (EC 1.13.11.5) (homogenisicase) (homogenisate oxygenase) (homogenisic acid oxidase); cDNA EST yk385c12.5 comes from this gene; cDNA EST EMBL:D73328 comes from this gene; cD... []"
21032	ENU04826	ANI6IS1672: 1..695			NAP		g2119707	77	55	0.000000	27	80	proline-rich protein precursor - rat []
21033	ENU04827	ANI6IC1097: 5:812..1721	71-90	805-829	NAP		g2496731	881	336	1.00E-91	67	92	hypothetical 30.2 KD protein Y4OV [Rhizobium sp. NGR234]
21034	ENU04828	ANI6IC3908: 798..1409	22-44	485-511	NAP		g586485	242	145	3.00E-34	35	50	hypothetical 45.5 KD protein in FIG1-GIP1 intergenic region [Saccharomyces cerevisiae]
21035	ENU04829	ANI6IS49:1..530			NAP		g416876	238	47	5.00E-11	38	60	dihydrodipicolinate synthase (DHDPs) (vegetative protein 81) (VEG81) [Bacillus subtilis]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21036	ENU04830	ANI61C1518:	22-43	659-678	NAP		g1168464	1254	212	2.00E-78	57	53	monamine oxidase N (MAO-N) [Aspergillus niger]
21037	ENU04831	ANI61C1133:	217-236	715-740	NAP		g118381	1019	228	6.00E-59	56	58	ornithine decarboxylase (ODC) [Neurospora crassa]
21038	ENU04832	ANI61C4437:	22-43	440-462	NAP		g4583351	113	64	5.00E-10	27	30	(AF114167) lysosomal peptidain insensitive protease [Canis familiaris]
21039	ENU04833	ANI61C2465:	57-76	795-815	NAP		g1546072	1287	147	1.00E-34	40	9	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21040	ENU04834	ANI61C9269:	26-53	808-829	NAP		g1805251	718	249	3.00E-65	44	51	(U58946) transposase [Aspergillus awamori]
21041	ENU04835	ANI61C9769:	102-127	526-551	NAP		g1870212	903	278	2.00E-74	94	97	(AC000133) ORF [Emmericella nidulans]
21042	ENU04836	ANI61C6563:	121-144	378-405	NAP		g1351598	398	167	5.00E-41	47	31	hypothetical 59.6 KD protein C4G8.07C in chromosome I [Schizosaccharomyces pombe]
21043	ENU04837	ANI61C6365:	39-57	728-749	NAP		g2342601	2803	145	3.00E-34	37	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21044	ENU04838	ANI61C2860:	161-187	714-740	NAP		g1346361	269	142	1.00E-35	41	32	serine/threonine-protein kinase SHK2 [Schizosaccharomyces pombe]
21045	ENU04839	ANI61C9769:	22-47	591-610	NAP		g1870213	1021	254	e-108	97	99	(AC000133) ORF [Emmericella nidulans]
21046	ENU04840	ANI61C1028	60-79	443-461	NAP		g609350	549	228	3.00E-59	63	22	(U15099) methionine synthase [Saccharomyces cerevisiae]
21047	ENU04841	ANI61C1045	105-132	426-447	NAP		g1709181	288	117	2.00E-27	39	27	high affinity methionine permease [Saccharomyces cerevisiae]
21048	ENU04842	ANI61C2802:	43-62	775-794	NAP		g4056555	849	86	3.00E-16			(AL034583) putative mitochondrial atp-dependent ma helicase precursor [Schizosaccharomyces pombe]
21049	ENU04843	ANI61S4378:			NAP		g1079170	144	31	0.04	31	69	larval glue protein Lgp-3 precursor - fruit fly (Drosophila virilis) [Drosophila virilis]
21050	ENU04844	ANI61C2758:	105-131	523-546	NAP		g2133266	875	319	1.00E-86	96	16	chromosome scaffold protein sudA - Emmericella nidulans [Emmericella nidulans]
21051	ENU04845	ANI61C5221:	22-45	806-828	NAP		g3282216	540	56	0.000000			(U68716) polyketide synthase homolog [Botryotinia fuckeliana]
21052	ENU04846	ANI61C1008	35-54	497-519	NAP		g135649	263	75	2.00E-13	41	31	"2,4-dichlorophenol 6-monoxygenase (2,4-dichlorophenol hydroxylase) (2,4-DCP hydroxylase) [Plasmid pJP4]"

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21053	ENU04847	ANI61C9706: 1522..6699	22-48	725-747	NAP		g1805262	3278	103	2.00E-45	39	13	"(U75347) fatty acid synthase, beta subunit [Emerticella nidulans]"
21054	ENU04848	ANI61C3226: 813..1	58-77	676-695	NAP		g1723578	359	96	3.00E-29	50	60	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
21055	ENU04849	ANI61C1235: 924..72	22-49	783-810	NAP		g4557168	1419	530	e-150	97	99	(AF104442) inhibitor resistant beta lactamase TEM-54 [Escherichia coli]
21056	ENU04850	ANI61S1182: 1..976			NAP		g3153821	177	34	0.99	26	29	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
21057	ENU04851	ANI61C7768: 1983..2496	24-51	468-492	NAP		g3005097	502	109	2.00E-48	67	99	"(AF046872) Cu,Zn-superoxide dismutase [Candida albicans]"
21058	ENU04852	ANI61C4396: 1322..413	55-76	768-787	NAP		g1293655	416	155	4.00E-37	41	37	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21059	ENU04853	ANI61C1049 0:4829..8034	22-46	775-802	NAP		g1834340	4837	489	e-138	95	18	(Z68904) ATP-binding cassette multidrug transporter [Emerticella nidulans]
21060	ENU04854	ANI61C6622: 552..1	81-100	479-500	NAP		g131768	555	226	9.00E-59	60	34	quinone permease (quinone transporter) [Emerticella nidulans]
21061	ENU04855	ANI61S1397: 1..369			NAP		g140011	497	182	1.00E-45	85	30	mitochondrial ribosomal protein S5 [Emerticella nidulans]
21062	ENU04856	ANI61C1122 4:1..504	122-144	458-482	NAP		g2493391	359	155	1.00E-37	49	38	probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) [Emerticella nidulans]
21063	ENU04857	ANI61C9762: 7481..7130	78-97	305-331	NAP		g731700	228	104	2.00E-22	41	31	hypothetical 42.4 KD protein in CDC12-ORC6 intergenic region [Saccharomyces cerevisiae]
21064	ENU04858	ANI61C957.1 ..653	102-125	516-543	NAP		g1703456	520	219	2.00E-56	52	18	cation-transporting ATPase PAT1 [Dictyostelium discoideum]
21065	ENU04859	ANI61C3989: 874..1	55-74	724-743	NAP		g1293655	332	78	8.00E-31	36	38	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21066	ENU04860	ANI61C5606: 1..829	66-85	760-786	NAP		g4106374	910	178	1.00E-89	73	46	(AF069777) mitogen-activated protein kinase kinase CPK1 [Cryphonectria parasitica]
21067	ENU04861	ANI61S4332: 397..1			NAP		g3170523	637	258	1.00E-68	99	10	(AF053883) coatomer alpha subunit [Emerticella nidulans]
21068	ENU04862	ANI61C9112: 4843..4071	22-48	725-752	NAP		g464738	138	58	0.000000			translocation protein SEC66 (HSS1 protein) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21069	ENU04863	ANI61C320:1			NAP		g940860	461	147	8.00E-35	51	29	(X90565) MYO2 [Saccharomyces cerevisiae]
21070	ENU04864	ANI61C6479: 744..2877	97-116	651-672	NAP		g1749498	176	95	5.00E-19	28	77	(D89145) similar to Saccharomyces cerevisiae ORF YGL092W
21071	ENU04865	ANI61C7648: 1..428	27-50	373-400	NAP		g1170421	180	60	3.00E-13	40	21	[Schizosaccharomyces pombe] HUS2 protein [Saccharomyces cerevisiae]
21072	ENU04866	ANI61C7910: 2260..1			NAP		g113314	3671	454	e-136	89	7	delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emertella nidulans]
21073	ENU04867	ANI61C1224: 1..844	64-91	638-663	NAP		g462071	797	290	7.00E-85			"fatty acid synthase, subunit beta [Yarrowia lipolytica]"
21074	ENU04868	ANI61C9303: 4520..2714	27-54	805-829	NAP		g4755188	521	73	8.00E-24			(AC007018) unknown protein [Arabidopsis thaliana]
21075	ENU04869	ANI61C2783: 1067..2183	22-44	677-695	NAP		g2414579	545	216	1.00E-55	49	44	(Z99292) flavoprotein [Schizosaccharomyces pombe]
21076	ENU04870	ANI61C1014 6:1022..265	50-69	635-657	NAP		g1730743	387	183	9.00E-46	46	77	hypothetical 34.9 KD protein in MSK1-PDA2 intergenic region [Saccharomyces cerevisiae]
21077	ENU04871	ANI61C3868: 3311..3872	22-49	436-461	NAP		g2949018	214	89	3.00E-17	35	79	maltose O-acetyltransferase (maltose transacetylase) [Escherichia coli]
21078	ENU04872	ANI61C1035 4:592..1	22-49	515-534	NAP		g2315274	419	76	1.00E-32	49	51	(Y11113) endoglucanase IV [Hypocrea jecorina]
21079	ENU04873	ANI61C8581: 3239..4082	22-42	799-819	NAP		g3980401	213	127	7.00E-29	33	97	(AC004561) putative tropinone reductase [Arabidopsis thaliana]
21080	ENU04874	ANI61C27:1.. 2171	24-51	715-742	NAP		g586352	1238	134	1.00E-30	34	22	hypothetical 124.0 KD protein in PCS60-ABD1 intergenic region [Saccharomyces cerevisiae]
21081	ENU04875	ANI61C1053 5:4916..3815	185-204	810-829	NAP		g2851424	181	100	1.00E-20	25	75	hypothetical 37.5 KD protein in DEGA-NPRB intergenic region [Bacillus subtilis]
21082	ENU04876	ANI61C7988: 770..1	40-59	665-691	NAP		g1175361	150	55	0.000000	29	51	hypothetical 48.5 KD protein C13C5.02 in chromosome I [Schizosaccharomyces pombe]
21083	ENU04877	ANI61C1202: 1..1694	22-41	786-808	NAP		g2342601	790	166	2.00E-40	37	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21084	ENU04878	ANI61C5153: 216..1177	40-59	768-787	NAP		g1706176	977	316	2.00E-85	71	25	cutinase transcription factor 1 alpha [Fusarium solani f. sp. pisi]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21085	ENU04879	ANI61C6712:	22-49	722-749	NAP		g10709997	726	48	0.0001			DNA repair protein RAD18 [Schizosaccharomyces pombe]
21086	ENU04880	ANI61C499:7	63-82	806-829	NAP		g2909648	548	157	5.00E-47	53	95	(AL021943) echA5 [Mycobacterium tuberculosis]
21087	ENU04881	ANI61C4145:	64-90	485-504	NAP		g1078626	954	346	5.00E-95	99	12	bimD protein - Emericella nidulans [Emericella nidulans]
21088	ENU04882	ANI61C7661:	102-123	291-310	NAP		g464435	303	126	6.00E-29	53	26	acid phosphatase precursor [Aspergillus niger]
21089	ENU04883	ANI61C6082:	68-87	804-826	NAP		g1805261	645	166	1.00E-44	40	13	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
21090	ENU04884	ANI61S373:1.	42-61	257-276	NAP		g2392764	335	141	4.00E-34	78	17	(AC002534) hypothetical protein [Arabidopsis thaliana]
21091	ENU04885	ANI61C3838:	23-46	807-826	NAP		g3806120	2179	466	e-130	96	23	(AF097728) pyruvate carboxylase [Aspergillus terreus]
21092	ENU04886	ANI61C1035	60-79	791-810	NAP		g3335173	373	71	1.00E-17			(AF071202) ABC transporter MOAT-B [Homo sapiens]
21093	ENU04887	ANI61C4237:	31-50	807-829	NAP		g1870208	2438	114	7.00E-25	99	58	(AC000133) ORF [Emmericella nidulans]
21094	ENU04888	ANI61C1042	22-43	810-829	NAP		g2495217	1971	436	e-121	78	57	glucokinase (glucose kinase) (GLK) [Aspergillus niger]
21095	ENU04889	ANI61C5224:	23-50	801-827	NAP		g1077569	1088	208	3.00E-75	53	37	probable membrane protein YDR109c - yeast [Saccharomyces cerevisiae]
21096	ENU04890	ANI61C3404:	22-48	790-810	NAP		g2131132	213	90	1.00E-17	24	19	[Saccharomyces cerevisiae] UDPglucose--glycoprotein glucosephosphotransferase (EC 2.7.8.19) - fission yeast
21097	ENU04891	ANI61C2738:	35-54	780-805	NAP		g4160575	539	122	2.00E-49	53	42	(Schizosaccharomyces pombe) [Schizosaccharomyces pombe] (AL035226) putative structure specific recognition protein, possible chromatin-associated HMG protein
21098	ENU04892	ANI61C1038	151-170	702-721	NAP		g1730665	121	67	2.00E-10	29	91	[Schizosaccharomyces pombe] hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region [Saccharomyces cerevisiae]
21099	ENU04893	ANI61C2329:	30-54	795-820	NAP		g4507295	250	85	4.00E-16	28	99	syntaxin 7 [Homo sapiens]



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21100	ENU04894	AN161C1038	22-46	535-562	NAP		g3790261	371	160	1.00E-38	43	65	(AL031966) putative quinone oxidoreductase [Schizosaccharomyces pombe]
21101	ENU04895	AN161S1377	70-89	378-397	NAP		g2494062	740	292	8.00E-79	98	51	hypothetical 30.8 KD protein in GIP-FDRA intergenic region [Escherichia coli]
21102	ENU04896	AN161C1013	22-49	766-789	NAP		g3873546	1129	190	6.00E-75	57	66	(AL033534) acetyl-coa acetyltransferase [Schizosaccharomyces pombe]
21103	ENU04897	AN161C1117	105-128	377-401	NAP		g129302	329	132	2.00E-30	43	47	D-amino acid oxidase (DAMOX) (DAO) (DAAO) [Nectria haematococca]
21104	ENU04898	AN161C4968	22-48	769-788	NAP		g135139	1151	348	3.00E-95	57	47	"lysyl-TRNA synthetase, cytoplasmic (lysine--TRNA ligase) (LYSRS) [Saccharomyces cerevisiae]"
21105	ENU04899	AN161C6717	27-46	806-829	NAP		g3660282	574	88	9.00E-30	39	54	"Chain A, Aspartate Aminotransferase From Saccharomyces Cerevisiae Cytoplasm [I]"
21106	ENU04900	AN161C6446	22-48	706-730	NAP		g1077167	152	73	3.00E-12	23	53	hypothetical protein YGL244w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21107	ENU04901	AN161C989	1	63-86	NAP		g1546072	903	55	0.000000	21	9	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21108	ENU04902	AN161C4177	22-44	428-447	NAP		g141305	472	172	6.00E-47			YPT1-related protein 2 [Schizosaccharomyces pombe]
21109	ENU04903	AN161C7502	27-50	795-822	NAP		g1351721	1692	296	2.00E-85	56	10	putative translational activator C18G6.05C (GCN1 homolog) [Schizosaccharomyces pombe]
21110	ENU04904	AN161C7090	23-43	794-813	NAP		g3170246	1708	398	e-128	98	49	(AF043230) trehalose-6-phosphate synthase subunit 1 [Emmericella nidulans]
21111	ENU04905	AN161C4732	96-115	302-321	NAP		g3287841	94	54	0.000000	30	19	glucose oxidase precursor (glucose oxyhydraz) (GOD) (beta-D-glucose:oxygen 1-oxido-reductase) [Talaromyces flavus]
21112	ENU04906	AN161C5835			NAP		g3283373	230	82	4.00E-15	30	28	(AF067650) sarcosine dehydrogenase [Rattus norvegicus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21113	ENU04907	ANT61C6337:	71-90	800-819	NAP		g3451309	427	140	6.00E-45	40	95	(AL031324) transcription initiation factor IIIe beta subunit (TFIIE-beta) [Schizosaccharomyces pombe]
21114	ENU04908	ANT61C6864:	22-48	804-824	NAP		g4063002	937	228	4.00E-59	42	35	(AB021703) fr [Neurospora crassa]
21115	ENU04909	ANT61S4630:			NAP		g2213547	201	95	1.00E-19	46	33	(Z97052) putative ubiquinone biosynthesis methyltransferase [Schizosaccharomyces pombe]
21116	ENU04910	ANT61C4391:	33-52	411-430	NAP		g1723516	327	144	4.00E-34	59	53	hypothetical 24.4 KD protein C22E12.02 in chromosome I [Schizosaccharomyces pombe]
21117	ENU04911	ANT61C1164:	31-53	247-266	NAP		g101797	469	195	8.00E-50	85	33	quininate 5-dehydrogenase (EC 1.1.1.24) - Emericella nidulans [] [Schizosaccharomyces pombe]
21118	ENU04912	ANT61C8818:	122-142	397-416	NAP		g3170523	546	191	2.00E-48	94	10	(AF053883) coatomer alpha subunit [Emericella nidulans]
21119	ENU04913	ANT61C2376:	30-49	786-805	NAP		g2497129	446	111	6.00E-24	38	72	hypothetical 38.2 KD protein in SUB1-ARGR1 intergenic region [Saccharomyces cerevisiae]
21120	ENU04914	ANT61C3368:	22-41	800-827	NAP		g1351682	425	82	3.00E-16	28	48	hypothetical 53.5 KD protein C1F5.07C in chromosome I [Schizosaccharomyces pombe]
21121	ENU04915	ANT61C9569:	24-43	804-829	NAP		g1154950	129	47	2.00E-11	27	35	(X94769) choline dehydrogenase [Rattus rattus]
21122	ENU04916	ANT61C8170:	28-47	775-794	NAP		g2147662	1979	238	4.00E-62	46	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium [Colletotrichum lagenarium]
21123	ENU04917	ANT61C6409:	95-114	551-577	NAP		g730338	774	289	1.00E-77	67	36	lysophospholipase precursor (phospholipase B) [Penicillium chrysogenum]
21124	ENU04918	ANT61C9456:	46-65	734-757	NAP		g1173091	497	171	4.00E-42	49	63	ran GTPASE activating protein 1 (RNAI protein) [Schizosaccharomyces pombe]
21125	ENU04919	ANT61C9369:	84-106	500-527	NAP		g1703371	253	93	8.00E-24	43	22	sterol O-acyltransferase 2 (sterol-ester synthase 2) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21126	ENU04920	ANI61C7770:	72-91	689-710	NAP		g1332918	517	179	6.00E-45	44	55	CAAX prenyl protease 1 (prenyl protein-specific endoprotease 1) (PSEP 1) (A-factor converting enzyme) [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]
21127	ENU04921	ANI61C8438:	37-56	745-764	NAP		g4499843	609	91	2.00E-19	38	53	(L47346) alpha-glucoside permease [Saccharomyces cerevisiae] (U32375) tartrate dehydrogenase [Agrobacterium vitis] (AL023534) putative methionine aminopeptidase 1 [Schizosaccharomyces pombe] (AL031179) ap synthase delta chain family, oligomycin sensitivity conferring protein [Schizosaccharomyces pombe] 4-carboxymuconolactone decarboxylase (CMD) [Acinetobacter calcoaceticus]
21132	ENU04926	ANI61C2478:	22-48	454-478	NAP		g118292	258	109	1.00E-23	38	100	hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae] (AC005313) unknown protein [Arabidopsis thaliana]
21133	ENU04927	ANI61C4431:	27-46	807-828	NAP		g2132120	139	175	5.00E-43	27	19	hypothetical protein SPAC8A4.01c - fission yeast (Schizosaccharomyces pombe) (fragment) [Schizosaccharomyces pombe] ORF5 - Alcaigenes eutrophus [Ralstonia eutrophal]
21134	ENU04928	ANI61C6376:	22-47	805-828	NAP		g3548818	348	134	1.00E-30	37	64	"dynactin, 150 KD isoform (150 KD dynein-associated polypeptide) (DP-150) (DAP-150) (P150-glied) [Neurospora crassa]"
21135	ENU04929	ANI61C8026:	26-45	613-632	NAP		g2130442	1140	129	5.00E-34	33	29	putative folypolyglutamate synthase (folypoly-gamma-glutamate synthetase) (FPGS) [Saccharomyces cerevisiae]
21136	ENU04930	ANI61C5280:	40-59	605-624	NAP		g2120955	387	175	2.00E-43	46	67	
21137	ENU04931	ANI61C7663:	24-43	704-731	NAP		g2493479	860	196	2.00E-49	47	21	
21138	ENU04932	ANI61S996.1:	28-48	249-273	NAP		g2494589	129	58	0.000000	37	22	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21139	ENU04933	ANI61C1866: 1576..1092	42-61	436-463	NAP		g2997731	650	222	1.00E-57	68	48	(AF054512) endoglucanase V [Aspergillus aculeatus]
21140	ENU04934	ANI61C7308: 1.637	113-132	524-543	NAP		g2117031	538	190	7.00E-51	62	37	(X94220) rhamnoglucuronase [Aspergillus niger]
21141	ENU04935	ANI61C6373: 1..3346	22-49	680-702	NAP		g1546072	828	75	7.00E-13			(U68040) polyketide synthase [Cochliobolus heterotrophus]
21142	ENU04936	ANI61C1004: 3:4535..1974	22-47	809-829	NAP		g2465160	1351	92	5.00E-38	41	24	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
21143	ENU04937	ANI61C6032: 1..657	152-171	533-558	NAP		g1723241	167	72	4.00E-12	29	29	hypothetical 60.7 KD protein C26A3.15C in chromosome I [Schizosaccharomyces pombe]
21144	ENU04938	ANI61C3309: 2809..1386	27-46	768-787	NAP		g2440206	1169	155	7.00E-59	56	33	(Z99532) putative integral membrane protein [Schizosaccharomyces pombe]
21145	ENU04939	ANI61C9915: 906..1	58-81	805-825	NAP		g1169440	1451	321	e-150	97	6	"dynein heavy chain, cytosolic (DYHC) [Emmericella nidulans]"
21146	ENU04940	ANI61C4247: 1..1862	23-45	752-778	NAP		g2342601	1009	261	6.00E-69	47	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21147	ENU04941	ANI61C3772: 1125..814	72-91	253-272	NAP		g549657	284	98	2.00E-20	54	24	hypothetical 49.0 KD protein UFD4-CAP1 intergenic region [Saccharomyces cerevisiae]
21148	ENU04942	ANI61C7930: 1..1336	44-63	611-632	NAP		g3334134	203	48	0.00006	30	36	chromatin assembly factor 1 P90 subunit (CAF-1 90 KD subunit) (RAP1 localization factor 2) [Saccharomyces cerevisiae]
21149	ENU04943	ANI61C9002: 1069..579	57-76	447-466	NAP		g3687473	191	52	2.00E-10	44	99	(AL031798) WD repeat protein [Schizosaccharomyces pombe]
21150	ENU04944	ANI61S3829: 1..529			NAP		g758803	90	46	0.0001	24	33	(U23828) peritrophin-95 precursor [Lucilia cuprina]
21151	ENU04945	ANI61C4391: 2057..1	22-40	712-731	NAP		g3114719	949	72	4.00E-12	38	13	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckelliana]
21152	ENU04946	ANI61C1720: 1181..1	116-138	721-748	NAP		g2791647	409	82	9.00E-23	29	48	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]
21153	ENU04947	ANI61C1069: 1:1..435	22-48	383-402	NAP		g2132249	348	123	6.00E-28	56	72	hypothetical protein YPL252c - yeast [Saccharomyces cerevisiae]
21154	ENU04948	ANI61S3700: 457..1	113-132	408-428	NAP		g2462832	700	184	6.00E-69	92	26	(AF000657) similar to Bacillus Cota [Arabidopsis thaliana]

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21155	ENU04949	AN161C8568:	22-45	453-475	NAP		g4176522	291	136	2.00E-31	30	47	(AL035263) hypothetical protein [Schizosaccharomyces pombe]
21156	ENU04950	AN161C8225:	39-62	806-829	NAP		g3264834	810	109	1.00E-45	46	77	(AF072541) xyliol dehydrogenase; XDH [Galactocandida mastotermiis]
21157	ENU04951	AN161C4401:	22-43	663-690	NAP		g1351102	282	124	2.00E-34	44	53	putative agmatinase precursor (agmatine ureohydrolase) (AUH) [Schizosaccharomyces pombe]
21158	ENU04952	AN161S4151:	31-51	245-271	NAP		g4514357	215	82	1.00E-17	35	100	(AB013376) unknown [Bacillus halodurans]
21159	ENU04953	AN161C1075	197-216	568-587	NAP		g730745	327	132	2.00E-30	38	17	osomolarity two-component system protein SLN1 [Saccharomyces cerevisiae]
21160	ENU04954	AN161C279:1	111-129	501-526	NAP		g3319315	271	104	5.00E-22	49	15	(AF074951) cellobiose dehydrogenase [Thiavia heterothalica]
21161	ENU04955	AN161C1025:	23-48	428-447	NAP		g1723260	396	173	8.00E-43	52	27	hypothetical GTP-binding protein C3F10.16C in chromosome I [Schizosaccharomyces pombe]
21162	ENU04956	AN161C9690:	27-54	688-715	NAP		g1166378	569	111	8.00E-24	32	25	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" (AF095741) unknown [Rattus norvegicus]
21163	ENU04957	AN161C1050	32-51	472-491	NAP		g3747107	96	67	1.00E-10	35	38	alpha-glucuronidase precursor (alpha-glucosiduronase) [Aspergillus tubingensis]
21164	ENU04958	AN161C7276:			NAP		g3912991	237	110	8.00E-24	39	19	coat assembly complex beta adaptin subunit [Rattus norvegicus]
21165	ENU04959	AN161C5836:	56-77	597-624	NAP		g4557469	620	185	4.00E-66			hypothetical 62.3 KD protein in PTP3-II V1 intergenic region [Saccharomyces cerevisiae]
21166	ENU04960	AN161C5110:	22-43	712-731	NAP		g731485	811	159	5.00E-73	51	48	(D64006) Ap-4-A phosphoriylase II [Synechocystis sp.]
21167	ENU04961	AN161C5433:			NAP		g1001338	87	65	2.00E-12	27	50	hypothetical 36.4 KD protein in POP2-HOL1 intergenic region [Saccharomyces cerevisiae]
21168	ENU04962	AN161C3958:	79-98	370-389	NAP		g1730686	96	39	0.014	25	45	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21169	ENU04963	AN161C84:10	22-41	712-731	NAP		g2132651	712	249	3.00E-65	42	48	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]
21170	ENU04964	AN161S1096:	38-57	445-464	NAP		g2673951	655	210	3.00E-58	66	16	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21171	ENU04965	ANI61C5094:	107-126	353-372	NAP		g584806	431	180	4.00E-45	62	23	"ATP synthase alpha chain, mitochondrial precursor [Neurospora crassa]"
21172	ENU04966	ANI61C3659:	48-68	291-310	NAP		g849206	519	213	4.00E-55	74	26	(U28373) Etf1p: Elongation factor 2 (Swiss Prot. accession number P32324). Note that the entire gene is not included in this cosmid.
21173	ENU04967	ANI61C2382:	49-76	614-641	NAP		g1351604	150	52	2.00E-10	26	66	[Saccharomyces cerevisiae] hypothetical 40.0 KD protein C4G8.14C in chromosome I []
21174	ENU04968	ANI61C1180:	22-47	684-709	NAP		g2408064	161	94	9.00E-19	29	23	(Z99165) hypothetical protein [Schizosaccharomyces pombe]
21175	ENU04969	ANI61C2243:	22-41	728-749	NAP		g2408021	352	120	1.00E-26	37	41	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
21176	ENU04970	ANI61C2141:	22-43	658-677	NAP		g4249560	1044	268	1.00E-90	72	51	(AB003109) beta-glucosidase [Hunnicola grisea var. thermoides]
21177	ENU04971	ANI61C9921:	24-51	539-565	NAP		g549643	191	79	3.00E-14	33	18	hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region [Saccharomyces cerevisiae]
21178	ENU04972	ANI61C2170:	23-42	714-740	NAP		g1709064	782	314	5.00E-85	57	75	MNN9 protein [Candida albicans]
21179	ENU04973	ANI61C7073:	68-88	360-381	NAP		g454438	317	111	2.00E-30	60	10	(L28110) LON gene of S. cerevisiae is downstream of the HAP 3 gene; Putative ATP-binding motif bp 1960 to bp 1986.; Putative catalytic site serine of serine proteases from bp 3109 to bp 3111 [Saccharomyces cerevisiae]
21180	ENU04974	ANI61C1121	52-71	601-628	NAP		g731024	387	138	3.00E-32	40	49	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) [Saccharomyces cerevisiae]"
21181	ENU04975	ANI61C2031:	69-96	356-383	NAP		g2687850	120	77	9.00E-14	24	25	(Y15839) fatty acid transporter protein [Coeliobolus heterotrophus]
21182	ENU04976	ANI61S4631:			NAP		g4589850	142	62	0.000000	32	26	(AB025967) chorogenin Hminor [Oryzias latipes]
21183	ENU04977	ANI61C7290:			NAP		g2072023	420	138	3.00E-32	53	100	(U93506) symbiosis-related protein [Laccaria bicolor]
21184	ENU04978	ANI61C6657:	103-123	421-440	NAP		g1073534	185	89	2.00E-17	39	43	incB protein - Escherichia coli [Escherichia coli]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21185	ENU04979	ANT61C1051	28-55	807-829	NAP		g10855432	147	38	0.07			mucin (clone PGM-2A) - pig [Sus scrofa]
21186	ENU04980	ANT61C7282: 2:5237..3644	31-58	465-489	NAP		g4262216	336	138	2.00E-32	35	64	(AC006161) putative DNA binding protein [Arabidopsis thaliana]
21187	ENU04981	554..1 ANT61S1306: 1..655			NAP		g4218005	179	49	0.00003	21	31	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21188	ENU04982	ANT61C1082	116-135	662-686	NAP		g4538673	116	70	1.00E-11	26	57	"(AL049474) putative lipid metabolism protein, sphingomyelinase family similarity [Schizosaccharomyces pombe]"
21189	ENU04983	ANT61C1252: 729..1091	36-55	418-436	NAP		g773414	434	183	8.00E-46	92	66	(U23751) beta galactosidase [Cloning vector pBBR1MCS-5]
21190	ENU04984	ANT61C439:9			NAP		g2330831	228	108	3.00E-23	26	53	(Z98530) myo-inositol transporter [Schizosaccharomyces pombe]
21191	ENU04985	ANT61C8782: 319..9705	29-50	720-739	NAP		g1351343	1615	547	e-155	98	26	positive regulator of purine utilisation [Emeticella nidulans]
21192	ENU04986	942..1 ANT61C295:6	157-184	797-824	NAP		g2648302	278	103	2.00E-32	44	86	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"
21193	ENU04987	ANT61C6797: 1073..1	62-81	715-735	NAP		g2146821	548	91	1.00E-17	36	39	alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) []
21194	ENU04988	ANT61C346:8	139-166	433-452	NAP		g3136049	132	63	0.000000	36	38	(AL023592) putative phosphatidylinositol- glycan-class c protein [Schizosaccharomyces pombe]
21195	ENU04989	2155..1 ANT61C7116:			NAP		g2599548	1110	223	1.00E-57	40	34	(AF029346) chloride channel protein 3 [Oryctolagus cuniculus]
21196	ENU04990	441..1 ANT61C4598:	22-42	437-461	NAP		g1651554	745	294	2.00E-79	98	65	(D90748) Spermidine/putrescine transport system permease protein PotB. [Escherichia coli]
21197	ENU04991	724..1 ANT61C5425:	96-115	597-616	NAP		g2492660	334	129	2.00E-29	36	11	afatoxin biosynthesis polyketide synthase (PKS) [Aspergillus parasiticus]
21198	ENU04992	2325..3743 ANT61C8486:	22-42	807-829	NAP		g1176339	671	209	2.00E-53	43	60	hypothetical 50.8 KID protein in MIR1-STE18 intergenic region [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21199	ENU04993	ANI61C948:1..580			NAP		g2190551	170	108	4.00E-23	28	38	"(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb Z71181). ESTs
21200	ENU04994	ANI61C4231: 1926..2480	22-41	414-435	NAP		g3859773	141	73	1.00E-12	32	20	gb H36844.gb AA394956 come from this gene. [Arabidopsis thaliana]"
21201	ENU04995	ANI61C6504: 1220..1	65-84	729-747	NAP		g728850	110	35	0.61			(Z98598) hypothetical protein [Schizosaccharomyces pombe]"
													"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase)
													[Saccharomyces cerevisiae var. diastaticus]"
21202	ENU04996	ANI61C1933: 1..571			NAP		g4249560	560	225	2.00E-58	66	34	(AB003109) beta-glucosidase [Humicola grisea var. thermoides]"
21203	ENU04997	ANI61C6870: 1120..1	22-49	806-829	NAP		g2388995	360	148	4.00E-35	36	56	(Z98981) hypothetical protein [Schizosaccharomyces pombe]"
21204	ENU04998	ANI61S913:1..754			NAP		g107749	124	71	1.00E-11	27	34	synapsin I splice form a - human []
21205	ENU04999	ANI61C2450: 1269..1	74-93	712-731	NAP		g1360744	340	84	3.00E-25	34	14	"ankyrin 1, erythrocyte form 3 - human []"
21206	ENU05000	ANI61S719:4 91..1	23-41	451-470	NAP		g2656001	211	92	2.00E-18	39	20	(Z98977) hypothetical protein [Schizosaccharomyces pombe]"
21207	ENU05001	ANI61C1120 5:9128..8237	22-49	802-829	NAP		g3879734	269	79	2.00E-18	38	93	(Z93388) predicted using GeneFinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727... []
21208	ENU05002	ANI61C7395: 906..2125	22-47	744-764	NAP		g1723736	720	187	7.00E-47	43	43	hypothetical 68.3 KD protein in PDX1-SNG1 intergenic region [Saccharomyces cerevisiae]"
21209	ENU05003	ANI61C3250: 1100..1	60-79	726-743	NAP		g2625138	574	233	1.00E-60	39	17	(AF032443) ABC1 transporter: ABC-type ATPase [Magnaporthe grisea]"
21210	ENU05004	ANI61C5872: 1..969	22-42	804-829	NAP		g2492658	1336	314	7.00E-85	99	12	putative stigmastocytin biosynthesis fatty acid synthase beta subunit [Emerticella nidulans]"



# Genomic Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21211	ENU05005	ANT61C9398:	102-124	523-547	NAP		g2851654	282	71	4.00E-22	43	31	2-dehydro-3-deoxyphosphogalactonate aldolase (6-phospho-2-dehydro-3-deoxygalactonate aldolase) (2-oxo-3-deoxygalactonate 6-phosphate aldolase) / galactonate dehydratase [Escherichia coli]
21212	ENU05006	ANT61C1139	22-47	795-814	NAP		g2498757	378	96	3.00E-19	31	52	peroxisomal membrane protein PAS2 (peroxin-3) [Pichia pastoris]
21213	ENU05007	ANT61C5990:	3:2741..4047	102-124	250-267	NAP	g2499716	206	94	3.00E-19	45	22	"exopolygalacturonase precursor (exoPg) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
21214	ENU05008	ANT61C5102:	139-163	426-445	NAP		g3116147	179	67	2.00E-14	34	27	(AL023290) amino acid permease [Schizosaccharomyces pombe]
21215	ENU05009	ANT61C1061	26-46	722-749	NAP		g730745	63	48	0.00006	27	16	osomolarly two-component system protein SLN1 [Saccharomyces cerevisiae]
21216	ENU05010	ANT61C5586:	1296..2033		NAP		g101797	1141	455	e-127	91	74	quinate 5-dehydrogenase (EC 1.1.1.24) - Emericella nidulans []
21217	ENU05011	ANT61C1129	164-183	336-358	NAP		g417321	189	83	8.00E-16	46	33	methylentetrahydrofolate dehydrogenase (NAD+) [Saccharomyces cerevisiae]
21218	ENU05012	ANT61C1543:	928..625		NAP		g1870219	78	45	0.0002	30	99	(AC000133) ORF [Emericella nidulans]
21219	ENU05013	ANT61C8821:	24-50	791-818	NAP		g2498849	263	123	1.00E-27	33	86	replication factor-A protein 2 (single-stranded DNA-binding protein P30 subunit) [Schizosaccharomyces pombe]
21220	ENU05014	ANT61C7941:	118-137	719-736	NAP		g2257514	387	157	6.00E-40	38	51	(AB004535) ATP-dependent RNA helicase MSS116 precursor [Schizosaccharomyces pombe]
21221	ENU05015	ANT61C5148:	110-129	454-473	NAP		g2493491	44	46	0.0002	25	92	hypothetical protein MJ0304 [Methanococcus jannaschii]
21222	ENU05016	ANT61C7063:	1..550		NAP		g2342601	1262	77	1.00E-13	27	4	(X89442) peptide synthetase [Metarhizium anisopliae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21223	ENU05017	ANT61C2576: 3088..4293	24-44	786-805	NAP		g1711573	610	156	6.00E-46	48	76	"probable succinyl-CoA ligase (GDP-forming), alpha-chain precursor (succinyl-CoA synthetase, alpha chain) (SCS-alpha) ["]
21224	ENU05018	ANT61S335:5 39..1	63-90	486-509	NAP		g3860271	877	353	7.00E-97	97	20	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
21225	ENU05019	ANT61C1118 5:657..1	22-45	525-548	NAP		g585169	422	129	4.00E-45	49	27	UDP-glucose 4-epimerase (galactowaldenase) / aldose 1-epimerase (mutarotase)
21226	ENU05020	ANT61C9007: 1.605	102-125	558-584	NAP		g730017	282	83	5.00E-20	50	26	[Saccharomyces cerevisiae] cystathionine gamma-synthase (O-succinylhomoserine (thiol)-lyase) [probable ATP-dependent DNA helicase C4H3.05 [Schizosaccharomyces pombe]
21227	ENU05021	ANT61C1183: 2222..1	68-87	717-736	NAP		g1723281	1051	122	3.00E-27	33	29	hypothetical 95.4 KD protein in SEC4-MSH4 intergenic region [Saccharomyces cerevisiae]
21228	ENU05022	ANT61C8411: 754..2343	30-57	779-799	NAP		g1175914	811	248	4.00E-65	42	34	(AF015561) RO10 [Neurospora crassa]
21229	ENU05023	ANT61C1834: 1947..2749	104-131	756-782	NAP		g2353165	186	46	0.0002	34	97	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emeticella nidulans]
21230	ENU05024	ANT61S578:6 24..1			NAP		g1705828	157	69	9.00E-12	33	18	(AL021246) echA14 [Mycobacterium tuberculosis]
21231	ENU05025	ANT61C1040 4:1486..565	41-60	795-822	NAP		g2791526	118	41	0.000000	32	63	putative tartarate transporter [Agrobacterium vitis]
21232	ENU05026	ANT61C1120 1:1734..2597	22-48	781-802	NAP		g4033481	233	69	2.00E-20	29	53	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
21233	ENU05027	ANT61C3812: 545..1	22-49	503-524	NAP		g3522935	63	57	0.000000	25	59	HOS3 protein [Saccharomyces cerevisiae]
21234	ENU05028	ANT61C2852: 1883..1	84-103	714-736	NAP		g2833193	594	85	6.00E-16	28	34	(AF009417) cytochrome P450 [Myrothecium roridum]
21235	ENU05029	ANT61C5843: 1..941	61-81	806-829	NAP		g2267601	306	120	1.00E-26	33	47	(Y17243) cytochrome P450 [Gibberella fujikuroi]
21236	ENU05030	ANT61C626:1 233..1	80-99	718-735	NAP		g4127832	601	144	6.00E-47	41	51	hypothetical 118.6 KD protein C29E6.03C in chromosome I [Schizosaccharomyces pombe]
21237	ENU05031	ANT61C8459: 9479..5897	33-53	805-828	NAP		g1351618	585	67	1.00E-10			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21238	ENU05032	ANI61C1121: 4754..3724	22-42	802-829	NAP		g124871	489	151	6.00E-46	40	87	Inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) (PPASE) [Kluyveromyces lactis]
21239	ENU05033	ANI61C4611: 1755..1	28-47	728-747	NAP		g3417410	1275	252	2.00E-66	50	31	(AL031261) sulfate permease [Schizosaccharomyces pombe]
21240	ENU05034	ANI61C1027: 8:2501..4162	22-48	782-808	NAP		g1870209	2360	476	e-134	85	51	(AC000133) ORF [Emeticella nidulans]
21241	ENU05035	ANI61C1047: 1:862..1278	33-52	413-432	NAP		g4056552	379	114	2.00E-36	59	43	(AL034583) putative nucleotide binding protein [Schizosaccharomyces pombe]
21242	ENU05036	ANI61C8687: 2011..1	43-62	626-645	NAP		g3912991	2086	419	e-116	67	33	alpha-glucuronidase precursor (alpha-glucosiduronase) [Aspergillus tubingensis]
21243	ENU05037	ANI61C7437: 1159..637	102-126	454-473	NAP		g2980827	114	80	8.00E-15	41	32	(AL022172) protein kinase [Schizosaccharomyces pombe]
21244	ENU05038	ANI61C6321: 3230..2423	62-80	747-766	NAP		g1680605	442	100	1.00E-42	52	99	(S59774) RNA polymerase subunit [Saccharomyces cerevisiae]
21245	ENU05039	ANI61C2198: 983..1	141-162	718-745	NAP		g547861	611	246	2.00E-64	48	32	ATP-dependent protease LA 2 [Myxococcus xanthus]
21246	ENU05040	ANI61C4414: 259..1253	22-46	801-828	NAP		g1730705	400	90	6.00E-38	42	92	hypothetical 27.5 KD protein in SPO1-SIS1 intergenic region [Saccharomyces cerevisiae]
21247	ENU05041	ANI61C6703: 3118..4359	51-73	805-829	NAP		g3261634	474	171	7.00E-42	42	40	(Z79700) hypothetical protein Rv0976c [Mycobacterium tuberculosis]
21248	ENU05042	ANI61C1053: 3:1539..2879	22-42	616-634	NAP		g3080527	872	206	2.00E-52	43	65	(AL022600) putative mannose-1-phosphate gaunyl transferase [Schizosaccharomyces pombe]
21249	ENU05043	ANI61S1767: 1..595	39-58	457-478	NAP		g539079	698	285	2.00E-76	70	16	peroxisomal assembly protein 5 - yeast [Pichia pastoris] []
21250	ENU05044	ANI61S3339: 1..831			NAP		g1076802	116	37	0.000002	30	21	extensin-like protein - maize [Zea mays]
21251	ENU05045	ANI61C1089: 7:1..972	66-85	711-731	NAP		g731288	185	64	0.000000	25	35	hypothetical 87.5 KD protein in ACS1-GCV3 intergenic region [Saccharomyces cerevisiae]
21252	ENU05046	ANI61C9718: 665..328	25-48	292-316	NAP		g4100190	153	87	5.00E-17	40	26	"(U95181) 2,5 dihydroxyphenylacetate oxidase [Caenorhabditis elegans]"
21253	ENU05047	ANI61S371:1..490			NAP		g539218	96	43	0.002	16	30	hypothetical protein YKL201c - yeast [Saccharomyces cerevisiae] []

Seq num	Seq id	Contig source	5 pos	3 pos	Primer	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21254	ENU05048	AN161C8803:	31-50	806-829	NAP	NAP	g4502091	410	160	1.00E-38	33	7		"ankyrin 2, neuronal [Homo sapiens]"
21255	ENU05049	AN161C8498:	22-47	808-829	NAP	NAP	g4176530	2328	277	3.00E-86	57	22		(AL035263) putative condensin subunit [Schizosaccharomyces pombe]
21256	ENU05050	AN161C1137:	5241..1481		NAP	NAP	g4468948	1258	490	e-138	92	49		(X00790) cytochrome oxidase I [Emmericella nidulans]
21257	ENU05051	AN161C4514:	431..1282		NAP	NAP	g729967	150	75	1.00E-13	36	39		homocitrate dehydratase [Saccharomyces cerevisiae]
21258	ENU05052	AN161C5723:	23-50	665-692	NAP	NAP	g3318897	453	221	4.00E-57	41	42		"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ["]
21259	ENU05053	AN161C7280:	22-46	802-821	NAP	NAP	g3914344	344	128	6.00E-29				3-phlytase precursor [Bacillus sp.]
21260	ENU05054	AN161C1544:	112-132	711-733	NAP	NAP	g2828341	165	98	1.00E-19	30	18		(AB004305) mBLVR [Mus musculus]
21261	ENU05055	AN161C8211:	69-87	747-766	NAP	NAP	g1077413	809	260	2.00E-87	66	99		hypothetical protein YLR186w - yeast [Saccharomyces cerevisiae]
21262	ENU05056	AN161S9.1..5			NAP	NAP	g2465558	162	79	2.00E-14	37	74		[Saccharomyces cerevisiae] (AF011545) YedB [Bacillus subtilis]
21263	ENU05057	AN161C9836:	22-45	804-828	NAP	NAP	g1351714	749	154	8.00E-37	34	55		putative transporter C11D3.18C [Schizosaccharomyces pombe]
21264	ENU05058	AN161C8454:	48-68	766-785	NAP	NAP	g2132208	739	210	1.00E-53	41	31		hypothetical protein YPL150w - yeast [Saccharomyces cerevisiae]
21265	ENU05059	AN161S13:69	157-174	618-645	NAP	NAP	g2804470	120	81	7.00E-15	28	16		[Saccharomyces cerevisiae] (AF043701) contains similarity to ankyrin repeats and protein kinases [Caenorhabditis elegans]
21266	ENU05060	AN161C5161:	34-53	627-647	NAP	NAP	g3668157	513	82	5.00E-15				(AL031764) putative exocyst complex component [Schizosaccharomyces pombe]
21267	ENU05061	AN161C229:1	33-59	624-643	NAP	NAP	g419963	226	73	3.00E-12	44	83		snRNP protein B - fruit fly (Drosophila melanogaster) [Drosophila melanogaster]
21268	ENU05062	AN161C728:2			NAP	NAP	g3025214	231	80	1.00E-17	36	36		hypothetical 65.9 KD protein in SSP120-HAP1 intergenic region [Saccharomyces cerevisiae]
21269	ENU05063	AN161C9372:	115-134	388-407	NAP	NAP	g2146853	325	90	1.00E-17	45	32		alpha-galactosidase (EC 3.2.1.22) III precursor - fungus (Trichoderma reesei) [Hypocrea jecorina]

Seq num	Seq id	Contig source	5 pos	3 pos	Primer	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21270	ENU05064	ANI61C6066:	192-211	455-479		NAP		g83697	633	254	4.00E-67	83	100	catabolic 3-dehydrogenase - Emericella nidulans [Emericella nidulans]
21271	ENU05065	ANI61C1113	64-82	786-804		NAP		g2507475	365	93	2.00E-18	36	9	Paired amphipathic helix protein [Saccharomyces cerevisiae]
21272	ENU05066	ANI61C3518:	210-237	571-598		NAP		g538067	157	44	0.0008	29	14	(M77661) putative pol polyprotein [Magnaporthe grisea]
21273	ENU05067	ANI61C9741:	55-74	794-813		NAP		g2970627	725	289	2.00E-77	50	86	(AF051914) C-4 methyl sterol oxidase [Candida albicans]
21274	ENU05068	ANI61C9993:	107-130	673-699		NAP		g1723552	325	130	1.00E-29	44	62	putative mitochondrial carrier protein C12B10.09 [Schizosaccharomyces pombe]
21275	ENU05069	ANI61C4742:	73-92	621-638		NAP		g3183171	784	318	2.00E-86	61	25	"probable alanyl-tRNA synthetase, cytoplasmic (alanine--tRNA ligase) (ALARS) [Schizosaccharomyces pombe]"
21276	ENU05070	ANI61S4634:				NAP		g731584	114	31	6	35	60	hypothetical 17.1 KD protein in PUR5 3region [Saccharomyces cerevisiae]
21277	ENU05071	ANI61C6461:	101-120	679-696		NAP		g2626826	170	137	2.00E-32	31	17	(D83967) YrkN [Bacillus subtilis]
21278	ENU05072	ANI61C720:1	47-66	800-824		NAP		g4505823	640	267	8.00E-71	48	94	pirin [Homo sapiens]
21279	ENU05073	ANI61C276:1	42-67	765-788		NAP		g2224775	595	226	2.00E-58	43	71	(Z97025) pyruvate carboxylase [Bacillus subtilis]
21280	ENU05074	ANI61C9649:	26-45	650-677		NAP		g1546072	555	167	8.00E-41	37	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21281	ENU05075	ANI61S1135:				NAP		g4008576	172	53	0.000002	34	37	"(AL034491) similar to yeast transcription initiation factor iif, alpha subunit [Schizosaccharomyces pombe]"
21282	ENU05076	ANI61S1439:				NAP		g3329623	156	45	0.0007	17	69	(AF078790) No definition line found [Caenorhabditis elegans]
21283	ENU05077	ANI61C1060	94-116	798-817		NAP		g1351343	1530	493	e-149	96	26	positive regulator of purine utilisation [Emericella nidulans]
21284	ENU05078	ANI61C8743:				NAP		g3646453	331	138	3.00E-32	38	100	(AL031603) putative succinate dehydrogenase cytochrome b subunit precursor [Schizosaccharomyces pombe]
21285	ENU05079	ANI61C7969:				NAP		g208131	126	64	5.00E-10	42	98	(M77169) beta-galactosidase alpha-peptide [Shuttle vector pJIR1457]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21286	ENU05080	AN161C9657:	44-63	800-820	NAP		g400269	1494	377	e-104	64	52	Methylmalonate-semialdehyde dehydrogenase precursor (acylating) (MMSDH) [Rattus norvegicus]
21287	ENU05081	AN161C6968:	28-48	808-829	NAP		g1399263	1443	469	e-131	96	60	(U28383) cystathionine beta-lyase [Emmericella nidulans]
21288	ENU05082	AN161C1441:	121-141	664-683	NAP		g462168	617	248	3.00E-65	46	9	translational activator GCN1 [Saccharomyces cerevisiae]
21289	ENU05083	AN161C249:5	93-112	317-344	NAP		g4757128	78	55	0.000000			(AJ238717) ZRP protein [Rattus norvegicus]
21290	ENU05084	AN161S3273:			NAP		g283032	92	49	0.00003	27	57	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
21291	ENU05085	AN161C6213:	22-41	805-829	NAP		g3283220	1109	200	1.00E-71	56	51	(AF061241) splicing factor hPRP17 [Homo sapiens]
21292	ENU05086	AN161C3458:	102-121	666-685	NAP		g2673947	594	226	2.00E-58	52	18	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
21293	ENU05087	AN161S1524:			NAP		g168082	69	48	0.00004	35	17	(M59935) negative-acting regulatory protein [Emmericella nidulans]
21294	ENU05088	AN161C5043:	38-57	750-769	NAP		g3006156	905	175	6.00E-70	52	52	(AL022299) putative serine palmitoyltransferase [Schizosaccharomyces pombe]
21295	ENU05089	AN161C1208:			NAP		g4867801	1922	49	0.00004			(AJ132442) phenylacetate 2-hydroxylase [Emmericella nidulans]
21296	ENU05090	AN161C2406:	118-137	638-658	NAP		g584839	599	239	1.00E-62			beta-glucuronidase (GUS) (beta-D-glucuronoside glucuronosohydrolase) [Escherichia coli]
21297	ENU05091	AN161C1087			NAP		g2224699	97	67	9.00E-11	27	18	(AB002377) KIAA0379 [Homo sapiens]
21298	ENU05092	AN161C721:5	65-87	468-492	NAP		g548669	313	151	3.00E-36	44	17	DNA repair protein RAD8 [Schizosaccharomyces pombe]
21299	ENU05093	AN161C1097	29-56	719-746	NAP		g4481954	1614	363	e-100	74	31	(AL035637) putative protease subunit; chaperonin [Schizosaccharomyces pombe]
21300	ENU05094	AN161C5311:	22-45	463-482	NAP		g543325	188	92	3.00E-20	33	56	small nuclear ribonucleoprotein U1A - mouse [Mus musculus]
21301	ENU05095	AN161S3796:			NAP		g4490609	361	109	6.00E-28	53	22	(AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]
21302	ENU05096	AN161S2956:	35-53	287-306	NAP		g2956768	109	45	0.00001	29	33	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]

# Database Hit

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
21303	ENU05097	AN161C9512: 23-50		736-757	NAP		g3183392	386	92	2.00E-36	45	99	hypothetical 24.1 KD protein C17A5.08 in chromosome I precursor [Schizosaccharomyces pombe]
		1490..2267											
21304	ENU05098	AN161C6112: 26-45		722-749	NAP		g2633022	585	225	4.00E-58	43	31	(Z99107) yeta [Bacillus subtilis]
		983..1											
21305	ENU05099	AN161C3343: 22-49		420-439	NAP		g1076211	101	33	1.6			hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii] (AF007865) bacitracin synthetase 1; BacA [Bacillus licheniformis] (AF052061) polygalacturonase [Ophiostoma novo-ulmi] (L35487) mannanase [Aspegillus aculeatus] putative sterigmatocystin biosynthesis ketoreductase STCE [Emericella nidulans]
		6378..5998											
21306	ENU05100	AN161C1093 22-44		808-829	NAP		g2982194	494	163	1.00E-39	38	5	(AF059534) severin kinase [Dictyostelium discoideum]
		4:2210..344											
21307	ENU05101	AN161C9439: 102-123		414-438	NAP		g2967835	312	70	1.00E-27	55	34	proline-rich protein MRP2 - mouse (fragment) []
		1..460											
21308	ENU05102	AN161C1118 104-130		396-422	NAP		g558311	294	132	9.00E-31	52	34	hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii] (Y07919) beta-prime-adaptin protein [Mus musculus]
		6:6780..6338											
21309	ENU05103	AN161C7701: 59-76		773-792	NAP		g2492756	1193	372	e-102	95	92	transcription elongation factor S-II (TFIIS) [Schizosaccharomyces pombe] (Z99531) ubiquitin system protein [Schizosaccharomyces pombe]
		1654..687											
21310	ENU05104	AN161C2235: 45-64		799-826	NAP		g3075511	823	58	0.000000	27	49	ARP2/3 complex 20 KD subunit (P20-ARC) [Homo sapiens] (AF068065) GP900; mucin-like glycoprotein [Cryptosporidium parvum]
		3153..1469											
21311	ENU05105	AN161C5581: 1..502			NAP		g91209	123	57	0.000000	29	67	hypothetical 49.1 KD protein C11D3.06 in chromosome I [Schizosaccharomyces pombe]
		1675..1088											
21312	ENU05106	AN161C9514: 118-138		525-552	NAP		g1076211	60	43	0.001	27	34	
		2141..1											
21313	ENU05107	AN161C4192: 42-61		722-749	NAP		g2398720	1362	271	4.00E-72	51	27	
		892..390											
21314	ENU05108	AN161C2192: 40-58		431-450	NAP		g1351227	385	148	2.00E-35	43	57	
		1:1..2848											
21315	ENU05109	AN161C1130 48-71		782-806	NAP		g2440180	473	32	6.9			
		1616..1089											
21316	ENU05110	AN161C7737: 60-80		484-507	NAP		g3121766	329	128	8.00E-30	72	68	
		1..755											
21317	ENU05111	AN161S2227: 1..755			NAP		g4063042	154	39	0.033	30	11	
		66..1											
21318	ENU05112	AN161C123:9 24-43		794-813	NAP		g1351703	856	284	7.00E-76	56	58	

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21319	ENU05113	ANI61C5332: 1091..2649	27-46	802-829	NAP		g4033486	299	75	7.00E-13			putative tartrate transporter [Agrobacterium vitis]
21320	ENU05114	ANI61C4918: 1107..1	22-44	724-749	NAP		g1352677	1333	369	e-101	91	37	serine/threonine protein phosphatase 2B catalytic subunit (calmodulin-dependent calcineurin A subunit) [Emmericella nidulans] (AB001995) Tel1p [Schizosaccharomyces pombe]
21321	ENU05115	ANI61C3944: 3311..1	23-50	797-817	NAP		g3764029	825	168	6.00E-53	43	9	emopamil-binding protein - human [Homo sapiens]
21322	ENU05116	ANI61C8015: 35..834	69-88	756-775	NAP		g1362793	263	69	5.00E-11	33	99	(X98690) Pristinamycin I synthase 2 [Streptomyces pristinaespiralis]
21323	ENU05117	ANI61C5643: 1526..2246	27-45	671-694	NAP		g1483603	128	105	3.00E-22	36	8	(X89442) peptide synthetase [Metarhizium anisopliae]
21324	ENU05118	ANI61C3986: 925..1	41-60	776-796	NAP		g2342601	437	188	5.00E-47	34	5	"(Z98978) SPAC27E2.06c, putative methionyl-tRNA synthetase, le n:539aa, similar eg. to YGR171C, SYMM_YEAST, P22438, methi onyl-tRNA synthetase; mitochondrial, (575aa), fasta scores, opt:396, E0:0, (39.9% identity in 546 aa o... ["]
21325	ENU05119	ANI61C8013: 1411..3361	45-71	805-829	NAP		g2388946	958	85	2.00E-33	36	48	putative sterigmacystin biosynthesis polyketide synthase (PKS) [Emmericella nidulans]
21326	ENU05120	ANI61C2723: 1..998	34-53	735-754	NAP		g2492661	1471	440	e-123	97	11	(U20808) auxin-induced protein [Vigna radiata]
21327	ENU05121	ANI61S2128: 94..537	107-125	390-407	NAP		g1184121	130	66	1.00E-10	31	46	DNA-directed RNA polymerase I 190 KD polypeptide (A190) [Saccharomyces cerevisiae]
21328	ENU05122	ANI61C1070: 6:2792..1	23-47	656-683	NAP		g2507346	1768	335	2.00E-91	54	16	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni]
21329	ENU05123	ANI61C4506: 496..1	102-128	453-472	NAP		g1790870	214	75	4.00E-13	44	50	(AL021070) ppsB [Mycobacterium tuberculosis]
21330	ENU05124	ANI61C4658: 1919..3382	23-43	799-823	NAP		g3261497	676	232	3.00E-60	43	18	(AC002292) Phosphatidylinositol 3-kinase [Arabidopsis thaliana]
21331	ENU05125	ANI61C4699: 489..1			NAP		g2462752	404	167	5.00E-41	51	20	hypothetical 83.4 KD protein in DSK2-CAT8 intergenic region [Saccharomyces cerevisiae]
21332	ENU05126	ANI61C4285: 2701..4130	42-61	765-784	NAP		g2497216	610	244	5.00E-64	49	35	



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21333	ENU05127	ANT61C7878: 1..585	22-42	528-547	NAP		g1945326	184	91	5.00E-18	27	13	(Z72902) ORF YGR116w [Saccharomyces cerevisiae]
21334	ENU05128	ANT61S1312: 1..671			NAP		g1572721	137	41	0.008	28	15	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
21335	ENU05129	ANT61C4899: 266..1409	34-53	781-800	NAP		g57554	201	101	5.00E-21	32	47	(X65296) carboxylesterase [Rattus rattus]
21336	ENU05130	ANT61C3565: 1..1113	74-93	711-730	NAP		g3913798	1464	439	e-122	72	52	"exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellobiohydrolase I) (beta-glucanocellobiohydrolase I) [Aspergillus aculeatus]"
21337	ENU05131	ANT61C9214: 3578..2562	218-244	802-829	NAP		g1729921	198	57	0.000000	39	55	Lipase 2 (triacylglycerol lipase) [Saccharomyces cerevisiae]
21338	ENU05132	ANT61S831:1..724			NAP		g1176993	383	168	3.00E-41	44	88	hypothetical 26.6 KD sensory transduction protein in IDH 3'region [Bacillus subtilis]
21339	ENU05133	ANT61C4796: 1633..2299	22-47	528-547	NAP		g3915105	474	160	8.00E-39	61	33	threonine dehydratase precursor (threonine deaminase) [Arxula adenivorans]
21340	ENU05134	ANT61C2653: 671..1	92-111	540-559	NAP		g1130507	141	83	2.00E-15	31	46	(L41670) fumarylacetoacetate hydrolase [Emeritella nidulans]
21341	ENU05135	ANT61S957:5 38..1	188-215	486-513	NAP		g1652748	345	150	5.00E-36	48	65	(D90908) hypothetical protein [Synecocystis sp.]
21342	ENU05136	ANT61C953:7 80..1	22-43	653-679	NAP		g417321	527	205	2.00E-52	59	64	methylenetetrahydrofolate dehydrogenase (NAD+)
21343	ENU05137	ANT61C1080: 6:1..675	114-133	550-570	NAP		g82852	614	231	3.00E-63	61	45	[Saccharomyces cerevisiae] hypothetical protein (LAC12 3' region) - yeast (Kluyveromyces marxianus var. lactis) [Kluyveromyces lactis]
21344	ENU05138	ANT61C4415: 673..1	51-70	537-555	NAP		g549009	201	67	4.00E-21	33	34	probable uroporphyrin-III C-methyltransferase (urogen III methylase) (SUMT) (uroporphyrinogen III methylase) (UROM) [Saccharomyces cerevisiae]
21345	ENU05139	ANT61C55:39 00..3276	113-132	458-476	NAP		g3378433	233	80	6.00E-19	38	34	(AF079317) flavoprotein subunit p-cresol methylhydroxylase [Sphingomonas aromaticivorans]
21346	ENU05140	ANT61C489:5 51..1	118-135	507-528	NAP		g4185903	717	291	2.00E-78	80	32	(AJ132432) fimbria [Gibberella pulicaris]

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21347	ENU05141	ANT61C3097:	113-132	625-647	NAP		g417038	640	193	2.00E-64	65	45	transcriptional activator GCN5 [Saccharomyces cerevisiae]
21348	ENU05142	ANT61C1204:	205-228	685-712	NAP		g4539186	192	111	7.00E-24	31	58	(AL049485) probable zinc-binding alcohol dehydrogenase [Streptomyces coelicolor]
21349	ENU05143	ANT61C1041	27-47	662-689	NAP		g731836	448	155	4.00E-50	51	37	probable mannosyltransferase KTR7 [Saccharomyces cerevisiae]
21350	ENU05144	ANT61C4688:	22-40	730-752	NAP		g549443	1580	257	e-126	96	12	condial green pigment synthase [Emertella nidulans]
21351	ENU05145	ANT61C8490:	40-59	773-792	NAP		g112984	1245	158	3.00E-70	68	53	"aspartate aminotransferase, mitochondrial precursor (Transaminase A) (glutamate oxaloacetate transaminase-2) [Mus musculus]" (AL031523) hypothetical protein [Schizosaccharomyces pombe]
21352	ENU05146	ANT61C1856:	22-46	449-476	NAP		g3560223	121	66	1.00E-10	29	48	(AL023776) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]
21353	ENU05147	ANT61C3386	22-47	718-744	NAP		g3184060	578	123	6.00E-50	49	26	(AF064069) aryl-alcohol oxidase precursor [Pleurotus eryngii]
21354	ENU05148	ANT61C726:6	22-46	562-581	NAP		g3851524	190	97	1.00E-19	30	32	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
21355	ENU05149	ANT61C2963:	32-59	331-354	NAP		g3850084	156	75	3.00E-13	32	46	(AL031824) putative transcriptional regulator [Schizosaccharomyces pombe]
21356	ENU05150	ANT61C8811:	49-68	336-356	NAP		g3702632	300	128	2.00E-29	48	18	hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]
21357	ENU05151	ANT61C2538:	53-73	410-434	NAP		g731385	165	72	2.00E-12	34	48	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
21358	ENU05152	ANT61S1367:			NAP		g82698	210	45	0.0008	32	70	"(U75347) fatty acid synthase, alpha subunit [Emertella nidulans]"
21359	ENU05153	ANT61C6372:			NAP		g1805261	169	67	9.00E-11	33	9	glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucose:oxygen 1-oxido-reductase) [Talaromyces flavus]
21360	ENU05154	ANT61C1057	22-44	700-719	NAP		g3287841	828	187	8.00E-47	63	43	hypothetical 68.5 KD protein in SCS3-SUP44 intergenic region [Saccharomyces cerevisiae]
21361	ENU05155	ANT61C7117:	25-48	375-398	NAP		g1723913	499	209	1.00E-53	63	27	

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21362	ENU05156	ANI61C3955:	120-138	486-505	NAP		g731968	486	203	1.00E-51	50	61	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region [Saccharomyces cerevisiae]
21363	ENU05157	ANI61C4224:	22-43	803-826	NAP		g4557481	761	148	4.00E-35	31	18	canalicular multispecific organic anion transporter [Homo sapiens]
21364	ENU05158	ANI61C7037:	1..1762		NAP		g4154078	195	93	7.00E-26	37	26	(AL035161) putative efflux protein [Streptomyces coelicolor]
21365	ENU05159	ANI61C856:2	57-76	451-470	NAP		g1170131	209	103	7.00E-22	37	35	glucarate dehydratase subunit (GDH) [Pseudomonas putida]
21366	ENU05160	ANI61C8308:	26-46	806-829	NAP		g1351678	130	43	0.003			hypothetical 41.5 KD protein C1F5.03C in chromosome I [Schizosaccharomyces pombe]
21367	ENU05161	ANI61C1012	26-53	723-749	NAP		g82798	844	197	4.00E-71	55	15	DNA-directed RNA polymerase (EC 2.7.7.6) I 189K chain - fission yeast (Schizosaccharomyces pombe) [Schizosaccharomyces pombe]
21368	ENU05162	ANI61S395:5	105-126	442-461	NAP		g4574121	146	85	4.00E-16	32	30	(AF009415) choline dehydrogenase [Staphylococcus xylosus]
21369	ENU05163	ANI61C9793:	22-48	781-803	NAP		g2342601	1701	158	4.00E-38	30	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21370	ENU05164	ANI61C7505:	69-88	774-796	NAP		g1363761	598	73	6.00E-15			probable membrane protein YPR194c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21371	ENU05165	ANI61C2147:	33-52	455-477	NAP		g1723578	296	130	2.00E-30	48	53	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
21372	ENU05166	ANI61C1526:	46-64	803-822	NAP		g4456821	1167	306	5.00E-99	76	56	(AL035548) casein kinase i homolog cki1 [Schizosaccharomyces pombe]
21373	ENU05167	ANI61C8658:	22-43	761-780	NAP		g3183368	810	191	7.00E-59	58	41	hypothetical 64.0 KD protein C20G4.05C in chromosome I [Schizosaccharomyces pombe]
21374	ENU05168	ANI61S2442:			NAP		g1805261	251	94	5.00E-19	43	9	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
21375	ENU05169	ANI61C8742:	22-47	728-749	NAP		g4106669	791	225	1.00E-69	73	57	(AL035064) protein kinase skp1p [Schizosaccharomyces pombe]
21376	ENU05170	ANI61C6713:	49-68	638-657	NAP		g3402279	415	152	9.00E-40	61	48	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]

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21377	ENU05171	ANT61C4226:	25-52	808-829	NAP		g2492658	5056	455	e-148	98	13	putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emmericella nidulans]
21378	ENU05172	ANT61S3081:			NAP		g100210	184	41	0.009	34	59	extensin precursor (clone Tom L-4) - tomato [Lycopersicon esculentum]
21379	ENU05173	ANT61C2460:	103-122	457-479	NAP		g3560221	161	58	8.00E-13	35	42	(AL031523) hypothetical protein [Schizosaccharomyces pombe]
21380	ENU05174	ANT61C8889:	38-57	789-808	NAP		g1800044	187	83	2.00E-15	32	56	(D90890) similar to [Escherichia coli]
21381	ENU05175	ANT61C3669:	46-71	677-695	NAP		g731763	576	245	3.00E-64	51	40	hypothetical 66.7 KD protein in EGD2-SUN1 intergenic region [Saccharomyces cerevisiae]
21382	ENU05176	ANT61C1049			NAP		g4218005	136	60	0.000000	19	30	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21383	ENU05177	ANT61S2866:			NAP		g854065	247	34	0.009	38	24	(X83413) U88 [Human herpesvirus 6]
21384	ENU05178	ANT61C2024:			NAP		g3646479	202	56	0.000000	36	100	(AJ010981) putative transposase [Talaromyces stipitatus]
21385	ENU05179	ANT61C9308:	45-64	492-511	NAP		g3878825	354	166	1.00E-40	50	47	(Z70782) similar to sorbitol dehydrogenase; cDNA EST EMBL.T00701 comes from this gene [Caenorhabditis elegans]
21386	ENU05180	ANT61C8487:	22-44	717-744	NAP		g3135994	689	142	4.00E-35	39	18	(AL023589) hypothetical protein [Schizosaccharomyces pombe]
21387	ENU05181	ANT61C518:	8-48	706-730	NAP		g1706695	303	114	9.00E-25	36	54	phosphomevalonate kinase [Saccharomyces cerevisiae]
21388	ENU05182	ANT61S4173:	215-233	416-435	NAP		g1351673	322	129	1.00E-29	45	53	hypothetical 37.7 KD protein ClF7.12 in chromosome I [Schizosaccharomyces pombe]
21389	ENU05183	ANT61C1188:	22-41	791-815	NAP		g631954	1952	362	e-119	99	28	chitin synthase (EC 2.4.1.16) chsB - Emmericella nidulans [Emmericella nidulans]
21390	ENU05184	ANT61C3528:	25-46	414-441	NAP		g2981719	252	106	7.00E-23	38	20	Crystal Structures Of The Copper-Containing Amine Oxidase From Arthrobacter Globiformis In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone [

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21391	ENU05185	ANT61C6380:	33-52	797-817	NAP	g2342601	653	101	9.00E-21	25	5	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21392	ENU05186	ANT61S2843:	2296..234		NAP	g1352946	366	136	1.00E-31	49	60	60	hypothetical 32.6 KD protein in DAL5-TIH11 intergenic region [Saccharomyces cerevisiae] (AC003972) pNORF1 [Homo sapiens]
21393	ENU05187	ANT61C5497:	27-54	808-829	NAP	g2739355	2771	429	e-119	71	25	25	TOXD protein [Cochliobolus carbonum] (Z70751) similar to 4-coumarate-CoA ligase; cDNA EST EMBL:C07240 comes from this gene; cDNA EST EMBL:C08540 comes from this gene [Caenorhabditis elegans]
21394	ENU05188	ANT61C5368:	22-44	787-806	NAP	g1729996	139	54	9.00E-11	32	75	75	betaine aldehyde dehydrogenase (BADH) []
21395	ENU05189	ANT61C9887:	191-218	533-556	NAP	g3875727	225	65	2.00E-22	49	28	28	dibenzothioephene desulfurization enzyme C (DBT sulfur dioxygenase) [Rhodococcus sp.]
21396	ENU05190	ANT61C8675:	24-43	725-744	NAP	g3121988	339	112	9.00E-30	34	48	48	kinesin-related protein unc-104 - Caenorhabditis elegans []
21397	ENU05191	ANT61C3613:	22-48	332-356	NAP	g1711469	257	116	6.00E-26	47	29	29	probable kynureninase (L-kynurenine hydrolase) [Saccharomyces cerevisiae] (U53863) Nopp44/46 [Trypanosoma brucei]
21398	ENU05192	ANT61C8895:	37-64	723-749	NAP	g102551	926	360	1.00E-98	65	17	17	NPL4 protein [Saccharomyces cerevisiae]
21399	ENU05193	ANT61C2996:	75-95	666-685	NAP	g3913980	435	157	9.00E-44	50	49	49	"(AC003970) Similar to Glucose-6-phosphate dehydrogenases, [Arabidopsis thaliana]"
21400	ENU05194	ANT61C5409:	71-90	265-284	NAP	g1314705	85	35	0.18	31	33	33	putative glycosyltransferase HOC1 precursor [Saccharomyces cerevisiae] probable helicase MOT1 []
21401	ENU05195	ANT61C1209:	22-44	748-775	NAP	g462739	216	106	3.00E-22	35	34	34	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger [Aspergillus niger]
21402	ENU05196	ANT61S3756:	27-47	553-572	NAP	g3482917	544	142	1.00E-51	74	26	26	Multidrug resistance-associated protein 4 [Homo sapiens]
21403	ENU05197	ANT61C1055	22-41	788-808	NAP	g1352891	153	95	7.00E-19	24	69	69	
21404	ENU05198	ANT61C4595:	67-87	492-516	NAP	g417308	457	94	8.00E-32				
21405	ENU05199	ANT61C4356:	40-59	600-621	NAP	g481285	356	159	1.00E-38	36	32	32	
21406	ENU05200	ANT61C3342:	22-41	476-495	NAP	g3219829	178	60	5.00E-15	36	99	99	

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21407	ENU05201	ANI61C1135	22-48	497-521	NAP		g481230	148	88	5.00E-17	32	43	L-idiol 2-dehydrogenase (EC 1.1.1.14) precursor - rat [Rattus norvegicus]
21408	ENU05202	ANI61C7939	22-41	519-539	NAP		g3567	217	96	2.00E-20	40	60	(X55731) COX11 (AA 1-277) [Saccharomyces cerevisiae]
21409	ENU05203	ANI61C7448			NAP		g1272506	444	125	7.00E-43	87	100	(D43686) L41 ribosomal protein [Candida maltosa]
21410	ENU05204	ANI61C2343			NAP		g1652639	52	75	3.00E-13	26	12	(D90907) sensory transduction histidine kinase [Synecocystis sp.]
21411	ENU05205	ANI61C1286	65-84	728-747	NAP		g2440190	606	187	1.00E-46	36	18	(Z98602) putative protein transport protein sec7 homolog
21412	ENU05206	ANI61S281	1		NAP		g433011	114	66	2.00E-10	29	53	[Schizosaccharomyces pombe] "(S62929) PRB1L precursor protein=basic proline rich proteins (Ps, PmF, PmS, and Pe) precursor (C-terminal) [Homo sapiens]" (AL031263) putative GTPase-activator protein for Rho-like GTPases
21413	ENU05207	ANI61C5167	221-239	605-624	NAP		g3417437	226	102	3.00E-21	34	64	[Schizosaccharomyces pombe] (U96090) myb-related transcription factor [Strongylocentrotus purpuratus] (U35661) colony 1 [Ophiostoma ulmi]
21414	ENU05208	ANI61C2551	27-47	775-795	NAP		g2072499	148	86	3.00E-16	29	31	hypothetical 72.5 KD protein C2F7.10 in chromosome 1
21415	ENU05209	ANI61C9694	217-238	722-741	NAP		g998355	239	127	8.00E-29	30	33	[Schizosaccharomyces pombe] (Z98977) hypothetical protein [Schizosaccharomyces pombe] (Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
21416	ENU05210	ANI61C9624	22-49	555-581	NAP		g1175373	390	137	6.00E-34	46	29	putative SEC14 cytosolic factor (phosphatidylinositol/phosphatidylcholine transfer protein) (P/PC TP) [Schizosaccharomyces pombe]
21417	ENU05211	ANI61C6114			NAP		g2388934	189	56	0.000000	38	23	NADH-ubiquinone dehydrogenase 24 KD subunit precursor [Neurospora crassa]
21418	ENU05212	ANI61C7669	24-51	730-749	NAP		g3282044	1676	390	e-113	76	18	(M77661) putative pol polyprotein [Magnaporthe grisea]
21419	ENU05213	ANI61C3906			NAP		g1710858	431	182	2.00E-45	50	65	
21420	ENU05214	ANI61C5852	120-139	726-746	NAP		g730212	798	180	2.00E-89	72	90	
21421	ENU05215	ANI61C9289	22-46	807-829	NAP		g538067	523	161	6.00E-39	34	20	

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21422	ENU05216	ANI61C7651:	28-51	787-806	NAP		g3978134	541	83	6.00E-32	48	24	(U65409) Sla2p [Yarrowia lipolytica]
21423	ENU05217	ANI61C320:1	102-129	654-677	NAP		g2995360	481	99	6.00E-36	56	48	(AL022243) nucleosome assembly protein. [Schizosaccharomyces pombe]
21424	ENU05218	ANI61C6917:	36-57	348-374	NAP		g4758126	241	62	0.000000			"DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome [Homo sapiens]"
21425	ENU05219	ANI61C9553:	23-44	801-828	NAP		g118233	452	55	2.00E-19			allantoate permease [Saccharomyces cerevisiae]
21426	ENU05220	ANI61C9720:	45-64	810-829	NAP		g1352079	1801	289	e-107	70	30	beta-glucosidase 1 precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucosylhydrolase) [Aspergillus aculeatus]
21427	ENU05221	ANI61C2169:	59-78	562-581	NAP		g4539264	662	241	4.00E-63	58	58	(AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]
21428	ENU05222	ANI61C4363:	27-50	711-731	NAP		g417305	702	190	1.00E-47	46	41	"mannosyl-oligosaccharide alpha-1,2-mannosidase (MAN9)-alpha-mannosidase [MAN9)-alpha-mannosidase] [Saccharomyces cerevisiae]"
21429	ENU05223	ANI61S1929:	111-134	521-544	NAP		g113314	891	356	5.00E-98	93	5	delta-(L-alpha-aminoacyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emerticella nidulans]
21430	ENU05224	ANI61C7050:	32-51	757-780	NAP		g2773302	270	179	2.00E-44	35	51	(AF040720) xylosidase/arabinosidase [Selenomonas ruminantium]
21431	ENU05225	ANI61C6970:	22-49	797-824	NAP		g543961	210	85	8.00E-16			cell division control protein 14 [Schizosaccharomyces pombe]
21432	ENU05226	ANI61C784:5	24-43	428-455	NAP		g2154997	247	134	3.00E-31	40	26	(Y12503) Man9-mannosidase [Sus scrofa]
21433	ENU05227	ANI61S3090:			NAP		g100210	156	37	0.09	32	45	extensin precursor (clone Tom L-4) - tomato [Lycopersicon esculentum]
21434	ENU05228	ANI61C3808:	101-120	617-640	NAP		g1363750	204	65	5.00E-20	30	15	hypothetical protein YLR419w - yeast [Saccharomyces cerevisiae]
21435	ENU05229	ANI61C1125	67-87	437-456	NAP		g4557587	157	70	4.00E-14	37	32	[Saccharomyces cerevisiae]
21436	ENU05230	ANI61C9186:	59-78	791-810	NAP		g4585936	1397	192	3.00E-48	38	21	funarylacetoacetase [Homo sapiens]
		4850..1262											(ACO07211) putative helicase [Arabidopsis thaliana]

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21437	ENU05231	ANI61C2296: 4890..5915	22-49	779-801	NAP		g1217600	149	92	3.00E-19	27	48	(D38215) tcr3 [Streptomyces aureofaciens]
21438	ENU05232	ANI61C8809: 310..1320			NAP		g416657	576	162	2.00E-42	52	73	Anti-silencing protein 1 [Saccharomyces cerevisiae]
21439	ENU05233	ANI61C1071 6:3239..1	64-83	719-738	NAP		g2342601	1457	214	1.00E-57	40	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21440	ENU05234	ANI61C79:28 29..3543	22-46	630-649	NAP		g1174617	494	129	1.00E-42	64	33	"T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon) ["]
21441	ENU05235	ANI61C9059: 1..533	99-120	490-512	NAP		g3116126	93	61	0.000000	28	30	(AL023287) Sat1p [Schizosaccharomyces pombe]
21442	ENU05236	ANI61C8724: 1944..3970	22-47	800-827	NAP		g1546072	493	70	2.00E-11			(U68040) polyketide synthase [Cochliobolus heterostrophus]
21443	ENU05237	ANI61C4628: 1..650	108-126	548-567	NAP		g2983756	265	119	2.00E-26	42	40	(AE000735) ATP-dependent protease ATPase subunit clpX [Aquifex aeolicus]
21444	ENU05238	ANI61C4376: 823..1527	22-45	646-673	NAP		g2347143	660	266	1.00E-70	59	99	(U48234) spU2AF23 [Schizosaccharomyces pombe]
21445	ENU05239	ANI61C4928: 1597..1	72-91	781-807	NAP		g2501339	673	207	9.00E-53	51	35	Copper amine oxidase I [Aspergillus niger]
21446	ENU05240	ANI61C9658: 2293..1816	72-89	434-456	NAP		g2132029	150	58	0.000000	37	56	Hypothetical protein YOR004w - yeast (Saccharomyces cerevisiae)
21447	ENU05241	ANI61C4358: 704..1569	31-49	719-738	NAP		g2842699	369	164	5.00E-40	42	50	[Saccharomyces cerevisiae] putative ubiquitin carboxyl-terminal hydrolase C6G9.08 (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
21448	ENU05242	ANI61C4668: 1..996	38-57	726-747	NAP		g1177622	216	49	0.00004	28	27	(X89715) AOF1001 [Saccharomyces cerevisiae]
21449	ENU05243	ANI61C1134 8:618..1	22-46	524-548	NAP		g4160578	154	79	2.00E-14	31	54	(AL035218) hypothetical protein [Schizosaccharomyces pombe]
21450	ENU05244	ANI61C639:7 12..322	22-45	452-479	NAP		g731385	158	94	8.00E-19	37	50	hypothetical 33.7 KID protein in ISC10 3region [Saccharomyces cerevisiae]
21451	ENU05245	ANI61C7684: 640..1399	72-91	718-739	NAP		g1175370	177	120	1.00E-26	30	39	hypothetical 68.8 KID protein C2F7.07C in chromosome I [Schizosaccharomyces pombe]



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21452	ENU05246	ANI61C8831: 22-43	458-478		NAP		g2132738	460	175	2.00E-43	61	98	probable membrane protein YNL044w - yeast (Saccharomyces cerevisiae)
		2353..2820											[Saccharomyces cerevisiae]
21453	ENU05247	ANI61C6666: 23-44	490-514		NAP		g2894269	245	117	7.00E-26	32	49	(AL021839) myb family DNA binding protein [Schizosaccharomyces pombe]
		734..1											[Saccharomyces cerevisiae]
21454	ENU05248	ANI61C5501: 23-50	725-748		NAP		g462414	1454	123	8.00E-64	69	45	amino-acid permease IND1A1 [Trichoderma harzianum]
		605..2159											(AC006250) putative Athila retroelement ORF1 protein
21455	ENU05249	ANI61S150:5	110-130	376-399	NAP		g4263543	584	229	9.00E-60	85	15	[Arabidopsis thaliana]
		74..155											"glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (G6PD) [Arabidopsis thaliana]"
21456	ENU05250	ANI61S310:5	183-210	340-365	NAP		g3913727	496	142	8.00E-38	98	20	methionine aminopeptidase 1 precursor (METAP 1) (peptidase M 1) (MAP) [Saccharomyces cerevisiae]
		86..201											"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
21457	ENU05251	ANI61C5962: 22-48	779-801		NAP		g1351928	292	66	3.00E-25	38	65	probable membrane protein YOL163w - yeast (Saccharomyces cerevisiae)
		1..1303											[Saccharomyces cerevisiae]
21458	ENU05252	ANI61C6706: 37-54	803-829		NAP		g1166378	515	79	2.00E-25	34	24	[Saccharomyces cerevisiae]
		2398..1											(AF002660) aflatoxin [Aspergillus parasiticus]
21459	ENU05253	ANI61C8887: 118-137	372-399		NAP		g2132861	92	45	0.00002	32	56	Periodic tryptophan protein 2 [Saccharomyces cerevisiae]
		1..420											(AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
21460	ENU05254	ANI61C1016	27-50	700-723	NAP		g2738309	251	98	8.00E-20	31	51	hypothetical 15.9 KD protein in GFP1-SYG1 intergenic region [Saccharomyces cerevisiae]
		0:827..1											(AB001995) Tellp [Schizosaccharomyces pombe]
21461	ENU05255	ANI61C6324: 29-56	723-742		NAP		g730431	914	258	6.00E-70	62	27	Myo-inositol-1-phosphate synthase (IPS) [Candida albicans]
		1123..1											(Z98951) hypothetical protein [Schizosaccharomyces pombe]
21462	ENU05256	ANI61C1002: 2743..3805			NAP		g2804298	532	118	3.00E-36	38	51	Candida cylindracea []
		2743..3805											
21463	ENU05257	ANI61C4431: 56-75	460-484		NAP		g731809	182	91	4.00E-18	40	99	
		2430..1926											
21464	ENU05258	ANI61C6829: 110-129	389-416		NAP		g3764029	318	146	6.00E-35	51	5	
		2880..2444											
21465	ENU05259	ANI61C1930: 1240..1			NAP		g1170566	697	172	4.00E-54	47	51	
		1240..1											
21466	ENU05260	ANI61C3261: 22-47	737-759		NAP		g2370466	2515	146	2.00E-34	29	5	
		1..3275											
21467	ENU05261	ANI61C2859: 23-42	785-804		NAP		g1421604	431	177	7.00E-44	40	48	
		99..1099											

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21468	ENU05262	ANI6IC4819: 2775..2475	121-146	256-280	NAP		g3219530	226	106	5.00E-23	52	52	(AJ006688) IgE-binding protein [Aspergillus fumigatus]
21469	ENU05263	ANI6IC1017 5:1..712	172-191	538-557	NAP		g558311	520	118	1.00E-51	57	51	(L35487) mannanase [Aspergillus aculeatus]
21470	ENU05264	ANI6IC9994: 26..1083	22-49	804-829	NAP		g4507293	354	185	3.00E-46	43	81	syntaxin 5A [Homo sapiens]
21471	ENU05265	ANI6IS1430: 1..745			NAP		g4218005	156	62	0.000000	21	35	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21472	ENU05266	ANI6IC746:1 ..380	122-142	337-358	NAP		g418296	268	123	5.00E-28			vacuolar ATP synthase 95 KD subunit (vacuolar ATPase 95 KD subunit) [Saccharomyces cerevisiae]
21473	ENU05267	ANI6IC2820: 629..1	22-44	490-509	NAP		g3169065	219	104	4.00E-22	32	19	(AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]
21474	ENU05268	ANI6IC7326: 1..356	50-75	308-335	NAP		g2499454	219	104	2.00E-22	46	34	pectinesterase precursor (pectin methylesterase) (PE) [Aspergillus aculeatus]
21475	ENU05269	ANI6IC7855: 3027..4065	22-43	801-828	NAP		g2132944	430	183	1.00E-45	40	87	probable membrane protein YOR311c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21476	ENU05270	ANI6IC1495: 1..635	102-126	464-483	NAP		g3850070	575	120	1.00E-56	58	28	(AL033385) transketolase [Schizosaccharomyces pombe]
21477	ENU05271	ANI6IC7628: 1..386	27-52	340-365	NAP		g2905657	323	138	1.00E-32	59	31	(AF047469) arsenite translocating ATPase [Homo sapiens]
21478	ENU05272	ANI6IC7236: 1..584	22-42	541-563	NAP		g1077557	101	55	0.000000	30	26	probable membrane protein YDR061w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21479	ENU05273	ANI6IC7050: 965..2783	22-40	802-829	NAP		g1929089	253	36	0.46			(Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis]
21480	ENU05274	ANI6IC5946: 1..992	39-58	789-807	NAP		g4160583	578	218	4.00E-56	50	73	(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]
21481	ENU05275	ANI6IC8772: 51..569	22-45	456-475	NAP		g2133256	318	129	2.00E-30	68	39	o-pyrocatechuate decarboxylase (EC 4.1.1.46) - Aspergillus niger (fragments) []
21482	ENU05276	ANI6IC1063 3:1017..1	47-66	755-780	NAP		g3130032	378	165	4.00E-40	35	48	(AL023534) major facilitator family transporter [Schizosaccharomyces pombe]

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21483	ENU05277	ANI6IS3800:			NAP		g119712	160	51	0.000009	32	78	extensin precursor (proline-rich glycoprotein) [Zea mays]
21484	ENU05278	ANI6IC4389:	93-112	387-406	NAP		g1652128	102	68	5.00E-11	27	9	(D90903) hypothetical protein [Synechocystis sp.]
21485	ENU05279	ANI6ISS30:5	43-70	396-423	NAP		g538067	149	50	0.000000	29	13	(M77661) putative pol polyprotein [Magnaporthe grisea]
21486	ENU05280	ANI6IC7970:	102-129	278-296	NAP		g442927	246	77	9.00E-17	50	18	Glucose Oxidase (E.C.1.1.3.4) []
21487	ENU05281	ANI6IC255:1	32-51	776-795	NAP		g4704282	236	88	9.00E-17			(AL049728) hypothetical protein [Schizosaccharomyces pombe]
21488	ENU05282	ANI6IC4337:	22-44	806-825	NAP		g3080521	391	149	9.00E-37	38	33	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
21489	ENU05283	ANI6IC9934:	56-75	380-399	NAP		g3123246	548	226	5.00E-59	71	28	serine-type carboxypeptidase F precursor (proteinase F) (CPD-II) [Aspergillus niger]
21490	ENU05284	ANI6IC1103	22-46	771-798	NAP		g1175933	206	92	5.00E-18	33	21	hypothetical 96.7 KID protein in STE2-FRS2 intergenic region [Saccharomyces cerevisiae]
21491	ENU05285	ANI6IC565:3	49-68	803-829	NAP		g1708073	1592	250	7.00E-66	66	45	GMP synthase (glutamine-hydrolysing) (glutamine amidotransferase) (GMP synthetase) [Saccharomyces cerevisiae]
21492	ENU05286	ANI6IC12:18	22-42	714-735	NAP		g4758416	281	121	6.00E-27			golgi-specific brefeldin A-resistance factor 1 [Homo sapiens]
21493	ENU05287	ANI6IC7103:	54-73	623-650	NAP		g3114278	698	281	3.00E-75	70	99	"Chain J, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution []" (AB011123) KIAA0551 protein [Homo sapiens]
21494	ENU05288	ANI6IC7913:	22-49	515-534	NAP		g3043626	81	34	0.85			(AF009417) cytochrome P450 [Myrothecium roridum]
21495	ENU05289	ANI6IC5607:	70-89	778-801	NAP		g2267601	244	59	1.00E-19	31	44	(X60499) rad15 [Schizosaccharomyces pombe]
21496	ENU05290	ANI6IC9702:	22-48	802-828	NAP		g5022	2884	429	e-119	68	36	HEFM1 protein [Saccharomyces cerevisiae]
21497	ENU05291	ANI6IC1121	28-47	759-784	NAP		g1708195	892	136	2.00E-31	50	22	(U58946) transposase [Aspergillus awamori]
21498	ENU05292	ANI6IC3793:	102-126	388-413	NAP		g1805251	143	52	0.000002	31	25	ATP-dependent bile acid permease [Saccharomyces cerevisiae]
21499	ENU05293	ANI6IC3447:	33-60	722-741	NAP		g3915963	503	154	6.00E-37	36	15	

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21500	ENU05294	ANI61C9040: 1009..1	31-58	723-749	NAP		g3915067	362	100	1.00E-38	41	43	aspartyl-TRNA synthetase (aspartate--TRNA ligase) (ASPRS) [Aquifex aeolicus]
21501	ENU05295	ANI61C1022	66-87	513-532	NAP		g1168269	278	123	1.00E-27	37	50	"arabian endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanASE A) (ABN A) [Aspergillus niger]"
21502	ENU05296	ANI61C9143: 322..1	145-164	454-479	NAP		g4731167	173	88	3.00E-17			(AF108357) c-myc binding protein MM-1 [Mus musculus]
21503	ENU05297	ANI61C7822: 3976..4512	44-63	477-502	NAP		g4519181	863	188	2.00E-75	98	16	(AB023911) chitin synthase [Emicella nidulans]
21504	ENU05298	ANI61C9203: 3211..802	54-73	778-797	NAP		g2147662	718	116	2.00E-25	28	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium [Colletotrichum lagenarium]
21505	ENU05299	ANI61C8314: 136..1241	22-45	808-829	NAP		g2501437	432	115	1.00E-27	30	79	DNA damage tolerance protein RHC31 (RAD31 homolog) [Saccharomyces cerevisiae]
21506	ENU05300	ANI61C9664: 520..4543	22-47	724-746	NAP		g2065438	1877	178	4.00E-71	48	19	(Y11989) Wsk1 protein [Schizosaccharomyces pombe]
21507	ENU05301	ANI61S3836: 1..901			NAP		g4760549	100	69	3.00E-11			(AB019494) IDN3 [Homo sapiens]
21508	ENU05302	ANI61C7667: 217..840	54-73	537-554	NAP		g1171737	199	76	3.00E-19	43	16	Nonsense-mediated mRNA decay protein 2 (up-frameshift suppressor 2) [Saccharomyces cerevisiae]
21509	ENU05303	ANI61C1021	108-130	447-469	NAP		g4210942	537	222	9.00E-58	65	60	(AF069518) 17beta-hydroxysteroid dehydrogenase [Cochliobolus lunatus]
21510	ENU05304	ANI61C7952: 1472..966	25-44	463-485	NAP		g1723793	212	105	2.00E-22			putative 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase (3beta-HSD) (3-beta-hydroxy-delta(5)-steroid dehydrogenase (3-beta-hydroxy-5-ene steroid dehydrogenase) (progesterone reductase) / steroid delta-isomerase.. [Saccharomyces cerevisiae]
21511	ENU05305	ANI61C3186: 4376..4770	35-62	369-396	NAP		g1723781	83	64	6.00E-10	31	45	hypothetical 34.3 KD protein in TAF145-YOR1 intergenic region [Saccharomyces cerevisiae]

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21512	ENU05306	ANT61C1003	63-82	495-512	NAP		g3024443	201	89	2.00E-18	38	52	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) [Zalorien arboricola]
21513	ENU05307	ANT61C378.4	22-47	784-803	NAP		g416820	164	75	5.00E-13	22	74	para-hydroxybenzoate--polyprenyltransferase precursor (PHB:polyprenyltransferase) [Saccharomyces cerevisiae]
21514	ENU05308	ANT61C3805: 1..1904	67-86	780-799	NAP		g1706176	1345	138	3.00E-32	44	26	cutinase transcription factor 1 alpha [Fusarium solani f. sp. pisi]
21515	ENU05309	ANT61C3630: 6980..5626	22-47	803-829	NAP		g538067	790	203	1.00E-51	37	20	(M77661) putative pol polyprotein [Magnaporthe grisea]
21516	ENU05310	ANT61C1203: 112..571	102-122	387-406	NAP		g1001163	600	137	8.00E-34	81	45	(D64001) hypothetical protein [Synechocystis sp.]
21517	ENU05311	ANT61C1698: 352..1311	22-44	781-807	NAP		g3121995	388	159	5.00E-48	39	26	DOM34 interacting protein 2 [Saccharomyces cerevisiae]
21518	ENU05312	ANT61C9662: 741..193	36-55	477-496	NAP		g3879850	270	98	6.00E-20	43	100	(Z81592) predicted using Genefinder [Caenorhabditis elegans]
21519	ENU05313	ANT61C1070: 0:1822..483	45-64	769-788	NAP		g2959374	712	148	4.00E-35	45	47	(AL022117) putative pre-mrna splicing factor [Schizosaccharomyces pombe]
21520	ENU05314	ANT61S1429: 1..610			NAP		g2996650	121	54	0.000000	24	11	(AC004493) KIAA0324 [Homo sapiens]
21521	ENU05315	ANT61C2295: 696..1	26-45	576-595	NAP		g3411013	484	213	1.00E-54	49	24	(AF000232) protein mannosyltransferase 1 [Candida albicans]
21522	ENU05316	ANT61C8866: 1887..4165	63-82	745-765	NAP		g173384	2075	429	e-119	74	26	(L07734) DNA polymerase delta [Schizosaccharomyces pombe]
21523	ENU05317	ANT61C8004: 2211..880	22-48	700-721	NAP		g3080532	404	120	1.00E-26	39	62	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
21524	ENU05318	ANT61C914:4	22-47	805-826	NAP		g3878905	180	121	7.00E-27	28	65	(Z46794) similarity to enoyl CoA hydratase. Amino terminus shows similarity to acyl-CoA binding domains; cDNA EST EMBL:C08977 comes from this gene; cDNA EST EMBL:C09386 comes from this gene; cDNA EST yk447c11.5 comes from this... []
21525	ENU05319	ANT61C5448: 30..818	22-48	625-644	NAP		g786117	73	48	0.00007	20	52	(L41834) nuclear protein [Ensis minor]

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21526	ENU05320	ANI61C1071	22-45	790-809	NAP		g549602	195	50	0.000002	32	75	hypothetical 32.0 KD protein in SAP190-SP014 intergenic region [Saccharomyces cerevisiae]
21527	ENU05321	ANI61C2481	61-80	806-829	NAP		g1654028	262	49	0.00005			(Z81360) hypothetical protein Rv1726 [Mycobacterium tuberculosis]
21528	ENU05322	ANI61S2482			NAP		g2465144	86	58	0.000000	32	63	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
21529	ENU05323	ANI61C7829	211-235	626-649	NAP		g2266908	143	86	3.00E-16	38	70	(AE001274) PXNC; L4171.2 [Leishmania major]
21530	ENU05324	ANI61C2803	29-53	386-405	NAP		g1711410	106	64	4.00E-10	27	34	Pristinamycin IIa synthase subunit A (PIIA synthase subunit A) [Streptomyces pristinaespiralis]
21531	ENU05325	ANI61C1039	22-42	728-751	NAP		g1706694	601	238	3.00E-63	52	34	"lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene—lanosterol cyclase) (OSC) [Schizosaccharomyces pombe]" HUS1 protein [Schizosaccharomyces pombe]
21532	ENU05326	ANI61C5507	25-44	802-829	NAP		g3219811	312	77	2.00E-13	32	70	(AL031534) Chaperonin hsp78p [Schizosaccharomyces pombe]
21533	ENU05327	ANI61C8456	27-48	611-638	NAP		g3560150	2216	359	1.00E-98	65	34	[Schizosaccharomyces pombe]
21534	ENU05328	ANI61S1345			NAP		g135153	105	52	0.000004	26	32	Synapsins IA and IB []
21535	ENU05329	ANI61C1768	70-89	721-740	NAP		g584806	1414	492	e-138	83	51	"ATP synthase alpha chain, mitochondrial precursor [Neurospora crassa]"
21536	ENU05330	ANI61C5226	22-49	804-823	NAP		g1723540	910	61	3.00E-13	36	27	hypothetical 100.5 KD protein C1B9.04 in chromosome I [Schizosaccharomyces pombe]
21537	ENU05331	ANI61C3227	22-47	732-755	NAP		g2501559	681	142	5.00E-61	45	38	hypothetical 77.8 KD protein in MRPS28-HXT7 intergenic region [Saccharomyces cerevisiae]
21538	ENU05332	ANI61C2826	67-87	651-672	NAP		g63628	107	40	0.000000	35	79	(X14612) myb protein [Gallus gallus]
21539	ENU05333	ANI61C991	1 46-70	280-299	NAP		g1945500	98	59	0.000000	30	25	(U13644) F56D2.2 gene product [Caenorhabditis elegans]
21540	ENU05334	ANI61C1082	22-41	577-603	NAP		g3249039	245	120	1.00E-26	36	53	(AF071221) N-carbamyl-L-amino acid amidohydrolase [Arthrobaacter aureus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21541	ENU05335	ANI61C1043: 1228..2077	22-45	803-822	NAP	g3687510	372	123	2.00E-27	58	65	65	(AL031788) ubiquitin-conjugating enzyme [Schizosaccharomyces pombe]
21542	ENU05336	ANI61C4716: 3207..3737	22-41	313-332	NAP	g1084771	445	183	7.00E-46	70	77	77	ribosomal protein L18ac.c13 - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21543	ENU05337	ANI61C2614: 1522..1	39-62	724-749	NAP	g543806	1224	299	2.00E-80	58	40	40	"glucoamylase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) [Aspergillus oryzae]" (Z99163) WD repeat protein [Schizosaccharomyces pombe]
21544	ENU05338	ANI61C1067: 3..1..1254	36-55	802-829	NAP	g4884474	624	121	7.00E-49				[Schizosaccharomyces pombe]
21545	ENU05339	ANI61C7406: 1100..398	41-62	645-664	NAP	g2076715	737	288	2.00E-78	67	46	46	(Y11322) SEC61 protein [Yarrowia lipolytica]
21546	ENU05340	ANI61C1013: 1..2643..3799			NAP	g1834315	855	217	1.00E-55	52	67	67	(D78351) nuclease O [Aspergillus oryzae]
21547	ENU05341	ANI61S2200: 1..459	23-45	415-438	NAP	g3738162	502	180	6.00E-45	70	32	32	(AL031856) putative involvement in protein glycosylation in the golgi [Schizosaccharomyces pombe]
21548	ENU05342	ANI61C9766: 4104..4449	46-65	375-398	NAP	g3913082	99	53	0.000000	33	38	38	Aquaporin 9 [Homo sapiens]
21549	ENU05343	ANI61C8029: 1..315	45-72	265-284	NAP	g485111	168	73	6.00E-13	36	26	26	(U00050) similar to enoyl-CoA hydratases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]
21550	ENU05344	ANI61S1642: 1..369	22-49	327-348	NAP	g1335873	264	108	2.00E-23	50	24	24	(U46690) ATP-dependent RNA helicase [Mus musculus]
21551	ENU05345	ANI61C659:1 412..1029	174-193	342-361	NAP	g4581500	133	64	4.00E-10	33	18	18	(AL034352) putative oxalyl-CoA decarboxylase [Schizosaccharomyces pombe]
21552	ENU05346	ANI61C2064: 1484..1	40-59	726-751	NAP	g458284	1502	269	1.00E-94	85	37	37	(U05811) serine/threonine protein kinase [Trichoderma reesei]
21553	ENU05347	ANI61C4060: 1116..1			NAP	g3023651	435	172	3.00E-42	37	48	48	D-lactate dehydrogenase [Kluveromyces lactis]
21554	ENU05348	ANI61S4097: 1..331			NAP	g2499312	127	57	0.000000	36	22	22	NADH-ubiquinone oxidoreductase 51 KD subunit precursor (complex I-51KD) (CI-51KD) [Aspergillus niger]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21555	ENU05349	ANI61C2044: 488..893			NAP		g2851654	219	110	7.00E-24	46	22	2-dehydro-3-deoxyphosphogalactonate aldolase (6-phospho-2-dehydro-3-deoxygalactonate aldolase) (2-oxo-3-deoxygalactonate 6-phosphate aldolase) / galactonate dehydratase [Escherichia coli]
21556	ENU05350	ANI61C9912: 1396..2092	22-47	480-505	NAP		g1125833	569	167	3.00E-55	80	78	(U43283) Similar to ras-related protein; coded for by C. elegans cDNA CEESK32F; coded for by C. elegans cDNA yk82h5.3; coded for by C. elegans cDNA yk82h5.5; coded for by C. elegans cDNA yk168c1.3; coded for by C. elegans cDNA yk168c1.5 [Caecili
21557	ENU05351	ANI61C55:78 1..1323	24-47	498-520	NAP		g4895135	87	78	4.00E-14			(AF127374) Mmcr [Streptomyces lavendulae]
21558	ENU05352	ANI61C8078: 450..4089	37-59	722-749	NAP		g3355628	1981	267	6.00E-71	48	17	(X91867) CPC3 protein [Neurospora crassa]
21559	ENU05353	ANI61C806:2 543..1	22-43	725-745	NAP		g3114719	1435	217	1.00E-67	50	16	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
21560	ENU05354	ANI61C2673: 850..36	58-83	729-746	NAP		g547901	760	262	6.00E-78	64	70	"MAlate dehydrogenase, mitochondrial precursor [Saccharomyces cerevisiae]"
21561	ENU05355	ANI61C1129 4:1..562	103-122	516-535	NAP		g2497072	315	96	3.00E-32	47	18	hypothetical 103.0 KD protein in RAD10-PRS4 intergenic region [Saccharomyces cerevisiae]
21562	ENU05356	ANI61C1032 7:1..1791	108-127	727-748	NAP		g2673947	1501	272	2.00E-72	52	21	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
21563	ENU05357	ANI61C949:5 42..1402	22-47	787-814	NAP		g1938424	293	94	3.00E-22	35	25	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
21564	ENU05358	ANI61C7361: 1583..2751	37-56	773-800	NAP		g1077257	282	111	8.00E-24	27	27	hypothetical protein YPL009c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21565	ENU05359	ANI61C179:1 ..1794	22-44	755-780	NAP		g3288709	1767	377	e-104	63	19	(AB010442) PMR1 [Penicillium digitatum]
21566	ENU05360	ANI61C9217: 135..888	31-56	707-733	NAP		g3183391	118	78	7.00E-14	29	97	hypothetical 27.3 KD protein C9G1.08C in chromosome I [Schizosaccharomyces pombe]



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21567	ENU05361	ANI61C1120	22-45	786-805	NAP		g3702641	498	124	9.00E-28	41	86	(AL031825) similar to human 75k autoantigen [Schizosaccharomyces pombe]
21568	ENU05362	ANI61C1045	34-55	728-747	NAP		g2342601	1392	174	8.00E-43	32	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21569	ENU05363	ANI61C8576	23-41	802-829	NAP		g586858	223	81	1.00E-14	42	94	hypothetical 21.4 KD protein in DACA-SERS intergenic region [Bacillus subtilis]
21570	ENU05364	ANI61C258:1	46-65	773-792	NAP		g2132903	436	73	2.00E-12	24	33	probable membrane protein YOR165w - yeast [Saccharomyces cerevisiae]
21571	ENU05365	ANI61C1091			NAP		g2144323	357	143	1.00E-33	46	14	[Saccharomyces cerevisiae] xanthine dehydrogenase (EC 1.1.1.204) / xanthine oxidase (EC 1.1.3.22) - rat []
21572	ENU05366	ANI61S4059	183-208	527-554	NAP		g1020096	596	252	1.00E-66	76	41	(D49832) stearyl-acyl carrier protein desaturase [Sesamum indicum]
21573	ENU05367	ANI61C1047	63-82	806-825	NAP		g2506150	325	101	5.00E-21	35	88	Versicolorin reductase (VER-1) [Aspergillus parasiticus]
21574	ENU05368	ANI61C7245	22-41	596-618	NAP		g2493389	343	159	2.00E-38	35	53	probable sterigmatocystin biosynthesis P450 MONOoxygenase STCF (cytochrome P450 60A2) [Emericella nidulans]
21575	ENU05369	ANI61S3950			NAP		g1572721	143	40	0.022	27	18	(U70136) megakaryocyte stimulating factor: MSF [Homo sapiens]
21576	ENU05370	ANI61C5314	22-44	666-693	NAP		g2245026	104	78	6.00E-14	35	100	(Z97341) hypothetical protein [Arabidopsis thaliana]
21577	ENU05371	ANI61C4173	24-43	629-652	NAP		g2624405	163	98	6.00E-20	27	30	(X92655) gluconate [Schizosaccharomyces pombe]
21578	ENU05372	ANI61C1147	22-46	669-688	NAP		g731806	1647	347	6.00E-95	63	23	probable calcium-transporting ATPase 7 [Saccharomyces cerevisiae]
21579	ENU05373	ANI61C5508	2:1..2042		NAP		g2511761	1185	458	e-128	86	34	(AF023156) carnitine acetyl transferase FacC [Emericella nidulans]
21580	ENU05374	ANI61C8155	104-123	352-371	NAP		g1073534	165	75	2.00E-15	38	36	iucB protein - Escherichia coli [Escherichia coli]
21581	ENU05375	ANI61S365:5	182-204	462-484	NAP		g131154	895	364	e-100	94	23	Photosystem I P700 chlorophyll A apoprotein A2 [Nicotiana tabacum]
21582	ENU05376	ANI61C4338	38-57	550-573	NAP		g2239236	674	255	3.00E-67	66	16	(Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe]

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21583	ENU05377	ANI61C2934: 335..1201	27-46	748-768	NAP		g1345571	376	104	2.00E-40	47	25	(X80010) starch branching enzyme II [Pisum sativum]
21584	ENU05378	ANI61C403:1 ..2381	71-90	806-824	NAP		g2842700	1133	155	4.00E-56	41	15	hypothetical 192.5 KD protein C6G9.10C in chromosome I [Schizosaccharomyces pombe]
21585	ENU05379	ANI61C196:1 130..2491	22-44	764-790	NAP		g538067	809	227	7.00E-59	43	20	(M77661) putative pol polyprotein [Magnaporthe grisea]
21586	ENU05380	ANI61S822:6 60..160	215-234	414-433	NAP		g3913995	217	63	0.000000	39	19	ATP-dependent protease LA [Azospirillum brasilense]
21587	ENU05381	ANI61C2843: 533..1	72-91	409-428	NAP		g120609	238	93	9.00E-20			uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTase) [Saccharomyces cerevisiae]
21588	ENU05382	ANI61C9743: 2636..1864	26-45	731-752	NAP		g1730032	230	89	4.00E-17	32	99	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) [Escherichia coli]
21589	ENU05383	ANI61C1137: 1..333			NAP		g83727	544	218	1.00E-56	96	33	hypothetical nox3 protein - Emmericella nidulans mitochondrion (SGC3) [Emmericella nidulans]
21590	ENU05384	ANI61C3195: 68..609	40-59	468-487	NAP		g1168269	223	95	3.00E-22	38	53	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) [Aspergillus niger]" (AB010442) PMR1 [Penicillium digitatum]
21591	ENU05385	ANI61C966:6 8..566	37-62	390-417	NAP		g3288709	623	245	5.00E-66	78	11	probable aflatoxin biosynthesis P450 monooxygenase ORD1 (cytochrome P450 60A1) [Aspergillus parasiticus]
21592	ENU05386	ANI61C3723: 1163..494	162-182	621-648	NAP		g2493388	228	107	6.00E-27	39	49	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) [Aspergillus niger]" (AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
21593	ENU05387	ANI61C2144: 1..645	103-122	520-540	NAP		g1168269	189	103	1.00E-21	31	64	mitochondrial respiratory function protein homolog [Schizosaccharomyces pombe]
21594	ENU05388	ANI61S1049: 1..735			NAP		g3153821	127	50	0.00001	23	27	
21595	ENU05389	ANI61C6621: 621..1	26-45	497-520	NAP		g1709097	286	121	2.00E-29	37	50	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21596	ENU05390	ANI61C5111:	108-127	654-673		NAP		g3560142	252	123	1.00E-27	36	29	(AL031534) Major facilitator superfamily protein
		885..1782												[Schizosaccharomyces pombe]
21597	ENU05391	ANI61C7295:	22-45	800-827		NAP		g3139137	259	98	2.00E-26	41	22	(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
		928..1												[Schizosaccharomyces pombe]
21598	ENU05392	ANI61C5341:	22-49	766-787		NAP		g3395584	868	273	8.00E-73	52	24	(AL031179) importin beta subunit [Schizosaccharomyces pombe]
		1491..1												[Schizosaccharomyces pombe]
21599	ENU05393	ANI61C6532:	118-137	448-473		NAP		g2388906	396	183	6.00E-46	57	54	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
		1..494												[Schizosaccharomyces pombe]
21600	ENU05394	ANI61C986:1	113-139	476-503		NAP		g3023676	495	187	5.00E-49	48	31	probable translation initiation factor EIF-2B epsilon subunit (EIF-2B GDP-GTP exchange factor) [Schizosaccharomyces pombe]
		..646												[Schizosaccharomyces pombe]
21601	ENU05395	ANI61C7272:	54-73	372-399		NAP		g1723230	305	123	6.00E-28	45	58	hypothetical 28.5 KD protein C1D4.08 in chromosome I [Schizosaccharomyces pombe]
		4101..4547												[Schizosaccharomyces pombe]
21602	ENU05396	ANI61C1104	107-129	609-628		NAP		g3978466	567	215	2.00E-55	51	31	(AF086822) dihydroxyacetone synthase [Candida boidinii]
		5:1..681												(U68040) polyketide synthase [Cochliobolus heterostrophus]
21603	ENU05397	ANI61C1017	137-156	722-749		NAP		g1546072	249	118	6.00E-26	34	10	AXL2 protein precursor (SRO4 protein) [Saccharomyces cerevisiae]
		3:859..1												(K03205) salivary proline-rich protein precursor [Homo sapiens]
21604	ENU05398	ANI61C6174:	39-57	555-574		NAP		g731878	197	105	3.00E-22	29	25	regulator Y protein GAL4 [Saccharomyces cerevisiae]
		1218..1848												(X89442) peptide synthetase [Metarhizium anisopliae]
21605	ENU05399	ANI61S1311:				NAP		g190504	97	45	0.0004			(AF132563) BcDNA.LD14392 [Drosophila melanogaster]
		1..713												Maltese permease MAL3T (maltose transport protein MAL3T) [Saccharomyces cerevisiae]
21606	ENU05400	ANI61C9864:	54-73	803-822		NAP		g1169823	368	33	3.1			(X05204) arom polypeptide [Emeticella nidulans]
		455..2549												putative mitochondrial carrier C17H9.08 [Schizosaccharomyces pombe]
21607	ENU05401	ANI61C1033	24-41	625-645		NAP		g2342601	2035	119	1.00E-42	43	5	
		0:1..4071												
21608	ENU05402	ANI61C9342:	36-55	703-723		NAP		g4689350	727	298	3.00E-80			
		2795..2015												
21609	ENU05403	ANI61C4212:	23-48	707-730		NAP		g585446	660	180	9.00E-45	33	45	
		1230..2470												
21610	ENU05404	ANI61C6072:	26-47	803-829		NAP		g3834343	1545	436	e-121	97	17	
		1..926												
21611	ENU05405	ANI61C958:	126-149	287-306		NAP		g3219962	210	88	2.00E-17	46	33	
		1437..1101												

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21612	ENU05406	ANI61C937:1	102-127	440-465	NAP		g4587971	772	277	2.00E-74	96	12	(AF082072) ABC transporter protein AtcC [Emmericella nidulans]
21613	ENU05407	ANI61C2980:586..1	56-77	527-546	NAP		g2462911	321	105	9.00E-32	42	28	(Z83832) UDP-glucose:sterol glucosyltransferase [Avena sativa]
21614	ENU05408	ANI61S3826:1..664	146-165	507-524	NAP		g2327063	174	45	0.0005	22	23	(AF001305) protease 1 [Pneumocystis carinii f. sp. carinii]
21615	ENU05409	ANI61C9451:4893..5790	41-61	625-649	NAP		g2076715	914	231	6.00E-91	76	51	(Y11322) SEC61 protein [Yarrowia lipolytica]
21616	ENU05410	ANI61C199:6			NAP		g539218	106	42	0.003	20	25	hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []
21617	ENU05411	ANI61C1002:5:4341..3161	25-52	807-829	NAP		g1586814	736	205	3.00E-52	48	63	glycerol-3-phosphate dehydrogenase [Schizosaccharomyces pombe]
21618	ENU05412	ANI61C3264:1240..2489	22-45	766-783	NAP		g2414609	1146	354	4.00E-97	69	53	(Z99295) citrate lyase [Schizosaccharomyces pombe]
21619	ENU05413	ANI61C7483:1457..719	22-46	691-718	NAP		g584766	537	173	2.00E-42	66	99	ADP-ribosylation factor-like protein 1 [Saccharomyces cerevisiae]
21620	ENU05414	ANI61C9092:1..1170	54-73	765-782	NAP		g4581500	838	252	2.00E-66	50	47	(AL034352) putative oxalyl-CoA decarboxylase [Schizosaccharomyces pombe]
21621	ENU05415	ANI61C3548:1816..1030			NAP		g126791	816	233	2.00E-73	88	42	MRNA maturase BII (COBA intron protein) []
21622	ENU05416	ANI61C2656:1..644	87-114	562-581	NAP		g731288	474	175	3.00E-43	43	27	hypothetical 87.5 KD protein in ACS1-GCV3 intergenic region [Saccharomyces cerevisiae]
21623	ENU05417	ANI61C1514:1..1308			NAP		g2493965	1869	244	e-108	84	20	xanthine dehydrogenase (purine hydroxylase J) [Emmericella nidulans]
21624	ENU05418	ANI61C305:2	22-44	723-749	NAP		g2459997	1553	144	3.00E-49	45	20	(AF012898) protein phosphatase Ssd1 homolog [Candida albicans]
21625	ENU05419	ANI61C9125:1..431	22-44	378-397	NAP		g3646447	92	53	0.000001	35	69	"(AL031603) peroxisomal membrane protein pmp20p, Ahpc-TSA family protein [Schizosaccharomyces pombe]"
21626	ENU05420	ANI61C5598:513..1	100-118	462-481	NAP		g1805262	292	131	3.00E-30	49	7	"(U75347) fatty acid synthase, beta subunit [Emmericella nidulans]"
21627	ENU05421	ANI61C2807:844..335	109-130	465-487	NAP		g4262222	299	105	2.00E-22	39	30	"(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]"
21628	ENU05422	ANI61C8964:6972..6519	108-127	375-394	NAP		g2493143	335	72	3.00E-23	74	66	vacuolar ATP synthase 16 KD proteolipid subunit [Candida tropicalis]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21629	ENU05423	ANI61C9643: 1704..1	34-53	724-743	NAP		g1723575	515	83	2.00E-15			hypothetical protein C26F1.01 in chromosome I [Schizosaccharomyces pombe]
21630	ENU05424	ANI61C4970: 1460..125	22-46	795-822	NAP		g699196	560	141	8.00E-33	42	52	(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]
21631	ENU05425	ANI61C1099: 1:1..1013	22-49	766-785	NAP		g3114719	588	196	1.00E-49	48	15	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
21632	ENU05426	ANI61C5574: 556..1	59-86	410-437	NAP		g3947855	244	67	2.00E-20	45	60	(AL034381) putative Golgi membrane protein [Schizosaccharomyces pombe]
21633	ENU05427	ANI61C9448: 4363..3345	22-48	806-829	NAP		g403179	367	114	3.00E-42	34	55	(L24441) kinesin light chain [Loligo pealii]
21634	ENU05428	ANI61S991:1..576			NAP		g3329623	165	57	0.000000	21	57	(AF078790) No definition line found [Caenorhabditis elegans]
21635	ENU05429	ANI61C9118: 1..1241	25-47	802-824	NAP		g3163927	1659	187	e-106	99	63	(AJ001157) hymA [Emmericella nidulans]
21636	ENU05430	ANI61C1327: 804..1520			NAP		g3850093	228	124	7.00E-28	30	47	(AL033389) putative allantoin permease [Schizosaccharomyces pombe]
21637	ENU05431	ANI61C9639: 9628..9095	122-141	489-513	NAP		g2137308	66	42	0.003	23	47	G protein beta subunit like - mouse [Mus musculus]
21638	ENU05432	ANI61C1236: 3252..1	36-60	714-736	NAP		g1805261	1628	259	1.00E-68	48	15	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
21639	ENU05433	ANI61C1001: 1:314..1	79-98	275-294	NAP		g2612805	142	80	1.00E-14	37	21	(AL008883) glnA4 [Mycobacterium tuberculosis]
21640	ENU05434	ANI61C2961: 1431..2728	31-50	770-789	NAP		g2342601	645	152	4.00E-36	41	4	(X89442) peptide synthetase [Metarhizium anisopliae]
21641	ENU05435	ANI61C1258: 1..467	53-75	398-417	NAP		g732372	90	50	0.000000	37	38	hypothetical oxidoreductase in PTA-ROCC intergenic region [Bacillus subtilis]
21642	ENU05436	ANI61C2743: 1213..1800	22-49	542-567	NAP		g2707191	124	36	0.22	38	53	(U94186) glutamine rich protein similar to glutenins [Glomerella cingulata]
21643	ENU05437	ANI61C3684: 1985..2821	28-55	784-811	NAP		g4502229	435	122	7.00E-40	53	100	ADP-ribosylation factor-like 2 [Homo sapiens]
21644	ENU05438	ANI61C9235: 1..631	106-128	561-580	NAP		g549795	384	161	4.00E-39			GTP-binding protein YPT51/VP521 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21645	ENU05439	ANT61C6976:	23-45	638-657	NAP		g2706459	179	85	5.00E-16	26	75	(AL021046) hypothetical PHD finger domain protein [Schizosaccharomyces pombe]
21646	ENU05440	ANT61C8570:			NAP		g2408082	806	96	1.00E-27	37	28	(Z99167) putative helicase [Schizosaccharomyces pombe]
21647	ENU05441	ANT61C1109			NAP		g1709159	449	120	2.00E-49	42	39	putative methylenetetrahydrofolate reductase [Saccharomyces cerevisiae]
21648	ENU05442	ANT61C4289:	24-44	803-829	NAP		g238482	269	135	4.00E-31	36	73	"long chain alpha-hydroxy acid oxidase=FMN-dependent alpha-hydroxy acid-oxidizing enzyme (EC 1.1.3.15) [rats, kidney, Peptide, 352 aa]"
21649	ENU05443	ANT61C1038	27-49	722-749	NAP		g3123262	1765	341	e-115	73	33	DNA repair protein RHP54 [Schizosaccharomyces pombe]
21650	ENU05444	ANT61C5267:	222-241	503-530	NAP		g2266427	229	99	1.00E-21	43	67	(Y13917) ynfF [Bacillus subtilis]
21651	ENU05445	ANT61C1038	22-43	802-829	NAP		g3929362	648	92	4.00E-36	42	45	Pisatin demethylase (cytochrome P450 57A1) [Nectria haematococca mp VII] (Z69793) R03A10.3 [Caenorhabditis elegans]
21652	ENU05446	ANT61C7643:	22-45	760-779	NAP		g3878874	351	124	9.00E-28	34	49	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) - Emericella nidulans mitochondrion (SGC3) [] (AL023517) putative iron-sulfur binding oxidoreductase [Streptomyces coelicolor]
21653	ENU05447	ANT61S4583:			NAP		g101813	585	141	1.00E-33	91	99	26S protease regulatory subunit 4 homolog (MTS2 protein) [Schizosaccharomyces pombe]
21654	ENU05448	ANT61C1798:	120-141	260-279	NAP		g3130015	75	50	0.000005	27	19	(Z98560) hypothetical protein [Schizosaccharomyces pombe]
21655	ENU05449	ANT61C9805:	186-213	551-570	NAP		g547935	581	106	1.00E-47	72	41	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
21656	ENU05450	ANT61C1029	72-91	717-736	NAP		g2330803	2374	353	1.00E-96	58	19	putative 60S ribosomal protein YEL050C [Saccharomyces cerevisiae]
21657	ENU05451	ANT61C617:	96-120	700-727	NAP		g1834342	1276	472	e-139	97	18	probable membrane protein YDL246c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21658	ENU05452	ANT61C1022	27-48	810-829	NAP		g418426	594	233	1.00E-60	54	59	
21659	ENU05453	ANT61S4056:			NAP		g2117435	101	64	5.00E-10	27	33	

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21660	ENU05454	ANI61C9713:	98-118	336-362	NAP		g2995374	273	120	6.00E-27	53	56	(AL022245) hypothetical 21.5 kd protein [Schizosaccharomyces pombe]
21661	ENU05455	ANI61C6683:	110-129	451-471	NAP		g1565203	151	92	2.00E-18	32	41	(D87894) chitinase [Rhizopus microsporus var. oligosporus]
21662	ENU05456	ANI61C1044	28-48	686-710	NAP		g2132863	600	238	4.00E-62	45	38	probable membrane protein YOR001w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21663	ENU05457	ANI61C5918:	42-61	765-784	NAP		g416900	422	115	6.00E-25	42	46	probable aldehyde dehydrogenase [Pseudomonas sp.]
21664	ENU05458	ANI61S1481:			NAP		g1334398	166	32	6.9	29	75	(X15081) MURF2 protein (AA 1-348) [Cnithidia fasciculata]
21665	ENU05459	ANI61C9981:	42-62	724-749	NAP		g3023272	2834	458	e-128	76	28	alpha-glucosidase precursor (maltase) (AGL) [Aspergillus oryzae]
21666	ENU05460	ANI61C1118	31-50	616-641	NAP		g2308977	977	100	2.00E-52	99	11	(AB000125) chitin synthase [Emeticella nidulans]
21667	ENU05461	ANI61C6359:	23-50	803-829	NAP		g3021303	1362	359	e-127	100	10	(Y15996) acetyl-CoA carboxylase [Emericella nidulans]
21668	ENU05462	ANI61C540:	104-123	722-741	NAP		g3947883	562	215	4.00E-55	44	55	(AL034382) putative Trp-Asp repeat protein [Schizosaccharomyces pombe]
21669	ENU05463	ANI61C1212:	53-76	463-482	NAP		g4505739	119	45	0.0003	26	100	prefoldin 1 [Homo sapiens]
21670	ENU05464	ANI61C739:	6-33-54	626-650	NAP		g4210899	68	54	0.000001	22	48	(AF045609) OrfL [Sinorhizobium meliloti]
21671	ENU05465	ANI61C3278:	108-131	701-724	NAP		g3116113	454	212	3.00E-54	53	29	(AL023286) probable ahp-dependent ma helicase [Schizosaccharomyces pombe]
21672	ENU05466	ANI61C2706:	65-84	317-343	NAP		g1168403	183	81	4.00E-15	41	15	regulatory protein ALCR []
21673	ENU05467	ANI61C1097	90-114	370-389	NAP		g731385	147	68	4.00E-11	35	46	hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]
21674	ENU05468	ANI61C558:	3-26-46	803-829	NAP		g5222302	959	143	8.00E-45	39	23	(L35053) endonuclease [Magnaporthe grisea]
21675	ENU05469	ANI61C2976:	23-47	805-826	NAP		g3868931	342	125	9.00E-37	39	66	(AB014769) glutaminyl cyclase [Bothrops jararaca]
21676	ENU05470	ANI61C4309:	48-67	762-781	NAP		g1654096	1237	78	4.00E-50	54	8	(Y09076) RAD3 [Schizosaccharomyces pombe]
21677	ENU05471	ANI61S1014:			NAP		g3037018	170	33	0.011	27	92	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21678	ENU05472	ANI6IS1690:			NAP		g786117	159	49	0.00003	17	52	(L41834) nuclear protein [Ensis minor]
21679	ENU05473	ANI6IC1127:	63-90	551-575	NAP		g3006175	448	191	3.00E-48	53	33	(AL022305) putative transcription factor [Schizosaccharomyces pombe]
21680	ENU05474	ANI6IC6111:	22-44	810-829	NAP		g117619	450	122	4.00E-27	34	41	Choline transport protein [Saccharomyces cerevisiae]
21681	ENU05475	ANI6IC3619:	41-60	616-635	NAP		g4033411	533	222	3.00E-57	44	27	putative importin beta-2 subunit (karyopherin beta-2 subunit) (importin 104) (transportin) (TRN) [Schizosaccharomyces pombe]
21682	ENU05476	ANI6IC4102:	112-131	321-343	NAP		g416963	402	171	2.00E-42			C-5 sterol desaturase [Saccharomyces cerevisiae]
21683	ENU05477	ANI6IC1696:	70-89	625-644	NAP		g2501730	328	92	5.00E-18	29	75	Peroxisome assembly protein PEX8 (peroxin-10) [Pichia angusta]
21684	ENU05478	ANI6IC1763:	22-45	748-767	NAP		g4160581	644	227	2.00E-61	48	67	(AL035218) possible involvement in nuclear protein localisation [Schizosaccharomyces pombe]
21685	ENU05479	ANI6IC7954:	24-44	807-826	NAP		g2833327	329	100	2.00E-20	33	54	Hexokinase [Schistosoma mansoni]
21686	ENU05480	ANI6IC5158:	22-48	695-714	NAP		g140925	419	144	3.00E-37	37	99	hypothetical oxidoreductase in INLA 5'region (ORFA) [Listeria monocytogenes]
21687	ENU05481	ANI6IC3007:	23-46	714-741	NAP		g1916927	769	286	2.00E-76	55	48	(U87965) putative G-protein [Mus musculus]
21688	ENU05482	ANI6IC9656:	40-59	495-520	NAP		g2330829	307	123	8.00E-28	35	13	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
21689	ENU05483	ANI6IC4620:	183-203	528-548	NAP		g2780359	448	194	3.00E-49	49	34	(AB010110) ascorbate oxidase [Acremonium sp.]
21690	ENU05484	ANI6IC7917:	28-55	724-749	NAP		g1077412	376	136	3.00E-31	42	22	hypothetical protein YLR187w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21691	ENU05485	ANI6IC1002	38-56	764-784	NAP		g2492658	1339	111	6.00E-24	27	14	putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emmericella nidulans]
21692	ENU05486	ANI6IC3789:	221-240	738-764	NAP		g4481951	583	243	8.00E-64	41	11	(AL035637) putative alpha-glucan synthase [Schizosaccharomyces pombe]
21693	ENU05487	ANI6IC1946:	53-75	515-534	NAP		g113701	422	185	2.00E-46	46	38	Acetamidase [Emmericella nidulans]



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21694	ENU05488	AN161C2383: 22-45	438-457		NAP		g417567	136	84	8.00E-16			protein-tyrosine phosphatase 2 (PTPase 2) [Schizosaccharomyces pombe]
21695	ENU05489	AN161C8573: 22-47	798-825		NAP		g4836505	296	64	0.000000			(AF124929) putative deacetylcephalosporin C acetyltransferase [Streptomyces clavuligerus]
21696	ENU05490	AN161C1008 65-84	806-829		NAP		g559964	194	102	3.00E-21	40	74	(J05282) insect-type dehydrogenase [Pseudomonas cepacia]
21697	ENU05491	AN161C513:1 102-129	617-640		NAP		g4557525	590	208	2.00E-53	54	44	dihydroipoamide dehydrogenase precursor [Homo sapiens]
21698	ENU05492	AN161C8488: 68-86	435-453		NAP		g1723495	168	61	0.000000	39	23	hypothetical 63.2 KD protein C1F3.09 in chromosome I [Schizosaccharomyces pombe]
21699	ENU05493	AN161C9883: 25-44	661-687		NAP		g2326833	704	200	9.00E-51	38	33	(Z73502) ORF YPL147w [Saccharomyces cerevisiae]
21700	ENU05494	AN161C1003: 23-49	802-829		NAP		g1653242	559	70	2.00E-11	28	53	(D90912) hypothetical protein [Synecocystis sp.]
21701	ENU05495	AN161C855:1 128-147	408-428		NAP		g1749490	138	82	4.00E-15	31	69	"(D89141) similar to Saccharomyces cerevisiae hypothetical 27.6KD protein in chromosome VII, SWISS-PROT Accession Number P46948 [Schizosaccharomyces pombe]"
21702	ENU05496	AN161C1018 22-48	365-392		NAP		g1437475	134	64	8.00E-10	30	38	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralsstonia pickettii]"
21703	ENU05497	AN161C1003 51-70	515-534		NAP		g4049543	131	60	0.000000	33	39	(AL034564) putative protease; endopeptidase [Schizosaccharomyces pombe]
21704	ENU05498	AN161C1042 22-43	804-829		NAP		g2995339	199	91	8.00E-18	27	32	(AL022244) hypothetical protein [Schizosaccharomyces pombe]
21705	ENU05499	AN161C1057 41-60	788-807		NAP		g113314	4339	538	e-152	99	7	delta-(L-alpha-aminoadipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emmericella nidulans]
21706	ENU05500	AN161C5776: 206-225	681-701		NAP		g4826880	94	62	0.000000			oxidase (cytochrome c) assembly 1-like [Homo sapiens]
21707	ENU05501	AN161C6356: 22-49	725-749		NAP		g3702200	717	252	2.00E-66	47	43	(AJ011686) methylenetetrahydrofolate reductase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21708	ENU05502	ANI61C4103: 987..1	42-61	795-814	NAP		g1346660	464	145	5.00E-34	37	58	Salicylate hydroxylase (salicylate 1-monoxygenase) [Pseudomonas putida]
21709	ENU05503	ANI61C1102: 1..483	25-46	390-413	NAP		g133356	258	115	2.00E-25			DNA-directed RNA polymerase III largest subunit (C160) [Saccharomyces cerevisiae]
21710	ENU05504	ANI61C9104: 4840..5692	45-64	762-781	NAP		g1173383	328	163	1.00E-39	37	66	SCN1 protein [Schizosaccharomyces pombe]
21711	ENU05505	ANI61C1296: 1318..1	22-43	728-749	NAP		g4500377	415	143	6.00E-38	36	47	(AL035439) putative NADPH cytochrome reductase
21712	ENU05506	ANI61C6074: 1430..1			NAP		g1805262	2017	391	e-108	77	13	[Schizosaccharomyces pombe] "(U75347) fatty acid synthase, beta subunit [Emmericella nidulans]"
21713	ENU05507	ANI61C9521: 1556..843	37-57	661-679	NAP		g2826168	235	106	2.00E-22	39	49	(AB010714) salicylate hydroxylase [Pseudomonas putida]
21714	ENU05508	ANI61C4432: 892..547	40-66	303-325	NAP		g1790870	191	90	7.00E-18	38	44	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni]
21715	ENU05509	ANI61C7537: 1247..2374	23-42	740-765	NAP		g67385	736	154	7.00E-52	42	52	alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]
21716	ENU05510	ANI61C8019: 1..467	178-195	422-446	NAP		g113701	170	81	5.00E-15	28	28	Acetamidase [Emmericella nidulans]
21717	ENU05511	ANI61C3497: 1..606	61-80	388-413	NAP		g3122272	717	261	4.00E-69	70	37	Importin alpha subunit (karyopherin alpha subunit) (serine-rich RNA polymerase I suppressor protein) [Schizosaccharomyces pombe]
21718	ENU05512	ANI61C2554: 778..1	42-66	730-749	NAP		g2244898	254	132	3.00E-30	29	26	"(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]"
21719	ENU05513	ANI61C3764: 587..1	23-47	494-517	NAP		g730378	502	141	4.00E-48			Proteasome component C11 (macropain subunit C11) (proteinase YSCE subunit 11) (multicatalytic endopeptidase complex subunit C11) [Saccharomyces cerevisiae]
21720	ENU05514	ANI61C7285: 541..1312	23-42	729-751	NAP		g4105147	848	175	8.00E-69	68	100	"(AF043595) xyloglucan-specific endo-beta-1,4-glucanase precursor [Aspergillus aculeatus]"

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21721	ENU05515	ANI61C3973:	37-64	713-737	NAP		g730881	1645	210	1.00E-87	64	33		"threonyl-tRNA synthetase, cytoplasmic (threonine--tRNA ligase) (THRRS) [Saccharomyces cerevisiae]"
21722	ENU05516	ANI61C3026:	22-49	392-419	NAP		g1362793	168	84	8.00E-16	35	69		emopannil-binding protein - human [Homo sapiens]
21723	ENU05517	ANI61C4961:	121-140	799-824	NAP		g1666269	261	83	2.00E-29	40	75		(Z82021) cytochrome P450 [Agaricus bisporus]
21724	ENU05518	ANI61C7020:	23-42	762-780	NAP		g3219785	885	288	4.00E-77	58	65		putative cysteine synthase (O-acetylserine sulfhydrylase) (O-acetylserine (thiol)-lyase) (CSASE)
21725	ENU05519	ANI61S2922:	22-45	398-420	NAP		g1723436	610	221	2.00E-57	74	14		[Schizosaccharomyces pombe] hypothetical 119.9 KD protein C56F8.03 in chromosome I
21726	ENU05520	ANI61C7675:	146-168	506-525	NAP		g538605	828	265	8.00E-88	86	41		[Schizosaccharomyces pombe] glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - Emericella nidulans
21727	ENU05521	ANI61C8815:	117-136	570-589	NAP		g2894300	256	90	2.00E-17	43	36		[Emericella nidulans] (AL021837) hypothetical protein [Schizosaccharomyces pombe]
21728	ENU05522	ANI61C1562:	22-49	727-747	NAP		g1834342	1513	512	e-144	96	18		(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
21729	ENU05523	ANI61C2594:	22-46	810-829	NAP		g401013	4308	384	e-120	73	21		DNA-directed RNA polymerase II 138 KD polypeptide (RNA polymerase II subunit 2) [Schizosaccharomyces pombe]
21730	ENU05524	ANI61C8067:	62-81	780-799	NAP		g2407176	1822	553	e-157	98	27		(AF016850) alpha-mannosidase [Emericella nidulans]
21731	ENU05525	ANI61S775.1:			NAP		g4240179	204	39	0.029	26	29		(AB020652) KIAA0845 protein [Homo sapiens]
21732	ENU05526	ANI61C3351:	22-43	468-493	NAP		g3982753	86	70	1.00E-11	32	37		(AF070937) gibberellin 3 beta-hydroxylase [Arabidopsis thaliana]
21733	ENU05527	ANI61C1027	57-77	482-509	NAP		g1770576	154	51	8.00E-14	31	54		(X95073) Translin associated protein X [Homo sapiens]
21734	ENU05528	ANI61C5396:	24-43	805-829	NAP		g462156	1450	172	2.00E-42				GTPase-activating protein [Schizosaccharomyces pombe]
21735	ENU05529	ANI61C1028	35-54	809-829	NAP		g2117970	341	71	1.00E-11				triacylglycerol lipase (EC 3.1.1.3) I-yeast (Geotrichum candidum) (strain CBS 178.71) []

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21736	ENU05530	ANI61S302.1	41-60	438-457	NAP	g2245050	599	172	1.00E-63	72	6	(Z97342) resistance gene homolog [Arabidopsis thaliana]	
21737	ENU05531	ANI61C6674	31-50	487-507	NAP	g1906796	349	133	2.00E-32	44	70	(D85181) fungal sterol-C5-desaturase homolog [Homo sapiens]	
21738	ENU05532	ANI61S1332	321..887		NAP	g4759100	115	45	0.0004			"splicing factor, arginine/serine-rich 11 [Homo sapiens]"	
21739	ENU05533	ANI61C2473	48-67	658-677	NAP	g226788	501	178	6.00E-44	37	14	erythrocyte ankyrin [Homo sapiens]	
21740	ENU05534	ANI61C3738	107-126	546-565	NAP	g2924771	126	95	6.00E-19	27	53	(AC002334) putative dimethylaniline monooxygenase [Arabidopsis thaliana]	
21741	ENU05535	ANI61C3590	32-51	427-448	NAP	g1749552	224	72	8.00E-28	33	35	"(D89172) similar to Saccharomyces cerevisiae transketolase 2(TK2), SWISS-PROT Accession Number P33315 [Schizosaccharomyces pombe]"	
21742	ENU05536	ANI61C8544	25-44	804-828	NAP	g2791647	454	110	8.00E-35	33	47	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]	
21743	ENU05537	ANI61S3134			NAP	g4558826	242	106	2.00E-22	42	41	(AF076691) aureobasidin-resistance protein; AurA [Emericella nidulans]	
21744	ENU05538	ANI61C4840	34-53	770-797	NAP	g3914984	432	181	5.00E-45	39	7	Ferrichrome siderophore peptide synthetase [Ustilago maydis]	
21745	ENU05539	ANI61C1550	41-60	423-442	NAP	g4456808	130	52	0.000002	33	22	(A1236923) ifc3 protein [Shewanella frigidimarina]	
21746	ENU05540	ANI61C9547	118-138	478-503	NAP	g3136025	165	104	4.00E-22	33	62	(AL0233587) putative DNA repair protein [Schizosaccharomyces pombe]	
21747	ENU05541	ANI61C5119			NAP	g2909514	88	47	8.00E-10	34	48	(AL021932) hypothetical protein Rv0439c [Mycobacterium tuberculosis]	
21748	ENU05542	ANI61C6475	166-185	369-388	NAP	g121649	389	115	2.00E-42	52	14	GRR1 protein [Saccharomyces cerevisiae]	
21749	ENU05543	ANI61C1044	39-58	803-822	NAP	g1708621	930	231	1.00E-67	57	23	serine/threonine-protein kinase PMK1 [Schizosaccharomyces pombe]	
21750	ENU05544	ANI61C6941	62-81	804-829	NAP	g1171738	809	240	1.00E-62	48	52	nonsense-mediated mRNA decay protein 3 [Saccharomyces cerevisiae]	
21751	ENU05545	ANI61C1198	83-109	692-719	NAP	g1652509	1338	520	e-147	96	72	(D90906) poly(3-hydroxyalkanoate) synthase [Synechocystis sp.]	
21752	ENU05546	ANI61C3622	22-47	803-829	NAP	g538067	1959	143	1.00E-33	38	16	(M77661) putative pol polypeptide [Magnaporthe grisea]	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21753	ENU05547	ANI6IC7101: 1816..452	38-57	802-829	NAP		g82865	231	99	4.00E-20	28	23	regulatory protein LAC9 - yeast (Kluyveromyces marxianus var. lactis)
21754	ENU05548	ANI6IC7111: 430..1	102-120	444-471	NAP		g731968	281	100	6.00E-21	47	43	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region [Saccharomyces cerevisiae]
21755	ENU05549	ANI6IS878:1..614	187-206	408-431	NAP		g2494125	468	172	1.00E-48	48	44	(AC002376) Strong similarity to Cucumis acetyl-CoA acyltransferase (gb D70895). [Arabidopsis thaliana] (X89442) peptide synthetase [Metarhizium anisopliae] (AB009461) MUIS38 [Neurospora crassa]
21756	ENU05550	ANI6IC1047 2:1..1931	22-41	772-795	NAP		g2342601	1299	244	5.00E-64	45	5	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
21757	ENU05551	ANI6IC4808: 1813..2678			NAP		g3219304	463	131	3.00E-36	58	26	(AB009461) MUIS38 [Neurospora crassa]
21758	ENU05552	ANI6IC3351: 420..1	102-121	437-456	NAP		g2408015	200	73	2.00E-12	36	42	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
21759	ENU05553	ANI6IC1065 5:1469..1894	24-51	391-410	NAP		g1363742	442	182	2.00E-45	61	51	probable membrane protein YLR243w - yeast (Saccharomyces cerevisiae)
21760	ENU05554	ANI6IS835:1..787			NAP		g3097062	168	72	4.00E-12	32	50	[Saccharomyces cerevisiae] (Y17145) putative betaine transporter [Eubacterium acidaminophilum]
21761	ENU05555	ANI6IC3157: 1..418	111-130	370-397	NAP		g1172532	521	183	4.00E-46	72	39	Penicillolysin precursor (deuterolysin) [Penicillium citrinum]
21762	ENU05556	ANI6IC18:1..767	114-133	716-736	NAP		g2330791	188	83	5.00E-20	32	35	(Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]
21763	ENU05557	ANI6IC8494: 3514..3060	22-48	455-479	NAP		g1304227	167	91	5.00E-18	32	44	(D63781) Epoxide hydrolase [Glycine max]
21764	ENU05558	ANI6IC9184: 3881..3418	219-237	382-401	NAP		g129766	316	69	8.00E-19			methyle-fatty-acyl-phospholipid synthase (unsaturated phospholipid methyltransferase) [Saccharomyces cerevisiae]
21765	ENU05559	ANI6IC9126: 1..1738	22-44	765-789	NAP		g127736	1164	141	5.00E-33	28	18	Myosin-2 isoform [Saccharomyces cerevisiae]
21766	ENU05560	ANI6IC9707: 4373..1505	22-48	785-811	NAP		g3646452	569	93	2.00E-18	28	19	(AL031603) BTB domain and Ankaryin repeat containing protein. [Schizosaccharomyces pombe]
21767	ENU05561	ANI6IC6194: 1239..1	60-85	780-802	NAP		g1580818	1021	201	3.00E-98	71	34	(Z69254) alpha-galactosidase [Hypocrea jecorina]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21768	ENU05562	ANI61C9491:	22-43	570-594	NAP		g416922	381	100	9.00E-32	53	97	Deoxyuridine 5'-triphosphate nucleotidohydrolase (DUTPase) (DUTP pyrophosphatase) (P18) [Lycopersicon esculentum] (AL023534) hypothetical protein [Schizosaccharomyces pombe] (L11574) p68 RNA helicase [Schizosaccharomyces pombe] (AL023594) amino-acid permease [Schizosaccharomyces pombe]
21769	ENU05563	ANI61C1103:	118-143	508-527	NAP		g3130037	318	128	3.00E-29	45	45	
21770	ENU05564	ANI61C4837:	60-79	579-599	NAP		g173419	787	317	5.00E-86	70	38	
21771	ENU05565	ANI61C1966:	22-46	371-389	NAP		g3150139	181	61	2.00E-19	31	32	
21772	ENU05566	ANI61C5006:	22-45	782-801	NAP		g1078626	3748	328	e-122	97	17	bimD protein - Emericella nidulans [Emericella nidulans]
21773	ENU05567	ANI61C6675:	181-202	609-636	NAP		g1723187	397	116	4.00E-44	46	20	112.3 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]
21774	ENU05568	ANI61S2718:			NAP		g2967448	102	40	0.013	31	13	(AB008683) alpha2(I) collagen [Bos taurus]
21775	ENU05569	ANI61C4825:	76-95	728-747	NAP		g3978134	779	256	2.00E-67	52	26	(U65409) Sla2p [Yarrowia lipolytica]
21776	ENU05570	ANI61S4379:			NAP		g1572721	254	50	0.00002	29	19	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
21777	ENU05571	ANI61C7082:	22-41	805-829	NAP		g4490992	219	61	3.00E-11	31	55	(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
21778	ENU05572	ANI61C5323:	23-42	726-744	NAP		g117619	215	56	0.000000	32	38	Choline transport protein [Saccharomyces cerevisiae]
21779	ENU05573	ANI61C1707:	35-62	718-744	NAP		g2494820	518	134	1.00E-45	46	48	Rhamnogalacturonase B precursor (rhamnogalacturonan lyase) (RGASE B) (RHGB) [Aspergillus aculeatus]
21780	ENU05574	ANI61C8098:	22-49	550-575	NAP		g1351596	221	98	7.00E-20	32	19	hypothetical 86.2 KD protein C4G8.04 in chromosome I [Schizosaccharomyces pombe]
21781	ENU05575	ANI61C1069			NAP		g1351689	297	85	1.00E-22	44	36	Potential CAAX prenyl protease 1 (prenyl protein-specific endoprotease 1) (PPSEP 1) [Schizosaccharomyces pombe]
21782	ENU05576	ANI61C1129	23-42	720-739	NAP		g132845	598	137	1.00E-31	78	100	60S ribosomal protein L27A (L29) (CRP1) [Neurospora crassa]

# Sequence Statistics

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21783	ENU05577	ANI61C6931: 1..396			NAP		g1877482	65	53	0.000000	32	39	(U89271) short-chain alcohol dehydrogenase [Tripsacum dactyloides]
21784	ENU05578	ANI61C7468: 1494..592	69-88	776-795	NAP		g2213907	1272	438	e-122	81	93	(AF004837) putative vacuolar protein sorting homolog [Aspergillus fumigatus]
21785	ENU05579	ANI61S4063: 1..645	90-109	528-548	NAP		g3929649	463	167	6.00E-41	84	36	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]
21786	ENU05580	ANI61C1014 0:1..515	102-121	468-494	NAP		g1806234	120	63	6.00E-14	31	61	(Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis]
21787	ENU05581	ANI61C1014 8:1981..1	34-61	726-749	NAP		g4185560	3327	571	e-162	99	12	(AF112473) PyrABCN [Emericella nidulans]
21788	ENU05582	ANI61C6750: 1851..2553	34-53	625-644	NAP		g4759160	252	69	5.00E-17			small nuclear ribonucleoprotein D3 polypeptide (18kD) [Homo sapiens]
21789	ENU05583	ANI61C4308: 1..641	117-136	584-603	NAP		g4262650	245	98	5.00E-26	38	31	(AF125969) contains similarity to GTP-binding proteins [Caenorhabditis elegans]
21790	ENU05584	ANI61C1086 1:1263..821	43-64	395-422	NAP		g3023956	101	69	2.00E-11	34	9	Vegetable incompatibility protein HET-E-1 [Podospora anserina]
21791	ENU05585	ANI61C9585: 637..1	22-48	502-521	NAP		g1175439	599	258	3.00E-68	57	22	hypothetical 107.1 KD protein C24H6.11C in chromosome I [Schizosaccharomyces pombe]
21792	ENU05586	ANI61C4157: 3992..3384	102-127	562-588	NAP		g1723926	248	130	1.00E-29	40	24	hypothetical 78.1 KD protein in TTP20-MRF1 intergenic region [Saccharomyces cerevisiae]
21793	ENU05587	ANI61C3304: 827..1	56-75	699-717	NAP		g729611	371	122	3.00E-27			Vanadate resistance protein GOG5/VRG4/VAN2 [Saccharomyces cerevisiae]
21794	ENU05588	ANI61C8348: 1658..2190	22-42	447-472	NAP		g3560147	263	122	2.00E-27	38	24	"(AL031534) ribosomal processing, ma binding, nucleolar protein [Schizosaccharomyces pombe]"
21795	ENU05589	ANI61C700:1..887	122-141	712-731	NAP		g1580818	1013	312	5.00E-90	64	37	(Z69254) alpha-galactosidase [Hypocrea jecorina]
21796	ENU05590	ANI61C6928: 775..1	25-52	680-707	NAP		g2342691	167	68	8.00E-14	29	33	(AC000106) F7G19.26 [Arabidopsis thaliana]
21797	ENU05591	ANI61C1019 2:1383..2024	27-46	563-582	NAP		g544013	143	64	7.00E-16	35	28	endochitinase precursor [Manduca sexta]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21798	ENU05592	ANI61C1575: 22-49		594-614	NAP		g3004863	530	214	4.00E-55	54	27	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
21799	ENU05593	535..1227 ANI61C9237: 64-83		806-825	NAP		g1723929	1819	261	6.00E-69	51	17	hypothetical 171.5 KD helicase in NUT1-ARQ2 intergenic region [Saccharomyces cerevisiae]
21800	ENU05594	1..2437 ANI61C1582: 22-45		725-748	NAP		g2500542	247	105	4.00E-22	31	19	putative ATP-dependent RNA helicase YMR128W [Saccharomyces cerevisiae]
21801	ENU05595	936..1 ANI61C7665: 69-88		761-780	NAP		g586486	508	178	4.00E-44	37	41	hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region [Saccharomyces cerevisiae]
21802	ENU05596	278..1134 ANI61C2116: 1..964			NAP		g2105430	687	216	2.00E-55	48	24	(U97079) U5-116kD [Mus musculus]
21803	ENU05597	1230..568 ANI61C3561: 95-114		609-630	NAP		g1437475	194	105	4.00E-22	38	57	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii]"
21804	ENU05598	ANI61C5947: 58..1380			NAP		g2924313	552	120	1.00E-26	34	25	"(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]"
21805	ENU05599	ANI61C431:8 22-48		452-471	NAP		g4803936	138	80	1.00E-17			(AC006264) unknown protein [Arabidopsis thaliana]
21806	ENU05600	32..1303 ANI61C374:1 204-223		380-399	NAP		g2117310	70	39	0.032	22	63	(Z95620) hypothetical protein [Schizosaccharomyces pombe]
21807	ENU05601	..592 ANI61C6452: 27-54		805-829	NAP		g3810847	471	192	3.00E-48	37	41	(AL032684) zinc finger protein [Schizosaccharomyces pombe]
21808	ENU05602	22..1176 ANI61C9353: 72-90		496-518	NAP		g3851530	195	59	4.00E-17	41	32	(AF065435) nodulin [Glycine max]
21809	ENU05603	1..539 ANI61C32:1.. 22-45		522-549	NAP		g3929312	145	51	0.000007	34	7	(AF100426) fimbriae-associated protein FapI [Streptococcus parasanguis]
21810	ENU05604	573 ANI61S133:1. 407			NAP		g2804455	274	79	3.00E-23	47	10	(AF043699) similar to a human orf (GB:DL3642) and human UV-damaged DNA binding factor (GB:U32986) in separate non-overlapping regions [Caenorhabditis elegans]
21811	ENU05605	ANI61S618:5 212-232		456-476	NAP		g136600	886	360	3.00E-99			transcriptional regulator Y protein TYRR [Escherichia coli]
21812	ENU05606	73..1 ANI61C1008 70-89		727-746	NAP		g1708982	810	143	4.00E-62	53	54	Ammonium transporter MIEP3 [Saccharomyces cerevisiae]
21813	ENU05607	6..1023..1 ANI61S222:1 308..1			NAP		g1708463	131	78	5.00E-14	28	37	IAA-amino acid hydrolase [Arabidopsis thaliana]



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21814	ENU05608	ANI61C6473: 22-46		727-749	NAP		g2408055	154	59	3.00E-11	28	35	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
21815	ENU05609	ANI61C9354: 898..1			NAP		g2565275	361	146	1.00E-34	68	81	(AF023611) Dim1p homolog [Homo sapiens]
21816	ENU05610	ANI61C5269: 37-58		712-730	NAP		g550452	766	154	1.00E-65	57	39	"(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]"
21817	ENU05611	ANI61C8323: 164-183		361-386	NAP		g1084969	612	190	2.00E-58	94	23	sulfate adenylyltransferase (EC 2.7.7.4) - Emericella nidulans [Emericella nidulans]
21818	ENU05612	ANI61C3094: 98-125		805-829	NAP		g1652620	459	96	1.00E-47	55	45	(D90907) pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp.]
21819	ENU05613	ANI61C2132: 22-41		425-446	NAP		g3878950	252	80	2.00E-23	44	98	(Z32683) similar to RNA binding domain; cDNA EST EMBL:D74891 comes from this gene; cDNA EST EMBL:D75208 comes from this gene; cDNA EST EMBL:D72347 comes from this gene; cDNA EST EMBL:D75552 comes from this gene; cDNA EST EMBL:D... [] (AL049498) hypothetical rho1 gdp-gtp exchange protein
21820	ENU05614	ANI61C8419: 28-46		805-827	NAP		g4539278	553	81	2.00E-15			[Schizosaccharomyces pombe] hypothetical 51.7 KID protein in CTP1-SUL2 intergenic region
21821	ENU05615	ANI61S2455: 33-52		413-438	NAP		g586361	127	62	0.000000	30	32	[Saccharomyces cerevisiae] (L10328) o197 [Escherichia coli]
21822	ENU05616	ANI61S2364: 61-87		427-452	NAP		g290544	730	234	1.00E-74	98	72	(Z97208) hypothetical protein [Schizosaccharomyces pombe]
21823	ENU05617	ANI61C1143: 22-47		803-829	NAP		g2239185	1187	253	1.00E-66	45	45	[Schizosaccharomyces pombe] proline-rich protein MP3 - mouse (fragment) []
21824	ENU05618	ANI61S4374: 1..547			NAP		g91210	117	61	0.000000	30	73	DNA-directed RNA polymerase II largest subunit (B220) [Saccharomyces cerevisiae]
21825	ENU05619	ANI61C6626: 22-48		780-807	NAP		g2507347	1984	48	0.00008	56	14	(AL031262) hypothetical protein [Schizosaccharomyces pombe]
21826	ENU05620	ANI61C7149: 28-50		770-790	NAP		g3417430	359	90	1.00E-17	31	30	

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21827	ENU05621	AN161C2318:			NAP		g2267008	195	112	4.00E-24	32	10	(AF006827) adenylate cyclase [Magnaporthe grisea]
21828	ENU05622	AN161C1143	88-108	368-390	NAP		g3978466	217	103	5.00E-22	42	19	(AF086822) dihydroxyacetone synthase [Candida boidinii]
21829	ENU05623	AN161C1455:	122-143	491-510	NAP		g3738169	289	92	3.00E-18	41	41	(AL031856) putative mitochondrial protein import protein - DNAJ protein [Schizosaccharomyces pombe]
21830	ENU05624	AN161C1069:	23-46	590-612	NAP		g2967835	661	214	1.00E-61	66	54	(AF052061) polygalacturonase [Ophiostoma novo-ulmi]
21831	ENU05625	AN161C4657:			NAP		g1703456	1367	231	3.00E-68	53	23	Cation-transporting ATPase PAT1 [Dictyostelium discoideum]
21832	ENU05626	AN161C1004	51-71	641-660	NAP		g1352388	377	173	1.00E-42	38	32	"Lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene-lanosterol cyclase) (OSC) [Rattus rattus]"
21833	ENU05627	AN161C1035:	118-138	381-400	NAP		g4150918	263	109	7.00E-24	51	55	(Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
21834	ENU05628	AN161C9868:	29-49	805-824	NAP		g2133268	1616	457	e-128	91	32	DNA-binding protein amda - Emericella nidulans [Emericella nidulans]
21835	ENU05629	AN161C9030:	22-45	720-739	NAP		g2414578	251	68	2.00E-20	39	60	(Z99292) hypothetical protein [Schizosaccharomyces pombe]
21836	ENU05630	AN161C1122	116-142	423-448	NAP		g84160	98	64	8.00E-10	32	40	fragmin - slime mold (Physarum polycephalum) (fragments) []
21837	ENU05631	AN161C1120	25-48	808-828	NAP		g2133293	814	154	8.00E-84	72	98	pectate lyase (EC 4.2.2.2) C - fungus (Fusarium solani) []
21838	ENU05632	AN161C5075:	22-49	720-745	NAP		g3738146	528	75	7.00E-13			"(AL031852) putative cleavage and polyadenylation specificity factor subunit, yeast pre-mRNA 3'-end processing factor CF II homolog [Schizosaccharomyces pombe]"
21839	ENU05633	AN161C5115:	60-85	727-750	NAP		g4539609	279	101	9.00E-21	39	100	(AL049522) WD repeat protein [Schizosaccharomyces pombe]
21840	ENU05634	AN161C7762:	24-45	540-561	NAP		g2408044	695	287	5.00E-77	65	24	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
21841	ENU05635	AN161C6096:	202-223	454-479	NAP		g3242653	155	55	0.000000	45	26	(AB015510) FII-CMCase [Aspergillus aculeatus]

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21842	ENU05636	ANI61C3621:	22-45	419-440	NAP		g2664240	476	199	1.00E-50	59	47	(AL009227) electron transfer flavoprotein alpha-subunit precursor [Schizosaccharomyces pombe]
21843	ENU05637	ANI61C2544:	22-43	805-824	NAP		g3287941	210	101	5.00E-21	45	26	hypothetical 44.3 KD protein C25H2.15 in chromosome II [Schizosaccharomyces pombe]
21844	ENU05638	ANI61C6113:	44-71	806-826	NAP		g1723894	806	238	6.00E-67	56	40	hypothetical GTP-binding protein in SEH1-PRP20 intergenic region [Saccharomyces cerevisiae]
21845	ENU05639	ANI61C2481:	22-42	581-600	NAP		g1787798	482	206	2.00E-52	43	91	(AE000249) putative enzyme [Escherichia coli]
21846	ENU05640	ANI61C8019:	38-58	485-507	NAP		g4106657	466	189	2.00E-47	57	46	(AL035064) activator 1 subunit (replication factor subunit) [Schizosaccharomyces pombe]
21847	ENU05641	ANI61C8982:	22-42	762-780	NAP		g1346661	337	74	1.00E-12	47	10	NAM9 protein precursor [Saccharomyces cerevisiae]
21848	ENU05642	ANI61C1079	24-45	775-794	NAP		g3133101	832	215	1.00E-64	56	72	(AL023554) conserved hypothetical protein. [Schizosaccharomyces pombe]
21849	ENU05643	ANI61C1061	43-62	709-734	NAP		g2133034	385	151	7.00E-36	26	45	probable membrane protein YPR156c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21850	ENU05644	ANI61C1799:	40-67	464-489	NAP		g1524045	165	63	1.00E-12	39	37	(X96943) Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi]
21851	ENU05645	ANI61S1588:	339..1098		NAP		g340613	112	41	0.007	25	68	(L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]
21852	ENU05646	ANI61C1255:	22-45	297-321	NAP		g4867840	299	137	5.00E-32			(Z99091) putative exocyst complex component [Schizosaccharomyces pombe]
21853	ENU05647	ANI61C1043	119-136	453-479	NAP		g732284	99	52	0.000002	30	31	hypothetical 29.7 KD protein in RPL1-CPDB intergenic region (F286) [Escherichia coli]
21854	ENU05648	ANI61S2100:	81-100	388-405	NAP		g4539261	197	61	0.000000	42	66	(AL049495) putative synaptobrevin-type protein transport protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21855	ENU05649	ANI61C5945: 1471..1055	221-240	373-396	NAP		g549725	90	50	5.00E-12			NADH-cytochrome B5 reductase precursor (P34/P32) [Saccharomyces cerevisiae]
21856	ENU05650	ANI61C1909: 1..546	71-92	504-525	NAP		g1827509	203	100	9.00E-21	33	24	(D83993) similar to pir: S52731 (23.4% identity in 273 aa overlap) [Schizosaccharomyces pombe]
21857	ENU05651	ANI61C1058: 2:545..1	62-81	470-487	NAP		g2494052	138	57	0.000000	41	45	purine nucleoside phosphorylase (inosine phosphorylase) (PNP) [Bacillus stearothermophilus]
21858	ENU05652	ANI61C5888: 2738..1935	22-44	731-750	NAP		g3121767	72	49	0.00003	31	99	ARP2/3 complex 16 KD subunit (P16-ARC) [Homo sapiens]
21859	ENU05653	ANI61C7786: 1..843	222-244	795-822	NAP		g2131466	205	55	5.00E-10	30	35	hypothetical protein YDR398w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21860	ENU05654	ANI61S4503: 777..1			NAP		g2330699	356	104	2.00E-28	39	53	(Z98529) putative mna polymerase ii transcription factor b subunit [Schizosaccharomyces pombe]
21861	ENU05655	ANI61C4705: 1..1508	22-40	792-811	NAP		g2133259	2209	485	e-136	77	48	tannase (EC 3.1.1.20) - Aspergillus oryzae [Aspergillus oryzae] (Z37980) ORF14 [Escherichia coli]
21862	ENU05656	ANI61C1133: 6948..6145	22-47	756-783	NAP		g953179	189	85	4.00E-16	28	98	(AF000232) protein mannosyltransferase 1 [Candida albicans]
21863	ENU05657	ANI61C1141: 1350..2351			NAP		g3411013	412	97	1.00E-37	46	27	Copper amine oxidase precursor (MAOXI) [Arthrobacter sp.] bystin-like [Homo sapiens]
21864	ENU05658	ANI61C1090: 1:1..499	35-57	436-460	NAP		g1351919	184	103	9.00E-22	37	24	hypothetical 66.7 KD protein in EGD2-SUN1 intergenic region [Saccharomyces cerevisiae]
21865	ENU05659	ANI61S1834: 1..670			NAP		g4757882	344	167	8.00E-41			Small nuclear ribonucleoprotein SM D1 (SNRNP core protein D1) (SM-D1) (SM-D autoantigen) [Mus musculus] (AL022117) asparagine synthetase [Schizosaccharomyces pombe]
21866	ENU05660	ANI61C6155: 3059..2512	107-130	504-527	NAP		g731763	318	109	8.00E-32	47	27	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
21867	ENU05661	ANI61C1098: 4:966..1386	22-42	421-440	NAP		g134039	337	71	7.00E-16	64	100	
21868	ENU05662	ANI61C7744: 8689..8335	24-44	313-334	NAP		g2959371	315	95	2.00E-29	63	18	
21869	ENU05663	ANI61C6500: 632..1	41-60	495-512	NAP		g1020413	120	57	8.00E-11	32	33	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchl gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21870	ENU05664	ANI61C6591: 1145..2267	34-52	808-827	NAP		g2132842	532	237	6.00E-62	51	87	probable membrane protein YOL077c - yeast (Saccharomyces cerevisiae)
21871	ENU05665	ANI61C1112 0:799..1	117-136	670-697	NAP		g3859709	344	176	2.00E-43	37	44	[Saccharomyces cerevisiae] (AL033497) nucleotide phosphodiesterase [Candida albicans]
21872	ENU05666	ANI61C1213: 864..2097	43-62	715-742	NAP		g2133333	215	50	9.00E-17	27	37	probable reverse transcriptase Mars1 (clone pCGC20) - fungus (Ascobolus immersus) (fragment) [Ascobolus immersus]
21873	ENU05667	ANI61C1105 7:851..1	50-69	755-781	NAP		g2293196	397	176	2.00E-43	34	65	(AF008220) YreT [Bacillus subtilis]
21874	ENU05668	ANI61C3631: 1..879			NAP		g2244802	208	101	5.00E-21	33	16	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
21875	ENU05669	ANI61C4225: 2092..1609	71-90	437-456	NAP		g1653493	403	153	2.00E-40	63	66	(D90914) hypothetical protein [Synechocystis sp.]
21876	ENU05670	ANI61C8023: 1..1115	40-66	738-765	NAP		g2342601	463	168	6.00E-41	33	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21877	ENU05671	ANI61C6494: 2741..1905	22-44	787-813	NAP		g1078030	294	79	2.00E-30	42	94	hypothetical protein YOR021c - yeast (Saccharomyces cerevisiae)
21878	ENU05672	ANI61C246:7 71..1	23-44	723-750	NAP		g585856	415	164	8.00E-40	43	60	[Saccharomyces cerevisiae] mitochondrial carrier protein RIM2
21879	ENU05673	ANI61C6363: 1281..1	23-42	718-737	NAP		g2133259	1584	467	e-131	78	48	[Saccharomyces cerevisiae] tannase (EC 3.1.1.20) - Aspergillus oryzae [Aspergillus oryzae]
21880	ENU05674	ANI61C7430: 3318..2845	36-62	430-453	NAP		g2967691	453	108	5.00E-46	68	45	"(AF038596) beta-1,3-glucanosyltransferase [Aspergillus fumigatus]"
21881	ENU05675	ANI61S1195: 1..938			NAP		g283032	192	64	0.000000	27	78	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
21882	ENU05676	ANI61C8808: 3399..4931	22-48	809-829	NAP		g3925779	177	42	0.005	24	48	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21883	ENU05677	ANI61C9823: 2105..910			NAP		g2492940	1531	200	e-127	95	77	Arginase [Emericella nidulans]
21884	ENU05678	ANI61C8194: 1..2472	24-48	779-801	NAP		g742559	1859	200	1.00E-50	41	10	TOR2(DRR2) gene [Saccharomyces cerevisiae]
21885	ENU05679	ANI61C3566: 2989..526	48-67	805-829	NAP		g3661614	1985	242	2.00E-63	50	35	(AF093142) aconitase [Aspergillus terreus]

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21886	ENU05680	ANI61C1218:	28-55	601-621	NAP		g1339938	428	185	2.00E-46	51	25	(D50430) glycerol-3-phosphate dehydrogenase [Mus musculus]
21887	ENU05681	1644..1003											
21887	ENU05681	ANI61S2611:	27-46	244-261	NAP		g2500536	283	79	5.00E-26	50	20	probable ATP-dependent RNA helicase DBP9 [Saccharomyces cerevisiae]
21888	ENU05682	1..368											
21888	ENU05682	ANI61C6784:	61-80	792-811	NAP		g1168351	198	49	0.00005	29	76	Alcohol dehydrogenase (ADH) [Bacillus stearothermophilus]
21889	ENU05683	3114..2036											
21889	ENU05683	ANI61S1114:			NAP		g2947228	184	39	0.054	25	16	(AF031886) erythrocyte binding protein [Plasmodium yoelii yoelii]
21890	ENU05684	1..857											
21890	ENU05684	ANI61C4594:	22-41	804-824	NAP		g1730777	1772	367	e-109	72	26	hypothetical 119.3 KD protein in FPR1-TOM22 intergenic region [Saccharomyces cerevisiae]
21891	ENU05685	1477..1											
21891	ENU05685	ANI61C4238:	102-125	335-361	NAP		g2132680	166	81	3.00E-15	40	3	probable membrane protein YLR087c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21892	ENU05686	1..382											
21892	ENU05686	ANI61C1030	22-49	801-828	NAP		g4007758	666	139	2.00E-32	53	55	(AL034433) conserved hypothetical protein [Schizosaccharomyces pombe] (Z95397) unknown [Schizosaccharomyces pombe]
21893	ENU05687	2:484..2062											
21893	ENU05687	ANI61C6614:	23-44	784-803	NAP		g2104465	627	87	2.00E-16			hypothetical 24.6 KD protein in MCK1-RP55B intergenic region [Saccharomyces cerevisiae]
21894	ENU05688	1648..159											
21894	ENU05688	ANI61C1031	22-47	457-479	NAP		g1353100	176	91	4.00E-18	43	45	delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Saccharomyces cerevisiae]
21895	ENU05689	5:1412..1739											
21895	ENU05689	ANI61C6286:	27-46	450-477	NAP		g730430	239	116	1.00E-25	49	22	alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]
21896	ENU05690	706..1089											
21896	ENU05690	ANI61C2164:	22-41	772-799	NAP		g67385	673	114	4.00E-66	45	55	"dynactin, 150 KD isoform (150 KD dynein-associated polypeptide) (DP-150) (DAP-150) (P150-glued) [Neurospora crassa]"
21897	ENU05691	68..1154											
21897	ENU05691	ANI61C1147	22-47	792-819	NAP		g2493479	1035	201	4.00E-51	36	21	(Y10542) homologous to 40kD subunit of RNA-polymerase I and III [Cricetus griseus]
21898	ENU05692	3:1..1399											
21898	ENU05692	ANI61C8423:	22-49	768-787	NAP		g1914859	814	282	2.00E-75	56	75	putative stergmatocystin biosynthesis protein STCQ [Emmericella nidulans]
21899	ENU05693	2330..1180											
21899	ENU05693	ANI61C7771:			NAP		g2498970	539	202	6.00E-52	78	54	(Y17332) proline-rich protein [Zea mays]
21900	ENU05694	4940..5391											
21900	ENU05694	ANI61S4257:			NAP		g4138732	194	55	0.000000	23	71	
		1..892											

# Genetic Information

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21901	ENU05695	ANI61C7923:	23-44	456-483	NAP		g1805251	184	61	0.000000	31	36	(U58946) transposase [Aspergillus awamori]
21902	ENU05696	ANI61C8749:	122-141	352-371	NAP		g3135990	365	157	4.00E-38	53	27	(AL023589) membrane transporter [Schizosaccharomyces pombe]
21903	ENU05697	ANI61C1122	35-62	537-564	NAP		g3925779	138	68	7.00E-11	32	27	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21904	ENU05698	ANI61C1033	23-42	786-813	NAP		g4583552	1171	327	e-103	74	75	"(AJ012316) arabinogalactan endo-1,4-beta-galactosidase [Aspergillus tubingensis]"
21905	ENU05699	ANI61C7064:	22-43	720-743	NAP		g113314	4318	575	e-163	98	7	delta-(L-alpha-aminoadipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emicella nidulans]
21906	ENU05700	ANI61C9189:	75-98	426-449	NAP		g1174433	146	78	4.00E-14	42	40	Signal recognition particle 19 KD protein homolog [Yarrowia lipolytica]
21907	ENU05701	ANI61C3701:	27-46	446-465	NAP		g3219956	168	44	0.0008	45	98	hypothetical protein C57A7.01 in chromosome I [Schizosaccharomyces pombe]
21908	ENU05702	ANI61C1058	36-63	531-556	NAP		g4160397	299	134	5.00E-31	39	53	(AL035210) halotolerance protein [Schizosaccharomyces pombe]
21909	ENU05703	ANI61C7089:	22-42	320-347	NAP		g2501094	96	52	0.000001	24	48	Syntaxin 6 [Rattus norvegicus]
21910	ENU05704	ANI61C908:1	22-42	363-382	NAP		g1085674	414	135	2.00E-31	75	79	blastocidin S deaminase - Aspergillus terreus [Aspergillus terreus]
21911	ENU05705	ANI61C1584:	92-111	391-413	NAP		g730406	106	46	0.0001	36	84	Profilin []
21912	ENU05706	ANI61C5748:	46-65	448-467	NAP		g3293344	150	77	7.00E-14	29	16	(AF059614) transportin; TRN [Xenopus laevis]
21913	ENU05707	ANI61C8295:	22-48	775-802	NAP		g2342601	436	92	8.00E-30	31	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21914	ENU05708	ANI61C9805:	24-45	805-829	NAP		g4512702	567	121	7.00E-27	30	41	(AC006569) hypothetical protein [Arabidopsis thaliana]
21915	ENU05709	ANI61C8160:			NAP		g3885836	414	69	8.00E-19	30	34	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
21916	ENU05710	ANI61C1615:	74-93	660-679	NAP		g4499837	276	88	2.00E-27	30	57	(AJ011963) dimethyl-allyl-trypphan-synthase [Claviceps purpurea]
21917	ENU05711	ANI61C6187:	35-54	722-749	NAP		g585965	1184	371	e-102	67	37	Vesicular-fusion protein SEC18 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
21918	ENU05712	ANI6IC8757: 1724..1329	121-140	332-351	NAP		g3560215	203	77	5.00E-14	36	28	"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe]" (AL035229) possible RanBP7-importin-beta-Cse1p superfamily [Schizosaccharomyces pombe] (X96767) U1 snRNP-specific protein C [Mus musculus]
21919	ENU05713	ANI6IC1104: 1..1964	24-43	802-821	NAP		g4176546	284	50	0.00003			
21920	ENU05714	ANI6IC2656: 2041..2589			NAP		g1360017	117	70	1.00E-11	45	62	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
21921	ENU05715	ANI6IS3099: 1..507			NAP		g82698	220	36	0.14	36	49	aminomethyltransferase precursor (glycine cleavage system T protein) [Saccharomyces cerevisiae]
21922	ENU05716	ANI6IC8555: 1..331	42-66	284-310	NAP		g1707880	154	84	3.00E-16			"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]"
21923	ENU05717	ANI6IS1431: 1..746			NAP		g2246532	170	46	0.0002	21	22	hypothetical 138.8 KD protein C11D3.14C in chromosome I [Schizosaccharomyces pombe]
21924	ENU05718	ANI6IC3881: 801..1	96-115	681-698	NAP		g1351710	415	203	2.00E-51	43	18	proline-rich protein - mouse (fragment) [Mus musculus]
21925	ENU05719	ANI6IS2549: 73..645			NAP		g91206	110	60	0.000000	29	96	[X81635) RAD26 [Saccharomyces cerevisiae]
21926	ENU05720	ANI6IC4525: 662..1	102-127	605-631	NAP		g550429	592	233	9.00E-61	53	20	hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
21927	ENU05721	ANI6IC5834: 446..2035	64-83	785-804	NAP		g731689	1635	491	e-138	61	7	(AF112473) PyrABCN [Emeticella nidulans]
21928	ENU05722	ANI6IC117: 1..1174	23-45	722-749	NAP		g4185560	1852	534	e-151	97	12	beta-galactosidase (lactase) [Arthrobacter sp.]
21929	ENU05723	ANI6IC9675: 2354..1	24-43	786-813	NAP		g3913155	1105	101	5.00E-21	30	22	(AL031740) putative calcium dependant serine-threonine protein kinase. [Schizosaccharomyces pombe]
21930	ENU05724	ANI6IC4143: 1..818	86-111	693-712	NAP		g3650382	253	115	5.00E-25	30	26	[AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]
21931	ENU05725	ANI6IC1116: 3:21..1728	22-43	807-829	NAP		g3184098	1329	173	1.00E-85	64	50	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
21932	ENU05726	ANI6IC4422: 1470..2350	26-45	720-739	NAP		g3150262	167	58	2.00E-14	31	65	[Schizosaccharomyces pombe]



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21933	ENU05727	ANI61C2800:	94-113	420-445	NAP		g4539248	339	132	2.00E-30	48	41	(AL049489) conserved hypothetical TBC domain-containing protein [Schizosaccharomyces pombe]
21934	ENU05728	ANI61C8872:	22-43	760-780	NAP		g2909783	511	187	1.00E-46	33	17	(AF020289) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]
21935	ENU05729	ANI61C1089	33-54	728-747	NAP		g3850091	199	73	1.00E-15	30	46	(AL033389) putative aminotransferase [Schizosaccharomyces pombe]
21936	ENU05730	ANI61C283:5	22-44	460-479	NAP		g2494072	256	127	4.00E-29	42	32	delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Agaricus bisporus]
21937	ENU05731	ANI61C9677:	202-223	804-829	NAP		g1352666	963	333	7.00E-98	82	83	"serine/threonine protein phosphatase PP2A-beta, catalytic subunit [Sus scrofa]"
21938	ENU05732	ANI61C9325:	22-43	729-749	NAP		g1345625	423	61	5.00E-14			Biotin--protein ligase (biotin apo-protein ligase) (biotin-- [Saccharomyces cerevisiae]
21939	ENU05733	ANI61C7546:	47-66	784-807	NAP		g3929399	1088	185	1.00E-67	46	51	proline-specific permease (proline transport protein) [Emmericella nidulans]
21940	ENU05734	ANI61C9605:	27-46	723-742	NAP		g729007	358	56	3.00E-14	43	49	CAJ1 protein [Saccharomyces cerevisiae]
21941	ENU05735	ANI61C601:6	63-84	294-314	NAP		g284071	175	83	7.00E-16	41	56	DTMP kinase (EC 2.7.4.9) - human [Homo sapiens]
21942	ENU05736	ANI61S645:1.	39-62	287-314	NAP		g2988417	43	46	0.0002	39	43	(U97573) peptidyl-prolyl cis-trans isomerase [Treponema pallidum]
21943	ENU05737	ANI61C678:8	27-46	729-747	NAP		g3914273	448	96	1.00E-34	49	65	Pectate lyase precursor [Emmericella nidulans]
21944	ENU05738	ANI61C8413:	30-49	797-816	NAP		g125348	1078	76	3.00E-19	33	31	KEX1 protease precursor [Kluyveromyces lactis]
21945	ENU05739	ANI61C2004:	54-73	740-759	NAP		g3088571	1869	485	e-136	86	47	(AF059523) heat shock protein 60 [Paracoccidoides brasiliensis]
21946	ENU05740	ANI61S2337:			NAP		g4325349	302	86	1.00E-24	52	43	(AF128394) contains similarity to Petunia PTTA' (GB:AF009516)
21947	ENU05741	ANI61C5790:	104-121	361-381	NAP		g4210461	260	87	8.00E-17	49	20	[Arabidopsis thaliana]
21948	ENU05742	ANI61C4064:	204-227	788-807	NAP		g2342601	301	116	2.00E-32	35	4	(Neurospora crassa)
													(X89442) peptide synthetase [Metarhizium anisopliae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21949	ENU05743	ANI61C8506: 1137..1	22-44	720-746	NAP		g3136057	427	153	1.00E-36	38	58	(AL023592) actin-like protein [Schizosaccharomyces pombe]
21950	ENU05744	ANI61C7482: 915..1	22-47	752-771	NAP		g2388975	336	67	2.00E-25	44	69	(Z98980) phosphotyrosyl phosphatase activator [Schizosaccharomyces pombe]
21951	ENU05745	ANI61S2702: 1..589			NAP		g3157413	113	44	0.0008	26	25	(AJ001386) catalase [Claviceps purpurea]
21952	ENU05746	ANI61C1084: 2:460..1			NAP		g731385	112	46	0.0002	33	49	hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]
21953	ENU05747	ANI61C1087: 2:1270..2819	22-45	806-825	NAP		g4176751	2421	443	e-130	92	43	(AF052391) heat shock protein 70 [Trichophyton rubrum]
21954	ENU05748	ANI61C5200: 1338..2380	22-42	780-799	NAP		g2388905	459	188	5.00E-47	48	59	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
21955	ENU05749	ANI61C21:96 5..1	37-56	728-749	NAP		g2132242	1203	379	e-104	81	56	hypothetical protein YPL235w - yeast (Saccharomyces cerevisiae)
21956	ENU05750	ANI61C7402: 1..1593	22-44	720-740	NAP		g83711	2184	314	e-135	94	34	[Saccharomyces cerevisiae] "nitrite reductase (NADH) (EC 1.6.6.4), short form - Emericella nidulans ["]
21957	ENU05751	ANI61C7966: 3747..3004	25-44	700-723	NAP		g2133240	196	50	8.00E-11	34	100	immunoreactive protein - Coccidioides immitis [Coccidioides immitis] (AL035065) putative urea active transporter [Schizosaccharomyces pombe]
21958	ENU05752	ANI61C8144: 449..2530	22-48	715-734	NAP		g4106690	946	104	6.00E-48	42	36	exonuclease II (exo II) (P140) [Schizosaccharomyces pombe]
21959	ENU05753	ANI61C9575: 4706..8327	22-41	749-769	NAP		g729456	2757	227	7.00E-59	44	21	(AL023592) ma binding protein [Schizosaccharomyces pombe]
21960	ENU05754	ANI61C7591: 1015..1722	22-43	666-687	NAP		g3136047	385	169	1.00E-41	44	53	[Schizosaccharomyces pombe] probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae)
21961	ENU05755	ANI61C1370: 533..4			NAP		g1363749	151	89	2.00E-17	38	35	[Saccharomyces cerevisiae]
21962	ENU05756	ANI61C7297: 576..1016	22-44	375-402	NAP		g3402004	273	94	6.00E-19	58	78	Mbp1 From Saccharomyces Cerevisiae []
21963	ENU05757	ANI61C543:1 ..1874	34-61	628-651	NAP		g3913210	1707	324	e-117	73	29	putative ATP-dependent RNA helicase CDC28 [Schizosaccharomyces pombe]
21964	ENU05758	ANI61C811:1 ..1042	22-43	756-781	NAP		g3417424	410	180	1.00E-44	38	10	(AL031261) putative transport protein [Schizosaccharomyces pombe]
21965	ENU05759	ANI61C1079: 5:2047..3775	28-48	806-828	NAP		g626178	834	204	6.00E-52	42	28	HIR1 protein - yeast [Saccharomyces cerevisiae] [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
21966	ENU05760	ANI61C9078: 4178..1	22-45	668-694	NAP		g2492604	2285	157	9.00E-38	37	15	multidrug resistance protein CDR2 [Candida albicans]
21967	ENU05761	ANI61C1585: 1..491	42-68	448-470	NAP		g2144467	267	120	6.00E-27	43	22	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae) []
21968	ENU05762	ANI61C1208: 6485..8096	22-44	810-829	NAP		g2894293	295	101	7.00E-21	24	54	(AL021837) hypothetical protein [Schizosaccharomyces pombe]
21969	ENU05763	ANI61C7167: 2698..3037	41-64	424-444	NAP		g3861442	255	83	1.00E-15	50	41	(AL033505) hypothetical protein SC1E6.19c [Streptomyces coelicolor]
21970	ENU05764	ANI61C3924: 920..1	22-46	719-738	NAP		g2656007	782	183	1.00E-77	50	44	(Z99126) putative dna helicases. [Schizosaccharomyces pombe]
21971	ENU05765	ANI61C4789: 1..431	118-137	307-326	NAP		g585856	211	96	2.00E-19	40	32	mitochondrial carrier protein RIM2 [Saccharomyces cerevisiae]
21972	ENU05766	ANI61C1039: 8:2329..550	35-54	803-829	NAP		g3925779	282	55	4.00E-10	23	45	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21973	ENU05767	ANI61S3461: 1..322	28-53	272-298	NAP		g3024528	435	176	5.00E-44	80	50	RAS-related protein RAB2BV [Beta vulgaris]
21974	ENU05768	ANI61C4749: 2526..4013	22-42	780-801	NAP		g4505651	524	54	8.00E-12	36	59	"phosphate cytidylyltransferase 2, ethanolamine [Homo sapiens]"
21975	ENU05769	ANI61C1954: 710..1			NAP		g1723566	534	196	3.00E-56	52	43	putative glucosyltransferase C17C9.07 [Schizosaccharomyces pombe]
21976	ENU05770	ANI61C4887: 1785..1260	105-123	396-415	NAP		g2244629	415	120	6.00E-32	58	94	(Z82019) sepin [Agaricus bisporus]
21977	ENU05771	ANI61C1913: 2849..1	31-50	806-829	NAP		g2492657	4813	558	e-158	98	18	putative sterigmatocystin biosynthesis fatty acid synthase alpha subunit [Emericella nidulans]
21978	ENU05772	ANI61S1288: 1..553	47-70	350-369	NAP		g4442927	133	54	0.000000	33	28	Glucose Oxidase (E.C.1.1.3.4) []
21979	ENU05773	ANI61C7281: 1246..1	28-46	716-735	NAP		g4539286	849	213	9.00E-55	44	47	(AL049498) activator of Hsp70 and Hsp90 chaperones [Schizosaccharomyces pombe]
21980	ENU05774	ANI61C243: 559..4334	23-50	692-712	NAP		g2132889	228	163	1.00E-39	32	22	probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21981	ENU05775	ANI61C7816: 1..546	46-65	498-525	NAP		g4502887	198	94	9.00E-19	40	28	"ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky disease) [Homo sapiens]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
21982	ENU05776	ANI61C525:7	22-47	799-818	NAP		g1077042	3207	122	9.00E-54	61	14	cadmium resistance protein YCF1 - yeast (Saccharomyces cerevisiae)
		159..2357											[Saccharomyces cerevisiae]
21983	ENU05777	ANI61C1705:	22-45	802-829	NAP		g586361	733	153	2.00E-36	45	54	hypothetical 51.7 KD protein in CTP1-SUL2 intergenic region [Saccharomyces cerevisiae]
		5289..6343											[Saccharomyces cerevisiae]
21984	ENU05778	ANI61S4513:	35-57	317-334	NAP		g136232	115	68	6.00E-11	30	18	"potassium transport protein, low-affinity [Saccharomyces cerevisiae]" (M20319) aminotriazole resistance protein [Saccharomyces cerevisiae]
		377..75											[Saccharomyces cerevisiae]
21985	ENU05779	ANI61C1142	48-67	784-803	NAP		g171124	411	101	7.00E-21	25	48	hypothetical protein YLR063w - yeast (Saccharomyces cerevisiae)
		7:3870..2510											[Saccharomyces cerevisiae]
21986	ENU05780	ANI61C9782:	49-70	446-465	NAP		g2131764	128	73	9.00E-13	33	40	hypothetical protein YLR063w - yeast (Saccharomyces cerevisiae)
		505..1											[Saccharomyces cerevisiae]
21987	ENU05781	ANI61C5615:			NAP		g3021303	2839	531	e-150	95	12	(Y15996) acetyl-CoA carboxylase [Emeticella nidulans]
		1694..1											(AL031261) putative transport protein [Schizosaccharomyces pombe]
21988	ENU05782	ANI61C8296:	24-43	804-828	NAP		g3417424	791	39	0.000000			hypothetical 88.2 KD protein C2F7.18C in chromosome I []
		2054..49											phosphoribosylformylglycinamide synthase (FGAM synthase) (formylglycinamide ribotide amidotransferase) (FGARAT)
21989	ENU05783	ANI61C8795:	22-47	807-826	NAP		g1175379	428	151	7.00E-36	30	36	[Saccharomyces cerevisiae]
		1067..1											[Z95395] putative taf; transcription factor TFHD complex component [Schizosaccharomyces pombe]
21990	ENU05784	ANI61C3558:			NAP		g1709924	491	214	5.00E-55	50	15	probable calcium-transporting ATPase 8 [Saccharomyces cerevisiae]
		1569..916											(AL049587) putative transcriptional regulator [Streptomyces coelicolor]
21991	ENU05785	ANI61C4915:	39-58	711-731	NAP		g2104421	1647	139	2.00E-32	34	23	"sodium channel" alpha subunit [human, skeletal muscle, Peptide, 1836 aa]
		2886..1											hypothetical 25.6 KD protein in SMI1-PHO81 intergenic region [Saccharomyces cerevisiae]
21992	ENU05786	ANI61C2010:	29-50	720-744	NAP		g2493011	732	254	8.00E-67	47	17	(AJ224922) ATP citrate lyase [Sordaria macrospora]
		1..1196											
21993	ENU05787	ANI61C6994:	27-49	563-590	NAP		g4584493	174	101	4.00E-21	35	58	
		783..1393											
21994	ENU05788	ANI61S1378:	41-59	219-239	NAP		g243989	474	192	5.00E-49	90	5	
		1..327											
21995	ENU05789	ANI61C385:4	30-57	808-829	NAP		g1723752	242	91	2.00E-23	35	99	
		068..4993											
21996	ENU05790	ANI61C4905:			NAP		g4107343	436	175	1.00E-43	62	23	
		1..545											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21997	ENU05791	ANI61C3311:	103-124	388-407	NAP		g4680709	322	97	3.00E-32			(AF132969) CGI-35 protein [Homo sapiens]
21998	ENU05792	ANI61C7708:	22-43	802-821	NAP		g3005587	326	33	2.3	30	33	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]
21999	ENU05793	ANI61C8066:	41-60	715-742	NAP		g1710663	1183	111	5.00E-69	58	22	putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) [Schizosaccharomyces pombe]
22000	ENU05794	ANI61C8202:	34-53	724-743	NAP		g553118	646	132	2.00E-54	38	53	(M27081) alkane hydroxylating cytochrome P-450 [Candida maltosa]
22001	ENU05795	ANI61C1091	43-62	780-799	NAP		g3024986	265	142	3.00E-33			hypothetical zinc-type alcohol dehydrogenase-like protein in AHPF-RNK intergenic region [Escherichia coli]
22002	ENU05796	ANI61C3211:	22-43	714-733	NAP		g3183035	1559	159	1.00E-41	41	27	importin beta-1 subunit (karyopherin beta-1 subunit) (importin 95) [Schizosaccharomyces pombe]
22003	ENU05797	ANI61C1633:	22-46	442-463	NAP		g1706221	211	62	3.00E-17	43	100	cytochrome B5 [Saccharomyces cerevisiae]
22004	ENU05798	ANI61C8674:	102-125	263-290	NAP		g409547	127	66	8.00E-11	33	19	(L07492) sugar transport protein [Saccharomyces cerevisiae]
22005	ENU05799	ANI61C1106	67-94	500-527	NAP		g2131422	184	83	2.00E-15	34	38	hypothetical protein YDR306c - yeast [Saccharomyces cerevisiae]
22006	ENU05800	ANI61C5670:			NAP		g83726	714	280	4.00E-75	97	42	[Saccharomyces cerevisiae] hypothetical nox2 protein - Emericella nidulans mitochondrion (SGC3)
22007	ENU05801	ANI61C7760:	29-56	306-331	NAP		g631806	233	104	3.00E-22	41	26	[Emericella nidulans] "beta2-chimerin, cerebellar - rat (fragment) []"
22008	ENU05802	ANI61C6462:	29-54	804-824	NAP		g1805251	924	159	6.00E-60	44	50	(U58946) transposase [Aspergillus awamori]
22009	ENU05803	ANI61C7280:	43-62	793-820	NAP		g2956768	400	122	4.00E-27	37	71	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22010	ENU05804	ANI61C4923:	39-60	804-823	NAP		g2507441	1041	135	4.00E-80	63	53	"T-complex protein 1, delta subunit (TCP-1-delta) (CCT-delta) [Saccharomyces cerevisiae]"
22011	ENU05805	ANI61C2862:	105-124	580-602	NAP		g4158188	147	74	1.00E-12	37	49	(AL035206) putative alcohol dehydrogenase [Streptomyces coelicolor]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22012	ENU05806	ANI61C1129	119-146	443-465	NAP		g2408082	398	169	8.00E-42	52	17	(Z99167) putative helicase [Schizosaccharomyces pombe]
22013	ENU05807	ANI61C9103	32-50	776-802	NAP		g2673955	1266	357	6.00E-98	87	32	(U62935) multidrug resistance protein 2 [Aspergillus fumigatus]
22014	ENU05808	ANI61C6282	112-135	711-738	NAP		g731262	220	125	4.00E-28	24	23	vacuolar protein sorting-associated protein VPS8 [Saccharomyces cerevisiae]
22015	ENU05809	ANI61C6738	57-76	810-829	NAP		g731597	300	94	2.00E-18	31	70	hypothetical 36.1 KD protein in YLF2-PRPS4 intergenic region [Saccharomyces cerevisiae]
22016	ENU05810	ANI61C1129	23-47	788-808	NAP		g1352980	778	300	1.00E-85	64	24	ATP-dependent RNA helicase DOB1 (MRNA transport regulator MTR4) [Saccharomyces cerevisiae]
22017	ENU05811	ANI61C850	7 22-46	601-626	NAP		g1706480	212	87	8.00E-18	34	19	DNA ligase I (polydeoxyribonucleotide synthase (ATP)) [Xenopus laevis]
22018	ENU05812	ANI61C3634	22-45	804-823	NAP		g1546072	1105	147	8.00E-35	32	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22019	ENU05813	ANI61C5125	22-47	770-797	NAP		g731899	947	280	6.00E-75	49	18	putative membrane glycoprotein in SDL 1 5'region precursor [Saccharomyces cerevisiae]
22020	ENU05814	ANI61C5245	31-58	604-631	NAP		g3738163	347	94	1.00E-18	38	99	(AL031856) putative DNA J domain containing protein [Schizosaccharomyces pombe]
22021	ENU05815	ANI61S1152	118-145	505-524	NAP		g2498506	271	85	3.00E-25	42	26	proline-rich protein LAS17 [Saccharomyces cerevisiae]
22022	ENU05816	ANI61C1643	78-97	720-740	NAP		g1261823	684	229	1.00E-59	48	25	(L77234) glycine rich protein [Neurospora crassa]
22023	ENU05817	ANI61S3304	52-71	285-312	NAP		g4097158	162	94	6.00E-19	37	7	(U46488) Nrps [Proteus mirabilis]
22024	ENU05818	ANI61C8526			NAP		g3004634	798	113	6.00E-53	59	81	(U96385) GATA transcription factor [Penicillium chrysogenum]
22025	ENU05819	ANI61C4111	27-46	807-826	NAP		g1076802	134	38	0.12			extensin-like protein - maize [Zea mays]
22026	ENU05820	ANI61C3323	32-59	603-622	NAP		g401335	526	114	1.00E-42	77	99	vacuolar ATP synthase 16 KD proteolipid subunit [Neurospora crassa]
22027	ENU05821	ANI61C1225	190-211	528-548	NAP		g131768	217	87	1.00E-16	41	31	quinate permease (quinate transporter) [Emeticella nidulans]

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22028	ENU05822	ANI61C9283:	107-126	444-463	NAP		g871830	113	39	0.017	35	60	(D30747) mini-collagen [Acropora done]
22029	ENU05823	ANI61C2431:	77-96	719-737	NAP		g3319315	977	290	7.00E-78	54	33	(AF074951) cellobiose dehydrogenase [Thielavia heterothallica]
22030	ENU05824	ANI61C1512:	26-53	796-819	NAP		g3929395	2040	328	4.00E-89	67	32	vacuolar ATP synthase 98 KD subunit (vacuolar ATPase 98 KD subunit) [Neurospora crassa]
22031	ENU05825	ANI61C5551:	22-48	785-809	NAP		g2120666	724	241	6.00E-63	42	48	"2,4-chlorocatechol 1,2-dioxygenase (EC 1.13.11.-) tdB - Pseudomonas putida [Pseudomonas putida]" (AL022071) hypothetical protein [Schizosaccharomyces pombe]
22032	ENU05826	ANI61S2863:	36-55	436-454	NAP		g2950458	228	88	3.00E-17	29	19	(AF019254) DNA polymerase epsilon homolog [Emicella nidulans]
22033	ENU05827	ANI61C5475:	22-46	792-812	NAP		g4102990	9834	578	e-164	98	12	(AJ223459) PmA protein [Emicella nidulans]
22034	ENU05828	ANI61C4262:	22-47	806-828	NAP		g2808662	854	122	3.00E-27	30	33	"glucan (1,4-alpha-), branching enzyme I (glycogen branching enzyme) [Homo sapiens]" (U07187) Mlh1p [Saccharomyces cerevisiae]
22035	ENU05829	ANI61C2219:	42-65	613-638	NAP		g4557619	1082	161	1.00E-87	66	35	protein kinase (EC 2.7.1.37) - fission yeast (Schizosaccharomyces pombe) [Schizosaccharomyces pombe]
22036	ENU05830	ANI61C8552:			NAP		g460627	92	53	0.000000	31	15	hypothetical 143.7 KD protein C11D3.15 in chromosome I [Schizosaccharomyces pombe]
22037	ENU05831	ANI61C1129	112-136	548-567	NAP		g2130466	719	290	7.00E-78	62	51	[Schizosaccharomyces pombe] containing protein in PMT6-PCT1 intergenic region [Saccharomyces cerevisiae]
22038	ENU05832	ANI61C4402:	27-48	622-649	NAP		g1351711	1351	311	4.00E-88	66	18	(AL049485) probable zinc-binding alcohol dehydrogenase [Streptomyces coelicolor]
22039	ENU05833	ANI61C1064	22-41	671-695	NAP		g1176045	1101	286	2.00E-76	50	35	(AF027687) beta glucosidase homolog [Cochliobolus heterotrophus]
22040	ENU05834	ANI61C1036	77-96	564-590	NAP		g4539186	228	102	7.00E-23	45	51	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emicella nidulans]
22041	ENU05835	ANI61C9204:	59-78	805-829	NAP		g2598192	900	375	e-103	67	30	
22042	ENU05836	ANI61C5575:			NAP		g1705828	123	63	0.000000	32	16	

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22043	ENU05837	ANI61C1100: 5121..4463	22-49	616-638	NAP		g3695005	256	115	3.00E-25	37	49	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays]
22044	ENU05838	ANI61S37:44 6..1	72-91	391-414	NAP		g1881271	210	78	4.00E-14	35	73	"(AB001488) function unknown, similar product in H. influenzae and synechocystis. [Bacillus subtilis]"
22045	ENU05839	ANI61C1145 1:441..1	102-124	455-479	NAP		g4760360	115	76	1.00E-13			"(AL035213) predicted using hexExon; L3291.5, Hypothetical protein, len: 300 aa [Leishmania major]"
22046	ENU05840	ANI61S2374: 1..339	66-86	257-276	NAP		g78837	517	205	9.00E-53	95	38	rimK protein - Escherichia coli [Escherichia coli]
22047	ENU05841	ANI61C7587: 2400..2047	33-55	294-313	NAP		g729611	286	126	5.00E-29			Vanadate resistance protein GOG5/VRG4/VAN2 [Saccharomyces cerevisiae]
22048	ENU05842	ANI61C8467: 1..411	189-208	367-388	NAP		g3059184	147	79	1.00E-14	33	40	(D88014) homologous to HpcE (HHDD isomerase) protein of E. coli [Rhodococcus erythropolis]
22049	ENU05843	ANI61C5479: 1309..2279	28-49	802-829	NAP		g114878	379	147	8.00E-35	37	83	carboxyvinyl-carboxyphosphonate phosphorylmunase (carboxyphosphonocoenolpyruvate phosphonmutase) (CPEP phosphonmutase) [Streptomyces hygroscopicus]
22050	ENU05844	ANI61C1078 6:1..423	102-124	354-373	NAP		g4249409	111	63	4.00E-13	33	29	(AC006072) putative sugar transporter [Arabidopsis thaliana]
22051	ENU05845	ANI61C4441: 1..966	22-48	633-659	NAP		g1351645	869	324	6.00E-88	55	52	hypothetical amino-acid permease C8A4.11 [Schizosaccharomyces pombe]
22052	ENU05846	ANI61C1134 6:1472..493	32-51	774-793	NAP		g4583351	380	185	4.00E-46	41	47	(AF114167) lysosomal peptatin insensitive protease [Canis familiaris]
22053	ENU05847	ANI61C2920: 387..1499	37-56	790-809	NAP		g1723578	381	102	1.00E-38	36	78	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
22054	ENU05848	ANI61C7166: 267..653	50-69	442-461	NAP		g3136036	128	82	2.00E-15	40	48	(AL023590) Glutathione S-transferase [Schizosaccharomyces pombe]
22055	ENU05849	ANI61C2437: 2082..3715	25-52	725-751	NAP		g728771	639	101	5.00E-42	52	23	Alanine/arginine aminopeptidase [Saccharomyces cerevisiae]
22056	ENU05850	ANI61C6823: 576..1	53-73	530-549	NAP		g2226425	124	71	6.00E-12	25	10	(Z97204) hypothetical protein [Schizosaccharomyces pombe]



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22057	ENU05851	ANI61C2391: 1406..2123	24-43	634-654	NAP		g3800835	205	67	2.00E-10	38	4	(AF079138) type I polyketide synthase PlkAII [Streptomyces venezuelae]
22058	ENU05852	ANI61S1602: 316..1	49-76	439-466	NAP		g2909465	110	56	0.000000	34	38	(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]
22059	ENU05853	ANI61C7205: 1..473	49-71	414-434	NAP		g1588283	463	205	2.00E-52	61	12	MSH6 gene [Saccharomyces cerevisiae]
22060	ENU05854	ANI61C4233: 71..904	101-126	791-813	NAP		g600810	228	90	2.00E-17	39	99	(Z46921) unknown [Saccharomyces cerevisiae]
22061	ENU05855	ANI61C918:2 37..1076	54-73	770-789	NAP		g731502	351	153	1.00E-36	32	25	importin beta-4 subunit (karyopherin beta-4 subunit) (ran binding protein YRB4) [Saccharomyces cerevisiae]
22062	ENU05856	ANI61C8801: 1..566	165-182	469-488	NAP		g130582	196	97	1.00E-19	35	12	Retrovirus-related pol polyprotein from transposon TNT 1-94 [Nicotiana tabacum]
22063	ENU05857	ANI61C3205: 1997..1	23-44	649-668	NAP		g3288709	1601	291	6.00E-78	52	19	(AB010442) PMR1 [Penicillium digitatum]
22064	ENU05858	ANI61C4172: 1..921	89-108	681-700	NAP		g3413518	506	231	5.00E-60	41	16	(AB010810) phospholipase D [Candida albicans]
22065	ENU05859	ANI61C3591: 1109..2671	29-48	793-811	NAP		g3116147	329	64	7.00E-17	30	47	(AL023290) amino acid permease [Schizosaccharomyces pombe]
22066	ENU05860	ANI61C5426: 653..1	43-63	522-549	NAP		g1731075	306	178	4.00E-44	43	53	probable NADH-dependent flavin oxidoreductase YQJM [Bacillus subtilis]
22067	ENU05861	ANI61C1073: 7..1064..2403	22-48	778-796	NAP		g3393022	397	176	2.00E-43	38	38	(AL031174) hypothetical protein [Schizosaccharomyces pombe]
22068	ENU05862	ANI61C7940: 1..685	127-145	642-664	NAP		g2498701	94	71	1.00E-11	26	46	sterigmatocystin 7-O-methyltransferase precursor [Aspergillus flavus]
22069	ENU05863	ANI61C3966: 918..16	24-46	760-781	NAP		g4539255	359	129	3.00E-29			(AL049495) hypothetical protein [Schizosaccharomyces pombe]
22070	ENU05864	ANI61S4253: 1..822			NAP		g3153821	160	47	0.0001	23	30	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22071	ENU05865	ANI61C9594: 1..503			NAP		g3282229	293	78	3.00E-14			(U68722) BcLHH [Botryotinia fuckeliana]
22072	ENU05866	ANI61C8675: 5936..6350	92-111	368-387	NAP		g1749656	105	73	2.00E-12	35	38	(D89224) similar to Saccharomyces cerevisiae ORF YCR028 [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22073	ENU05867	ANI6IC4988:	36-58	483-510	NAP		g1351666	316	119	4.00E-27	50	30	putative ATP-dependent RNA helicase C1F7.02C [Schizosaccharomyces pombe]
22074	ENU05868	ANI6IC5515:	115-134	391-410	NAP		g2501339	327	148	2.00E-35	44	24	Copper amine oxidase 1 [Aspergillus niger]
22075	ENU05869	ANI6IC7746:	22-49	615-635	NAP		g2133285	298	129	3.00E-29			tryptophan dimethyltransferase (EC 2.5.1.34) - ergot fungus [Claviceps purpurea]
22076	ENU05870	ANI6IC1105:			NAP		g135140	570	219	9.00E-63	54	22	"Leucyl"-TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS) [Neurospora crassa]
22077	ENU05871	ANI6IC6132:			NAP		g1730744	352	136	1.00E-31	56	45	hypothetical 33.5 KD protein in MKS1-MSK1 intergenic region [Saccharomyces cerevisiae]
22078	ENU05872	ANI6IC1070:	42-61	806-828	NAP		g998355	455	71	2.00E-22	31	31	(U35661) colony 1 [Ophiostoma ulmi]
22079	ENU05873	ANI6IC2660:	25-44	709-736	NAP		g2145937	415	57	7.00E-17	33	12	polyketide synthase pksE - Mycobacterium leprae [Mycobacterium leprae]
22080	ENU05874	ANI6IS2794:	113-139	459-486	NAP		g3327882	453	205	1.00E-52	54	43	(AB016221) SSL1 [Schizosaccharomyces pombe]
22081	ENU05875	ANI6IC8962:	31-58	754-773	NAP		g1407655	179	46	0.0003			(U58884) SH3P7 [Mus musculus]
22082	ENU05876	ANI6IC8475:	28-47	793-812	NAP		g4107343	1137	243	e-111	91	36	(AJ224922) ATP citrate lyase [Sordaria macrospora]
22083	ENU05877	ANI6IC5331:	117-134	425-444	NAP		g1723448	339	124	9.00E-31	46	28	hypothetical protein C56F8.17C in chromosome I [Schizosaccharomyces pombe]
22084	ENU05878	ANI6IS813:	1		NAP		g2635194	425	173	9.00E-43	47	99	(Z99117) similar to hypothetical proteins [Bacillus subtilis]
22085	ENU05879	ANI6IS617:	216-235	527-546	NAP		g4091929	422	185	2.00E-46	47	50	"(AF069752) C5,6 desaturase [Candida albicans]"
22086	ENU05880	ANI6IS564:	5		NAP		g2635812	276	125	1.00E-28	46	70	(Z99120) similar to hypothetical proteins [Bacillus subtilis]
22087	ENU05881	ANI6IC5372:	22-48	790-817	NAP		g2342601	820	242	3.00E-63	48	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22088	ENU05882	ANI6IC4407:	26-45	584-606	NAP		g118239	131	42	0.000000	31	71	Dihydrodipicolinate synthase (DHDPs) [Corynebacterium glutamicum]

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22089	ENU05883	ANI61C4408: 1363..1	22-44	633-652	NAP		g3116018	679	134	1.00E-46	44	53	(Y13067) vanillin: NAD+ oxidoreductase [Pseudomonas fluorescens]
22090	ENU05884	ANI61C1974: 1.699	133-152	494-517	NAP		g83673	183	96	3.00E-19	36	34	amidase (EC 3.5.1.4) - Aspergillus oryzae [Aspergillus oryzae]
22091	ENU05885	ANI61C409: 879..1	29-48	761-780	NAP		g114971	1192	181	6.00E-45	37	33	beta-glucosidase precursor (gentiobiose) (cellobiose) (beta-D-glucoside glucosylhydrolase) [Kluyveromyces marxianus]
22092	ENU05886	ANI61C938: 927..454	183-204	430-453	NAP		g3947883	172	68	3.00E-11	31	31	(AL034382) putative Trp-Asp repeat protein [Schizosaccharomyces pombe]
22093	ENU05887	ANI61C1941: 1..1874	22-43	792-819	NAP		g3915963	1019	192	2.00E-48	45	14	ATP-dependent bile acid permease [Saccharomyces cerevisiae]
22094	ENU05888	ANI61C9360: 882..1542	23-47	522-545	NAP		g2765195	214	101	7.00E-21	33	6	(Y12527) HMMWP1 protein [Yersinia enterocolitica]
22095	ENU05889	ANI61C7355: 925..159	22-43	727-746	NAP		g2132992	120	104	9.00E-22	34	21	probable membrane protein YPL183c - yeast (Saccharomyces cerevisiae)
22096	ENU05890	ANI61C7856: 1..541	24-43	485-504	NAP		g3080368	162	91	6.00E-18	34	24	[Saccharomyces cerevisiae] (AL022580) putative protein [Arabidopsis thaliana]
22097	ENU05891	ANI61S1700: 1..605	36-63	387-413	NAP		g2894215	104	71	6.00E-12	29	38	(AL021841) amB [Mycobacterium tuberculosis]
22098	ENU05892	ANI61C2695: 1..616	58-83	404-425	NAP		g4505499	213	119	1.00E-26	40	18	O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) [Homo sapiens]
22099	ENU05893	ANI61C2136: 5058..4203	115-134	805-829	NAP		g266448	648	252	3.00E-66			long-chain-fatty-acid--COA ligase 1 (long-chain acyl-COA synthetase 1) (fatty acid activator 1) [Saccharomyces cerevisiae]
22100	ENU05894	ANI61C1060: 5:839..1	153-176	654-679	NAP		g2499125	458	196	2.00E-49	37	8	vacuolar protein sorting-associated protein VPS13 [Saccharomyces cerevisiae]
22101	ENU05895	ANI61C7807: 1308..332	22-46	804-829	NAP		g3220205	166	55	0.000000			(AF054613) peroxin [Yarrowia lipolytica]
22102	ENU05896	ANI61C3104: 1..1521	61-80	807-826	NAP		g4007757	1872	368	e-126	72	51	(AL034433) glucose-6-phosphate isomerase [Schizosaccharomyces pombe]

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22103	ENU05897	ANI6IC6457: 22-47		801-826	NAP		g2052244	324	92	3.00E-18	37	52	[Schizosaccharomyces pombe] [] (Y12561) Cdc1 protein
22104	ENU05898	ANI6IC477:1 24-45		535-560	NAP		g3879684	151	85	4.00E-16	36	49	[Schizosaccharomyces pombe] [] (Z74042) predicted using GeneFinder; Similarity to Haemophilus 3-oxoacyl-(acyl-carrier protein) reductase (SW:FABG_HAEIN); cDNA EST yk470b2.3 comes from this gene; cDNA EST yk470b2.5 comes from this gene [Caenorhabditis elegans] (ABO10274) fatty acid synthetase [Schizosaccharomyces pombe]
22105	ENU05899	ANI6IC9467: 22-42		796-819	NAP		g4115480	1564	122	2.00E-43	42	12	[Schizosaccharomyces pombe] cell division-associated protein B1MB []
22106	ENU05900	ANI6IC9162: 27-49		434-456	NAP		g416716	917	254	3.00E-67	92	10	(AF080217) acetoacetyl-CoA synthetase; acetoacetyl-CoA ligase; acyl-activating enzyme [Sinorhizobium meliloti] (D90912) hypothetical protein [Synechocystis sp.] (AL031741) putative membrane transporter [Schizosaccharomyces pombe]
22107	ENU05901	ANI6IC1100 50-69		795-814	NAP		g3769519	982	209	2.00E-53	45	41	(AF080217) acetoacetyl-CoA synthetase; acetoacetyl-CoA ligase; acyl-activating enzyme [Sinorhizobium meliloti] (D90912) hypothetical protein [Synechocystis sp.] (AL031741) putative membrane transporter [Schizosaccharomyces pombe]
22108	ENU05902	ANI6IC4407: 34-54		707-730	NAP		g1653242	390	91	1.00E-23	32	58	(AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22109	ENU05903	ANI6IC1871: 22-49		640-660	NAP		g3650370	299	116	1.00E-25	37	41	(L10127) ORF17 [Molluscum contagiosum virus type 1] (AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22110	ENU05904	ANI6IC1015 37-54		764-790	NAP		g462768	85	41	0.008			(L10127) ORF17 [Molluscum contagiosum virus type 1] (AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22111	ENU05905	ANI6IC9626: 22-48		802-829	NAP		g3650405	960	216	2.00E-55	49	53	(L10127) ORF17 [Molluscum contagiosum virus type 1] (AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22112	ENU05906	ANI6IC9067: 26-49		806-825	NAP		g4574121	402	100	2.00E-20	36	27	(L10127) ORF17 [Molluscum contagiosum virus type 1] (AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22113	ENU05907	ANI6IC7016: 25-48		806-825	NAP		g2257494	737	122	4.00E-27	45	41	(L10127) ORF17 [Molluscum contagiosum virus type 1] (AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22114	ENU05908	ANI6IC7570: 24-50		803-822	NAP		g3169091	1112	199	4.00E-81	59	46	(L10127) ORF17 [Molluscum contagiosum virus type 1] (AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22115	ENU05909	ANI6IS1726: 1..791			NAP		g1572721	130	45	0.0008	25	18	(L10127) ORF17 [Molluscum contagiosum virus type 1] (AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22116	ENU05910	ANI6IC6647: 22-41		803-829	NAP		g3219964	455	158	4.00E-38	46	87	(L10127) ORF17 [Molluscum contagiosum virus type 1] (AL031739) putative dna primase large subunit [Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus] (AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe] (AL023706) hypothetical protein [Schizosaccharomyces pombe] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22117	ENU05911	ANI6IC7639: 22-49		807-829	NAP		g4587971	3918	501	e-141	99	20	(AF082072) ABC transporter protein Atrc [Emmericella nidulans]

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22118	ENU05912	ANT6IC2128: 1906..1	22-41	725-746	NAP		g1709029	1120	295	2.00E-79	56	27	MIC1 protein [Saccharomyces cerevisiae]
22119	ENU05913	ANT6IC1267: 1081..1	22-42	786-805	NAP		g2133039	685	218	4.00E-56	45	17	probable membrane protein YPR184w - yeast (Saccharomyces cerevisiae)
22120	ENU05914	ANT6IS4277: 1..568	69-88	527-547	NAP		g4733981	345	57	4.00E-18			[Saccharomyces cerevisiae] (AC007268) putative serine carboxypeptidase [Arabidopsis thaliana]
22121	ENU05915	ANT6IS4437: 465..1	204-225	414-436	NAP		g2414610	170	53	4.00E-13	43	48	"(Z99295) oxidoreductase, possible sorbitol utilization
22122	ENU05916	ANT6IC7381: 195..928	34-61	686-713	NAP		g1666269	430	90	6.00E-36	40	97	[Schizosaccharomyces pombe] (Z82021) cytochrome P450 [Agaricus bisporus]
22123	ENU05917	ANT6IC2718: 372..9	50-76	457-479	NAP		g229530	193	75	5.00E-20	43	97	cytochrome b2 1-103 [Saccharomycetales]
22124	ENU05918	ANT6IS3976: 136..520			NAP		g547782	162	73	1.00E-12	36	47	"aninoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3)) [Plasmid NTP16]"
22125	ENU05919	ANT6IC775:2 14..1041	24-51	682-709	NAP		g1730771	602	172	3.00E-42	55	25	hypothetical 110.9 KD protein in SPC98-TOM70 intergenic region [Saccharomyces cerevisiae]
22126	ENU05920	ANT6IC2389: 2144..1723	72-93	375-401	NAP		g1351972	666	153	7.00E-37	95	16	Nitrogen regulatory protein area [Emeticella nidulans]
22127	ENU05921	ANT6IC1098 7:1221..1	91-110	738-756	NAP		g3914054	447	131	5.00E-30	32	35	MUTS protein homolog 1 [Schizosaccharomyces pombe]
22128	ENU05922	ANT6IC3268: 2781..1885	22-44	802-829	NAP		g2132229	149	47	0.0002	31	94	hypothetical protein YPL199c - yeast (Saccharomyces cerevisiae)
22129	ENU05923	ANT6IC1371: 1175..482	112-133	640-667	NAP		g3702646	135	72	5.00E-12	26	38	[Saccharomyces cerevisiae] (AL031825) putative membrane transport protein
22130	ENU05924	ANT6IC6060: 740..1	22-47	597-624	NAP		g4495124	436	174	5.00E-43	43	62	[Schizosaccharomyces pombe] (AL035675) WD repeat protein; human U5 SNRNP-specific-like
22131	ENU05925	ANT6IC679:2 506..1	22-45	721-748	NAP		g2131263	2782	396	e-109	66	13	[Schizosaccharomyces pombe] GLT1 protein - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]

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22132	ENU05926	ANI61C1134:	52-71	781-800	NAP		g2132124	1978	445	e-124	75	25	hypothetical protein YOR304w - yeast (Saccharomyces cerevisiae)
		6666..8397											[Saccharomyces cerevisiae]
22133	ENU05927	ANI61C2187:	24-47	680-702	NAP		g2144167	351	70	7.00E-26	32	34	beta-glucosidase (EC 3.2.1.21) - yeast (Candida molischiana) [Pichia capsulata]
		1719..1											
22134	ENU05928	ANI61C7216:	22-48	793-815	NAP		g4033486	238	56	6.00E-20	33	51	putative tartrate transporter [Agrobacterium vitis]
		214..1063											(AL023554) conserved hypothetical protein [Schizosaccharomyces pombe]
22135	ENU05929	ANI61C247:1	29-48	797-816	NAP		g3133104	154	61	0.000000	34	74	cytochrome P450(BM-3) / NADPH-cytochrome P450 reductase [Bacillus megaterium]
		250..2139								008			
22136	ENU05930	ANI61C8055:	22-47	765-784	NAP		g117298	1073	194	9.00E-49			hypothetical 59.1 KD protein ZK637.1 in chromosome III []
		2141..227											beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Kluveromyces marxianus]
22137	ENU05931	ANI61C8057:	91-110	417-444	NAP		g586797	112	61	0.000000	26	28	beta-glucosidase 1 precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Aspergillus aculeatus]
		1..467								005			
22138	ENU05932	ANI61S1712:	22-41	395-420	NAP		g114971	415	173	5.00E-43	53	17	(L41834) nuclear protein [Ensis minor]
		1..453											
22139	ENU05933	ANI61C7085:	26-45	803-829	NAP		g1352079	1500	357	e-126	77	32	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
		2078..3434											(AL034352) putative phosphodiesterase-nucleotide pyrophosphatase precursor
22140	ENU05934	ANI61S2736:			NAP		g786117	236	48	0.0001	19	55	[Schizosaccharomyces pombe]
		1..906											probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae)
22141	ENU05935	ANI61C323:3	22-49	808-829	NAP		g2956768	907	242	3.00E-63	47	67	[Saccharomyces cerevisiae]
		652..2386											hypothetical 74.0 KD protein in CAI1-HOM3 intergenic region [Saccharomyces cerevisiae]
22142	ENU05936	ANI61S1621:	67-85	320-344	NAP		g3925755	110	62	0.000000	30	21	
		365..1								002			
22143	ENU05937	ANI61C978:8	22-48	718-737	NAP		g2132846	275	113	2.00E-24	31	48	
		38..1											
22144	ENU05938	ANI61C1138	26-48	442-461	NAP		g731462	179	94	9.00E-19	40	22	
		7:1..552											

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22145	ENU05939	ANI61C1146	22-45	714-732	NAP		g3810838	429	88	7.00E-17	37	38	"(AL032684) putative DNA polymerase epsilon, subunit b [Schizosaccharomyces pombe]"
22146	ENU05940	ANI61C1098	26-45	721-743	NAP		g3451448	195	80	3.00E-14	35	80	(AL031350) putative dehydrogenase [Streptomyces coelicolor]
22147	ENU05941	ANI61C1053	22-43	710-734	NAP		g3914984	1047	72	4.00E-12	22	7	Ferriochrome siderophore peptide synthetase [Ustilago maydis]
22148	ENU05942	ANI61C9561: 1:3372..1	32-51	758-785	NAP		g2342601	674	128	6.00E-43	39	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22149	ENU05943	ANI61C2459: 288..1649	22-49	788-812	NAP		g101795	1373	406	e-112	98	51	nitrate transport protein crmA - Emericella nidulans []
22150	ENU05944	ANI61C1143	24-46	735-756	NAP		g3869276	296	138	4.00E-32	33	97	(AF053764) NADP-dependent mannitol dehydrogenase [Agaricus bisporus]
22151	ENU05945	ANI61S973:1.511			NAP		g631954	402	145	2.00E-34	53	18	chitin synthase (EC 2.4.1.16) chsB - Emericella nidulans [Emericella nidulans]
22152	ENU05946	ANI61C8446: 608..1	34-53	480-506	NAP		g3850084	308	105	2.00E-29	44	52	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
22153	ENU05947	ANI61C6254: 1232..2582	58-77	768-787	NAP		g2501339	541	161	2.00E-47	49	37	Copper amine oxidase 1 [Aspergillus niger]
22154	ENU05948	ANI61C3968: 789..1	22-42	712-739	NAP		g470731	1194	269	e-126	97	60	(L31778) alkaline protease [Aspergillus nidulans]
22155	ENU05949	ANI61S75:52	215-232	463-482	NAP		g3915105	430	189	9.00E-48	55	31	threonine dehydratase precursor (threonine deaminase) [Arxula adenivorans]
22156	ENU05950	ANI61C6610: 702..1	30-50	577-601	NAP		g2559008	345	131	1.00E-32	57	30	"(AF026291) chaperonin containing t-complex polypeptide 1, delta subunit; CCT-delta [Homo sapiens]"
22157	ENU05951	ANI61S3152: 590..107	122-146	437-463	NAP		g1546698	456	111	3.00E-24	93	34	(X98808) peroxidase ATP3a [Arabidopsis thaliana]
22158	ENU05952	ANI61C9158: 1..560	22-43	446-464	NAP		g1708464	689	171	2.00E-62	73	31	"putative dihydroxy-acid dehydratase precursor (DAD) (2,3-dihydroxy acid hydrolyase) [Schizosaccharomyces pombe]"
22159	ENU05953	ANI61C5582: 1..745	103-128	683-706	NAP		g1351078	107	76	3.00E-13	25	26	High-affinity glucose transporter SNF3 [Saccharomyces cerevisiae]
22160	ENU05954	ANI61S2588: 580..188	205-232	343-370	NAP		g128192	514	209	8.00E-54	82	15	Nitrate reductase (NADPH) (NR) [Emericella nidulans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22161	ENU05955	ANT6IS4224: 997..549			NAP		g3329623	130	30	8.7	28	44	(AF078790) No definition line found [Caenorhabditis elegans]
22162	ENU05956	ANT6IC6104: 1..1195	22-49	810-829	NAP		g2499716	755	217	8.00E-56	46	59	"exopolylacturonase precursor (exoPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
22163	ENU05957	ANT6IC4643: 1007..1	72-89	777-796	NAP		g1346380	1126	383	e-105	81	30	Kinesin heavy chain []
22164	ENU05958	ANT6IC9251: 2690..2369	23-45	408-434	NAP		g3130014	63	61	0.000000	29	40	(AL023517) putative lipoprotein [Streptomyces coelicolor]
22165	ENU05959	ANT6IC1307: 317..1363	25-44	808-829	NAP		g114275	698	223	1.00E-57	46	80	L-Asparaginase precursor (L-asparagine amidohydrolase) [Erwinia chrysanthemi]
22166	ENU05960	ANT6IS4270: 610..1			NAP		g3738194	192	59	0.000000	41	26	(AL031854) hypothetical protein [Schizosaccharomyces pombe]
22167	ENU05961	ANT6IC1126: 71..477	24-43	394-421	NAP		g464369	108	64	5.00E-10	32	18	Phenol 2-monooxygenase (phenol hydroxylase) [Trichosporon cutaneum]
22168	ENU05962	ANT6IC1110: 0:8975..10390	46-65	723-744	NAP		g3650376	720	216	1.00E-55	44	30	(AL031740) dna ligase protein [Schizosaccharomyces pombe]
22169	ENU05963	ANT6IC2411: 2469..1213	22-41	803-829	NAP		g3395556	724	146	1.00E-63	58	70	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
22170	ENU05964	ANT6IC2118: 1698..2569	51-70	763-780	NAP		g2388904	528	173	8.00E-55	51	39	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
22171	ENU05965	ANT6IC3180: 242..753	23-42	436-455	NAP		g3036901	89	55	0.000000	28	55	(AJ222715) DapA [Sinorhizobium meliloti]
22172	ENU05966	ANT6IC1061: 5:1250..1	94-113	732-749	NAP		g461623	522	155	4.00E-37	38	25	beta-galactosidase precursor (lactase) [Aspergillus niger]
22173	ENU05967	ANT6IC5650: 327..1072	56-78	702-725	NAP		g227874	482	98	1.00E-41	50	28	Extracellular beta glucosidase [Trichoderma reesei]
22174	ENU05968	ANT6IC8513: 724..1	65-86	658-677	NAP		g1498245	324	151	6.00E-36	38	29	"(X99960) putative, YGL139w [Saccharomyces cerevisiae]"
22175	ENU05969	ANT6IC3470: 262..1249	22-49	806-829	NAP		g217326	396	82	3.00E-32	40	42	(D13332) Ca2+/calmodulin-dependent protein kinase II [Drosophila sp.]
22176	ENU05970	ANT6IC4698: 1522..1924	92-119	375-398	NAP		g3913326	173	88	3.00E-17	31	31	Cytochrome P450 52A9 (CYP11A9) (alkane-inducible P450-ALK5-A) [Candida maltosa]



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22177	ENU05971	ANI61C7088:	108-127	719-738	NAP		g2407970	666	209	2.00E-53	63	38	(Y14750) TOM70 [Podospora anserina]
22178	ENU05972	ANI61C8560:	60-87	519-546	NAP		g640053	144	50	2.00E-12	41	35	(U19714) 3-phosphoserine aminotransferase [Saccharomyces cerevisiae]
22179	ENU05973	ANI61C8579:	22-47	793-820	NAP		g4586928	449	155	5.00E-37	39	5	(AB017641) polyketide synthase [Micromonospora griseorubida]
22180	ENU05974	ANI61C1021	22-48	710-732	NAP		g3087842	624	152	8.00E-53	48	55	(Y08841) core protein II [Neurospora crassa]
22181	ENU05975	ANI61S557:1.	5:1152..1		NAP		g2213913	92	53	8.00E-10	21	9	(AF004884) neuronal calcium channel alpha 1A subunit isoform A-1 [Homo sapiens]
22182	ENU05976	ANI61C9522:	22-43	646-669	NAP		g4104764	293	119	2.00E-26	40	54	(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
22183	ENU05977	ANI61S3702:	1062..1831		NAP		g125462	90	38	0.046			"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3)I) [Cloning vector pHIND2.2]"
22184	ENU05978	ANI61C7393:	22-41	568-595	NAP		g113701	332	128	5.00E-33	48	36	Acetamidase [Emericella nidulans]
22185	ENU05979	ANI61C4935:	40-59	499-521	NAP		g4803681	131	73	2.00E-12			(AL049819) putative AraC-family transcriptional regulator [Streptomyces coelicolor]
22186	ENU05980	ANI61C5316:	47-65	533-552	NAP		g4008543	98	61	0.000000	29	62	(AL034492) putative deacetylase [Streptomyces coelicolor]
22187	ENU05981	ANI61C1030	22-45	633-660	NAP		g1708808	550	213	2.00E-59	47	79	Lactoylglutathione lyase (methylglyoxalase) (aldoketomutase) (glyoxalase I) (GLX I) (ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [Saccharomyces cerevisiae]
22188	ENU05982	ANI61C1103	102-127	453-479	NAP		g3860373	466	171	4.00E-42	57	47	(AJ012668) tomatinase [Fusarium oxysporum f. sp. lycopersici]
22189	ENU05983	ANI61C2278:	39-66	721-748	NAP		g2275095	185	109	2.00E-23	26	24	(X86179) phosphoprotein [Schizosaccharomyces pombe]
22190	ENU05984	ANI61S2170:	30-49	334-361	NAP		g3183329	297	126	6.00E-29	53	26	Hypothetical aminotransferase C6B12.04C [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22191	ENU05985	ANI61C2482:	102-125	653-680	NAP		g3850151	437	115	4.00E-44	58	70	(AL033396) rehydrin-like protein [Candida albicans]
22192	ENU05986	ANI61C1048	43-70	807-829	NAP		g1805251	1078	131	4.00E-43	41	50	(U58946) transposase [Aspergillus awamori]
22193	ENU05987	ANI61C1147:	22-45	705-730	NAP		g1749410	711	183	5.00E-59	59	41	"(D89101) similar to Saccharomyces cerevisiae Asparagine synthetase(glutamine-hydrolyzing)2, SWISS-PROT Accession Number P49090 [Schizosaccharomyces pombe]"
22194	ENU05988	ANI61C2507:	144-171	796-818	NAP		g2896707	511	138	4.00E-51	52	90	(AL021897) echA8 [Mycobacterium tuberculosis]
22195	ENU05989	ANI61S3763:	33-52	385-410	NAP		g4263063	213	98	7.00E-20	34	28	(AC005142) hypothetical protein [Arabidopsis thaliana]
22196	ENU05990	ANI61S1588:			NAP		g2500356	357	157	6.00E-38	54	69	60S ribosomal protein L10 (QM protein homolog) (SPQM) [Schizosaccharomyces pombe]
22197	ENU05991	ANI61C1133	105-125	379-398	NAP		g1749480	179	82	3.00E-15	43	26	"(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]"
22198	ENU05992	ANI61C4764:	22-46	723-744	NAP		g1711623	1646	372	e-102	67	29	"alanyl-tRNA synthetase, cytoplasmic (alanine-tRNA ligase) (ALARS) [Saccharomyces cerevisiae]"
22199	ENU05993	ANI61C8670:	35-54	793-815	NAP		g2956768	384	80	3.00E-14	27	61	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22200	ENU05994	ANI61C1074	53-78	261-288	NAP		g3850084	134	54	0.000000	36	30	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
22201	ENU05995	ANI61C487:6	114-136	474-493	NAP		g731294	247	79	3.00E-14	37	43	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region [Saccharomyces cerevisiae]
22202	ENU05996	ANI61C9976:	23-50	809-828	NAP		g3549899	332	78	6.00E-14			(Y15013) copalyl diphosphate synthase [Gibberella fujikuroi]
22203	ENU05997	ANI61C7223:	23-49	794-813	NAP		g1171890	885	261	3.00E-71			"pyruvate dehydrogenase E1 component, beta subunit precursor (PDHE1-B) [Schizosaccharomyces pombe]"

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22204	ENU05998	ANI61C553.2	27-46	342-361	NAP		g3378446	112	48	0.00005	30	63	(AF079317) 4-hydroxy-2-oxovalerate aldolase [Sphingomonas aromaticivorans]
22205	ENU05999	ANI61S2740.1..354			NAP		g4218005	122	39	0.014	31	16	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
22206	ENU06000	ANI61C9901.3907..4488			NAP		g2131340	358	127	8.00E-29	47	61	hypothetical protein YDL119c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22207	ENU06001	ANI61C9014.275..627	105-128	453-474	NAP		g1077357	232	99	4.00E-23	42	31	probable membrane protein YLR359w - yeast (Saccharomyces cerevisiae)
22208	ENU06002	ANI61C3570.331..1656	71-90	802-829	NAP		g4894182	652	183	2.00E-45			[Saccharomyces cerevisiae] (AJ24251) 12-oxophytodienate reductase [Lycopersicon esculentum]
22209	ENU06003	ANI61C7889.1..837	49-70	788-807	NAP		g730115	395	158	4.00E-38	38	35	Nitrate reductase [Synechococcus sp.]
22210	ENU06004	ANI61C9695.892..1	37-56	717-744	NAP		g4507007	267	128	6.00E-29	31	37	Calcium binding mitochondrial carrier superfamily member Aralar [Homo sapiens]
22211	ENU06005	ANI61C1230.4470..1314	22-45	805-829	NAP		g1166378	1020	101	5.00E-21			"(L76169) reverse transcriptase, RnaseH [Glomerella cingulata]"
22212	ENU06006	ANI61C2256.1842..633	22-43	777-796	NAP		g140965	346	173	1.00E-42	40	48	Probable serine/threonine-protein kinase YKL116C [Saccharomyces cerevisiae]
22213	ENU06007	ANI61S1491.1..981			NAP		g119714	466	36	0.38	41	43	Extensin precursor (cell wall hydroxyproline-rich glycoprotein) [Nicotiana tabacum]
22214	ENU06008	ANI61C4969.1048..17	22-41	711-730	NAP		g119791	181	80	2.00E-14	35	63	3-oxoacyl- [Cuphea lanceolata]
22215	ENU06009	ANI61C1471.1005..1	38-61	712-738	NAP		g4176721	683	196	1.00E-49	52	46	(AF038568) negative regulator Moel [Schizosaccharomyces pombe]
22216	ENU06010	ANI61C9067.114..1174	22-46	804-824	NAP		g2290999	409	163	2.00E-43	42	85	(AF006000) unknown [Bordetella pertussis]
22217	ENU06011	ANI61C1087.5:1444..2508	25-52	798-819	NAP		g1465804	295	143	1.00E-33	32	77	(U64852) W01A11.2 gene product [Caenorhabditis elegans]
22218	ENU06012	ANI61C5251.672..1	23-45	625-651	NAP		g113626	612	185	9.00E-56			fructose-bisphosphate aldolase [Saccharomyces cerevisiae]
22219	ENU06013	ANI61C1972.1260..386	202-221	802-822	NAP		g416875	353	116	6.00E-30	35	41	Allantoin permease (allantoin transport protein) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22220	ENU06014	ANT6IC1013			NAP		g2500936	447	196	2.00E-49	40	36	High-affinity glucose transporter RGT2 [Saccharomyces cerevisiae]
22221	ENU06015	ANT6IC4401: 4:1072..1	38-57	672-693	NAP		g549689	352	129	9.00E-32	51	99	Hypothetical 19.7 KD protein in LHS1-NUP100 intergenic region [Saccharomyces cerevisiae]
22222	ENU06016	ANT6IC6292: 2373..1660	22-45	745-765	NAP		g3015626	1262	227	e-119	98	68	(AF041976) nitrogen metabolite repression regulator NmrA [Emmericella nidulans]
22223	ENU06017	ANT6IC2265: 1012..1	72-91	623-645	NAP		g4758416	489	201	5.00E-51			golgi-specific brefeldin A-resistance factor 1 [Homo sapiens]
22224	ENU06018	ANT6IC1241: 1..3733	42-61	764-783	NAP		g1078633	5787	123	2.00E-69	97	21	myosin I myoA - Emmericella nidulans [Emmericella nidulans]
22225	ENU06019	ANT6IC8228: 1182..1	23-42	716-734	NAP		g2293233	152	76	3.00E-13	26	49	(AF008220) YtcJ [Bacillus subtilis]
22226	ENU06020	ANT6IC9644: 2543..1	40-59	725-749	NAP		g1546072	1051	144	9.00E-34	38	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22227	ENU06021	ANT6IC1915: 2189..2885	22-47	642-667	NAP		g462683	320	137	7.00E-32			putative N-acetylglucosamine-6-phosphate deacetylase (GLCNAC 6-P deacetylase) [Caenorhabditis elegans]
22228	ENU06022	ANT6IS4147: 1..360	62-81	310-329	NAP		g2633827	408	165	1.00E-40	63	65	(Z99111) similar to formylmethionine deformylase [Bacillus subtilis]
22229	ENU06023	ANT6IS2660: 399..1			NAP		g4249564	206	61	0.000000	48	30	(AB003111) actin [Hunnicola grisea var. thermoideal]
22230	ENU06024	ANT6IC8071: 516..1	27-46	447-474	NAP		g3560266	248	63	6.00E-20	44	72	(AL031535) putative n-terminal acetyltransferase complex su bunit [Schizosaccharomyces pombe]
22231	ENU06025	ANT6IS4267: 399..892			NAP		g730888	138	50	0.00001	31	85	Octapeptide-repeat protein T2 [Mus musculus]
22232	ENU06026	ANT6IC1090: 1..464	197-223	417-443	NAP		g585965	230	104	5.00E-22	37	19	Vesicular-fusion protein SEC18 [Saccharomyces cerevisiae]
22233	ENU06027	ANT6IC4878: 634..1			NAP		g3202046	117	80	2.00E-14	30	9	(AF069525) 190 kDa ankyrin isoform; AnkG190 [Rattus norvegicus]
22234	ENU06028	ANT6IC6400: 1..496	39-58	433-460	NAP		g3819717	165	52	1.00E-13	31	42	(AJ012408) citrate synthase [Anabaena PCC7120]
22235	ENU06029	ANT6IC532:6			NAP		g3023956	178	80	5.00E-15	34	11	Vegetable incompatibility protein HET-E-1 [Podospora anserinal]
22236	ENU06030	ANT6IC3032: 885..1	84-103	720-738	NAP		g1834342	800	292	2.00E-79	54	19	(Z68905) ATP-binding cassette multidrug transporter [Emerticella nidulans]

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22237	ENU06031	ANI61C1134	104-131	483-510	NAP		g1711561	177	67	5.00E-17	47	18	Sugar transporter STL1 [Saccharomyces cerevisiae]
22238	ENU06032	5:1958..1415 ANI61C4015:	24-51	341-365	NAP		g1255425	86	46	0.0001	21	42	(U53154) No definition line found [Caenorhabditis elegans]
22239	ENU06033	507..1 ANI61C8048:	43-62	804-829	NAP		g3184558	290	82	4.00E-15	31	77	(AF052290) unknown [Synecococcus PCC7002]
22240	ENU06034	2217..3278 ANI61S3246:			NAP		g4204304	259	129	2.00E-29	42	24	(AC003027) lc prt. seq No definition line found [Arabidopsis thaliana]
22241	ENU06035	169..616 ANI61C1043	22-45	774-801	NAP		g1743374	143	69	5.00E-19	28	36	(Y10034) 1-aminocyclopropane-1-carboxylic acid oxidase [Rumex palustris]
22242	ENU06036	4:2564..3682 ANI61C1041	22-41	808-827	NAP		g3738182	1083	287	5.00E-77	63	47	"(AL031854) probable t-complex protein 1, theta subunit [Schizosaccharomyces pombe]"
22243	ENU06037	1:6403..7672 ANI61S1333:			NAP		g3153821	140	45	0.0006	22	21	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22244	ENU06038	1..588 ANI61C6363:	24-43	809-828	NAP		g1890776	157	68	9.00E-11			(U88574) syringomycin biosynthesis enzyme [Pseudomonas syringae pv. syringae]
22245	ENU06039	3584..2480 ANI61C6186:	23-50	802-829	NAP		g418150	726	157	7.00E-38			GABA-specific permease (GABA-specific transport protein) [Saccharomyces cerevisiae]
22246	ENU06040	1283..1 ANI61C5013:	193-220	784-808	NAP		g731276	967	314	6.00E-91	71	65	hypothetical 40.7 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]
22247	ENU06041	1202..1 ANI61C5574:	53-72	371-394	NAP		g115943	334	103	4.00E-30	41	58	cytochrome C heme lyase (CCHL) (holocytochrome-C synthase) [Neurospora crassa]
22248	ENU06042	4289..4900 ANI61C9267:	56-82	455-474	NAP		g1890290	51	42	0.003	25	17	(U89999) Ski2 [Xenopus laevis]
22249	ENU06043	2297..2780 ANI61S2314:	65-84	392-411	NAP		g3891714	155	84	9.00E-16	32	38	Gal6 (Yeast Bleomycin Hydrolase) Mutant C73a []
22250	ENU06044	1..614 ANI61C7278:	29-48	444-463	NAP		g267125	511	154	1.00E-46	98	99	"Thioredoxin [Aspergillus nidulans, Peptide, 109 aa]"
22251	ENU06045	3793..4190 ANI61C3823:	22-41	650-675	NAP		g1171671	688	166	1.00E-71	74	100	hypothetical calcium-binding protein C18B11.04 in chromosome I [Schizosaccharomyces pombe]

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22252	ENU06046	ANI61C9568:	37-56	639-658	NAP		g399112	1005	242	4.00E-76	48	27	beta-galactosidase (lactase) [Kluveromyces lactis]
22253	ENU06047	ANI61C1019	1..1387		NAP		g1166378	376	72	4.00E-12	34	23	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
22254	ENU06048	ANI61C431:4	203-222	491-510	NAP		g2388991	206	69	2.00E-11	35	64	(Z98980) hypothetical protein [Schizosaccharomyces pombe]
22255	ENU06049	ANI61C4184:	22-45	723-741	NAP		g3850071	405	170	1.00E-41	37	54	(AL033385) cadmium resistance protein [Schizosaccharomyces pombe]
22256	ENU06050	ANI61C7503:	37-56	617-634	NAP		g1170811	2349	302	2.00E-81	53	25	putative mitochondrial ATP-dependent protease precursor
22257	ENU06051	ANI61C3397:	29-48	780-807	NAP		g4512354	202	71	1.00E-11			[Schizosaccharomyces pombe] (AB011836) alkyl hydroperoxide reductase large subunit [Bacillus halodurans]
22258	ENU06052	ANI61C3251:	39-58	804-824	NAP		g3738153	237	69	5.00E-23	39	25	(AL031852) putative cleavage and polyadenylation specificity factor [Schizosaccharomyces pombe]
22259	ENU06053	ANI61C9170:	22-47	806-829	NAP		g2225983	414	34	1			(Z97193) hypothetical protein Rv1877 [Mycobacterium tuberculosis]
22260	ENU06054	ANI61C2103:	111-130	456-480	NAP		g2370466	374	165	2.00E-40	46	3	(Z98951) hypothetical protein [Schizosaccharomyces pombe]
22261	ENU06055	ANI61C5199:	102-129	418-437	NAP		g2493134	299	50	4.00E-13	48	58	vacuolar ATP synthase subunit E (V-ATPase E subunit) (V-ATPase 26 KD subunit) [Neurospora crassa]
22262	ENU06056	ANI61C3111:	102-123	660-686	NAP		g1710848	428	138	3.00E-45	45	21	SIT4-associating protein SAP190 [Saccharomyces cerevisiae]
22263	ENU06057	ANI61C466:9	22-49	797-816	NAP		g4106672	57	37	0.16			(AL035064) hypothetical protein [Schizosaccharomyces pombe]
22264	ENU06058	ANI61C5033:	22-46	724-749	NAP		g3560147	522	117	1.00E-40	35	41	"(AL031534) ribosomal processing, ma binding, nucleolar protein [Schizosaccharomyces pombe]"
22265	ENU06059	ANI61S4450:	26-51	338-359	NAP		g1805251	275	79	2.00E-14	39	28	(U58946) transposase [Aspergillus awamori]
22266	ENU06060	ANI61C3498:	98-119	591-613	NAP		g3242651	554	187	2.00E-58	59	20	(AB015509) beta-mannosidase [Aspergillus aculeatus]
22267	ENU06061	ANI61C7525:	36-63	542-569	NAP		g2182006	76	56	0.000000	32	49	(Z96072) hypothetical protein Rv2715 [Mycobacterium tuberculosis]
22268	ENU06062	ANI61C6205:	66-85	794-813	NAP		g730569	888	238	4.00E-91	73	92	60S ribosomal protein YL6 (L5) (RP8) [Saccharomyces cerevisiae]

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22269	ENU06063	ANI61C9151: 27-48	27-48	703-727	NAP		g2497499	482	125	8.00E-54	52	100	Guanylate kinase (GMP kinase) [Mus musculus]
22270	ENU06064	2755..3502											
22271	ENU06065	ANI61C1564: 50-69	50-69	711-730	NAP		g1730729	441	79	4.00E-27	30	39	hypothetical 74.8 KD protein in ALG11-YTP3 intergenic region [Saccharomyces cerevisiae]
22272	ENU06066	1200..1											
22273	ENU06067	ANI61C7241: 27-46	27-46	722-748	NAP		g3006142	339	116	2.00E-25	36	43	(AL022229) hypothetical protein [Schizosaccharomyces pombe]
22274	ENU06068	ANI61C498:7 207-226	207-226	360-379	NAP		g1526987	117	66	3.00E-13	36	52	(U13050) pectate lyase D [Fusarium solani f. sp. pisi]
22275	ENU06069	072..6630											
22276	ENU06070	ANI61C4158: 22-49	22-49	799-818	NAP		g1764018	622	108	2.00E-43	44	66	(Z83760) COS41.8 [Ciona intestinalis]
22277	ENU06071	2015..756											
22278	ENU06072	ANI61C7648: 22-48	22-48	373-398	NAP		g4886445	209	34	0.59			(AL050269) hypothetical protein [Homo sapiens]
22279	ENU06073	710..1253											
22280	ENU06074	ANI61C3744: 56-78	56-78	803-829	NAP		g118498	1074	252	3.00E-66	45	55	aldehyde dehydrogenase (ALDH) [Emmericella nidulans]
22281	ENU06075	3348..4992											
22282	ENU06076	ANI61C4669: 111-130	111-130	736-758	NAP		g3114719	1141	336	1.00E-91	64	18	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
22283	ENU06077	1..983											
22284	ENU06078	ANI61C867:1 40-60	40-60	808-829	NAP		g1438951	581	115	4.00E-25	46	51	(U61842) cutinase negative acting protein [Fusarium solani f. sp. pisi]
22285	ENU06079	000..1											
22286	ENU06080	ANI61C1057 22-44	22-44	805-829	NAP		g3880602	127	74	1.00E-12			(Z82080) cDNA EST EMBL: D66071 comes from this gene; cDNA EST yk274a10.3 comes from this gene; cDNA EST yk289f12.3 comes from this gene; cDNA EST yk289f12.5 comes from this gene; cDNA EST yk274a10.5 comes from this gene; cDNA ES... []
22287	ENU06081	2:1..1132											
22288	ENU06082												
22289	ENU06083	ANI61C1041 22-39	22-39	413-432	NAP		g140338	258	106	2.00E-22			hypothetical 23.1 KD protein in DMSC-PFLA intergenic region [Escherichia coli]
22290	ENU06084	6:537..1											
22291	ENU06085												
22292	ENU06086	ANI61C2627: 31-50	31-50	724-743	NAP		g2995341	190	66	4.00E-10	25	46	(AL022244) hypothetical protein [Schizosaccharomyces pombe]
22293	ENU06087	1104..1											
22294	ENU06088	ANI61C1049 5:3803..6305					g1705915	2051	309	2.00E-83	51	16	Clathrin heavy chain [Bos taurus]
22295	ENU06089	22282											
22296	ENU06090	ANI61C1002: 23-42	23-42	604-631	NAP		g3130036	389	125	4.00E-28	50	49	(AL023534) putative methionine aminopeptidase I [Schizosaccharomyces pombe]
22297	ENU06091	732..1											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22283	ENU06077	ANT61C3365: 1394..1	23-49	721-740	NAP		g2290770	668	78	5.00E-37	45	21	(AF002163) delta-adapin [Homo sapiens]
22284	ENU06078	ANT61C3696: 1.671	113-132	561-581	NAP		g3874563	276	115	1.00E-32			(Z81042) similar to Yeast hypothetical protein YEF6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... [] (X58824) cdc21 protein [Schizosaccharomyces pombe]
22285	ENU06079	ANT61C6044: 895..1	203-222	701-720	NAP		g4165293	583	245	2.00E-64	59	22	[Schizosaccharomyces pombe]
22286	ENU06080	ANT61C3840: 1.659	102-119	599-618	NAP		g2500535	206	97	1.00E-19	37	20	putative ATP-dependent RNA helicase YDL031W [Saccharomyces cerevisiae]
22287	ENU06081	ANT61C1933: 1700..1181	64-84	472-499	NAP		g3850093	135	76	1.00E-13	28	33	(AL033389) putative allantoin permease [Schizosaccharomyces pombe]
22288	ENU06082	ANT61C6667: 1271..434			NAP		g3136096	1016	406	e-112	83	69	(AF032988) spindle assembly checkpoint protein SLDB [Emmericella nidulans]
22289	ENU06083	ANT61C130:1 ..788	197-215	624-648	NAP		g4206286	702	239	2.00E-62	63	24	(AF043332) plasma membrane H(+)-ATPase [Emmericella nidulans]
22290	ENU06084	ANT61C1055 5:1..5216	22-46	773-792	NAP		g1805261	8541	284	e-121	95	14	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
22291	ENU06085	ANT61C3890: 1104..1	32-52	623-646	NAP		g4056558	104	85	8.00E-16	30	28	(AL034583) related to yeast zds family proteins [Schizosaccharomyces pombe]
22292	ENU06086	ANT61C6567: 691..1	51-78	603-630	NAP		g3184109	673	259	2.00E-71	81	28	(AL023780) ABC transporter [Schizosaccharomyces pombe]
22293	ENU06087	ANT61C6142: 1290..1	35-54	790-809	NAP		g4185560	2042	460	e-147	99	12	(AF112473) PyrABCN [Emmericella nidulans]
22294	ENU06088	ANT61C4368: 2711..1864	119-138	802-827	NAP		g1723766	415	158	5.00E-38	40	57	ubiquinone biosynthesis monooxygenase COQ6 [Saccharomyces cerevisiae]
22295	ENU06089	ANT61C1060 2:1542..1	22-46	718-738	NAP		g3929290	727	190	1.00E-69	54	51	(AF094507) B-type cyclin [Candida albicans]
22296	ENU06090	ANT61C8408: 3444..1	57-76	711-730	NAP		g1597721	1958	110	1.00E-23	36	18	(X99021) putative helicase [Schizosaccharomyces pombe]



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22297	ENU06091	ANI61C1987: 30-57		477-504	NAP		g1813523	124	45	0.0005	28	28	(U67763) PbTRAP [Plasmodium berghei]
22298	ENU06092	ANI61C9063: 22-42		800-827	NAP		g2266911	600	156	3.00E-46	39	78	(AE001274) L4171.5 [Leishmania major]
22299	ENU06093	ANI61C9187: 29-50		522-544	NAP		g1346405	303	88	4.00E-30	39	28	Laccase precursor (benzenediol:oxygen oxidoreductase) (urishiol oxidase) (laccase I) [Emmericella nidulans]
22300	ENU06094	ANI61C1765: 22-45		779-801	NAP		g543923	692	203	9.00E-61			Calnexin homolog precursor [Schizosaccharomyces pombe]
22301	ENU06095	ANI61C6158: 22-42		803-826	NAP		g2330690	184	69	3.00E-11	31	18	(Z98529) putative cytoskeleton assembly control protein
22302	ENU06096	ANI61C8249: 22-49		621-646	NAP		g193271	752	213	2.00E-65	61	62	[Schizosaccharomyces pombe] (M59288) ferrochelatase [Mus musculus]
22303	ENU06097	ANI61C9171: 58-76		797-816	NAP		g1706692	1173	189	3.00E-58	50	50	C-24(28) sterol reductase [Saccharomyces cerevisiae]
22304	ENU06098	ANI61C8836: 24-45		784-803	NAP		g3929395	1129	195	1.00E-85	61	31	vacuolar ATP synthase 98 KD subunit (vacuolar ATPase 98 KD subunit) [Neurospora crassa]
22305	ENU06099	ANI61C3681: 285..1751			NAP		g2492863	2264	409	e-124	98	58	Ornithine aminotransferase (ornithine--oxo-acid aminotransferase) [Emmericella nidulans]
22306	ENU06100	ANI61C9107: 39-58		777-796	NAP		g1027486	805	73	3.00E-25	36	43	(D49538) dihydrogeodin oxidase [Aspergillus terreus]
22307	ENU06101	ANI61C5317: 114-133		281-300	NAP		g461830	176	86	1.00E-16	39	29	carboxypeptidase S1 [Penicillium janthinellum]
22308	ENU06102	ANI61C7469: 115-142		725-744	NAP		g461830	436	113	2.00E-24	35	52	carboxypeptidase S1 [Penicillium janthinellum]
22309	ENU06103	ANI61C8631: 22-49		799-826	NAP		g4468731	698	146	9.00E-44	46	50	(AL035592) hypothetical protein [Schizosaccharomyces pombe]
22310	ENU06104	ANI61C8596: 22-41		773-793	NAP		g1169885	1408	289	2.00E-77	51	26	putative glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system P-protein) [Schizosaccharomyces pombe]
22311	ENU06105	ANI61C2944: 212-231		500-524	NAP		g2494820	321	111	1.00E-25	52	28	Rhannogalacturonase B precursor (rhannogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus]

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22312	ENU06106	ANI61C6952:	99-118		652-673	NAP		g3549877	116	67	1.00E-10	32	37	(Y15902) nitrogen metabolite repression-(nmr)-responsible protein [Gibberella fujikuroi]
		759..1												phosphoribosylamine--glycine ligase (GARS) (glycinamide RIBOnucleotide synthetase) (phosphoribosylglycinamide synthetase) / phosphoribosylformylglycinamide cyclo-ligase (AIRS) (phosphoribosyl-aminimidazole synthetase) ... [Schizosaccharomyces pombe]
22313	ENU06107	ANI61C8294:	22-46		611-630	NAP		g131618	1083	259	1.00E-86			Vegetable incompatibility protein HET-E-1 [Podospira anserinal]
		1154..1												"glucan 1,3-beta-glucosidase precursor (exo-beta 1,3 glucanase) (1,3-beta-D-glucanohydrolase) [Cochliobolus carbonum]"
22314	ENU06108	ANI61C8529:	26-45		517-536	NAP		g3022956	369	166	8.00E-41	45	13	(Z99759) rna binding protein [Schizosaccharomyces pombe]
		1740..2296												(Z68905) ATP-binding cassette multidrug transporter [Emeticella nidulans]
22315	ENU06109	ANI61C3904:	35-54		714-735	NAP		g1352399	370	146	2.00E-34			(AL035548) meu14. ring zinc finger [Schizosaccharomyces pombe]
		2002..1												(D88802) ydhJ [Bacillus subtilis]
22316	ENU06110	ANI61C6018	40-59		586-605	NAP		g2467274	466	127	6.00E-36	66	100	"tyrosyl-TRNA synthetase, cytoplasmic (tyrosyl--TRNA ligase) (TYRRS) [Saccharomyces cerevisiae]"
		74..1208												hypothetical 41.8 KD protein (ORFM) [Schizosaccharomyces pombe]
22317	ENU06111	ANI61C1057	24-45		774-797	NAP		g1834342	1828	232	3.00E-60	70	15	hypothetical 103.6 KD protein in COX5B-PFK26 intergenic region [Saccharomyces cerevisiae]
		1..1.3158												(AF098669) pantothenate kinase [Emeticella nidulans]
22318	ENU06112	ANI61C4884:	64-91		451-478	NAP		g4456818	183	112	1.00E-24	27	47	(Z99759) hypothetical protein [Schizosaccharomyces pombe]
		481..1												(D88802) ydhJ [Bacillus subtilis]
22319	ENU06113	ANI61C4660:	52-78		444-464	NAP		g1945094	317	126	1.00E-28	42	51	"tyrosyl-TRNA synthetase, cytoplasmic (tyrosyl--TRNA ligase) (TYRRS) [Saccharomyces cerevisiae]"
		506..1												hypothetical 41.8 KD protein (ORFM) [Schizosaccharomyces pombe]
22320	ENU06114	ANI61C3441	22-49		786-805	NAP		g549037	845	103	4.00E-42	44	63	hypothetical 103.6 KD protein in COX5B-PFK26 intergenic region [Saccharomyces cerevisiae]
		726..475												(AF098669) pantothenate kinase [Emeticella nidulans]
22321	ENU06115	ANI61C7626:	22-48		595-617	NAP		g2828499	226	117	8.00E-26	28	64	(Z99759) hypothetical protein [Schizosaccharomyces pombe]
		1362..2185												(D88802) ydhJ [Bacillus subtilis]
22322	ENU06116	ANI61C2105:	22-41		656-675	NAP		g731857	267	118	4.00E-26	37	26	"tyrosyl-TRNA synthetase, cytoplasmic (tyrosyl--TRNA ligase) (TYRRS) [Saccharomyces cerevisiae]"
		257..1047												hypothetical 103.6 KD protein in COX5B-PFK26 intergenic region [Saccharomyces cerevisiae]
22323	ENU06117	ANI61C3464	106-123		623-642	NAP		g4191500	1045	199	2.00E-50	97	49	(AF098669) pantothenate kinase [Emeticella nidulans]
		053..3380												(Z99759) hypothetical protein [Schizosaccharomyces pombe]
22324	ENU06118	ANI61S4392:				NAP		g2467272	701	275	3.00E-73	61	31	"tyrosyl-TRNA synthetase, cytoplasmic (tyrosyl--TRNA ligase) (TYRRS) [Saccharomyces cerevisiae]"
		1..741												hypothetical 103.6 KD protein in COX5B-PFK26 intergenic region [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22325	ENU06119	ANI61C1002	102-121	499-526	NAP		g585377	550	220	2.00E-57	51	39	probable mannosyltransferase KTR4 [Saccharomyces cerevisiae]
22326	ENU06120	ANI61C9979:	82-101	394-418	NAP		g280164	63	62	0.000000	22	43	probable dehydrogenase (EC 1.-.-.-) - Vibrio cholerae [Vibrio cholerae]
22327	ENU06121	ANI61C1079	22-46	766-789	NAP		g135100	1254	276	8.00E-84			"aspartyl-TRNA synthetase, cytoplasmic (aspartate--TRNA ligase) (ASPRS) [Saccharomyces cerevisiae]"
22328	ENU06122	ANI61C9357:	30-57	810-829	NAP		g1176581	1120	300	7.00E-81	53	31	hypothetical 101.7 KD protein in EGT2-KRE1 intergenic region [Saccharomyces cerevisiae]
22329	ENU06123	ANI61S3452:	59-86	462-489	NAP		g807674	327	99	4.00E-24	45	21	(M23385) pol protein [Simian sarcoma virus]
22330	ENU06124	ANI61C1040	115-134	777-796	NAP		g3183028	370	159	2.00E-38	35	77	probable histidinol-phosphatase [Schizosaccharomyces pombe]
22331	ENU06125	ANI61C5831:	57-84	262-289	NAP		g3220154	235	107	3.00E-23	47	28	(AF022789) ubiquitin hydrolyzing enzyme I [Homo sapiens]
22332	ENU06126	ANI61C6438:	102-129	620-642	NAP		g1709240	518	175	4.00E-43	48	31	cell division control protein NDA4 []
22333	ENU06127	ANI61C8710:	57-77	802-829	NAP		g2132227	364	96	2.00E-31	42	76	hypothetical protein YPL196w - yeast [Saccharomyces cerevisiae]
22334	ENU06128	ANI61C3623:	211-238	448-467	NAP		g1169590	164	89	3.00E-17	37	43	Malonyl (COA-acyl) carrier protein transacylase (MCT) [Haemophilus influenzae Rd]
22335	ENU06129	ANI61C4966:	22-49	657-684	NAP		g83673	503	78	1.00E-34	37	45	amidase (EC 3.5.1.4) - Aspergillus oryzae [Aspergillus oryzae]
22336	ENU06130	ANI61C6896:	43-62	652-671	NAP		g2226418	178	75	5.00E-13	34	53	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
22337	ENU06131	ANI61C3102:	115-137	514-533	NAP		g4481949	581	226	1.00E-58	67	51	(AL035637) glycoprotein endopeptidase-like protein. [Schizosaccharomyces pombe]
22338	ENU06132	ANI61C7249:	22-42	810-829	NAP		g731481	500	114	1.00E-24	44	42	hypothetical 58.0 KD peptidase in PTP3-IL-V1 intergenic region [Saccharomyces cerevisiae]
22339	ENU06133	ANI61C651:1	23-43	730-755	NAP		g4507711	119	49	0.00003	36	62	tetratricopeptide repeat domain 1 [Homo sapiens]
22340	ENU06134	ANI61C9781:	95-116	403-422	NAP		g3702642	285	97	8.00E-20	52	36	(AL031825) ma binding protein - putative pre mna splicing factor [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22341	ENU06135	AN161C1861:	22-43	802-829	NAP		g1762781	1324	129	3.00E-29	44	27	(U65685) phosphoinositide-specific phospholipase C [Botryotinia fuckeliana]
22342	ENU06136	AN161S2460:			NAP		g913016	107	79	2.00E-14	27	12	(S76267) Snq2 homolog=bf1
22343	ENU06137	AN161C6319:	34-53	806-825	NAP		g4539662	252	74	8.00E-22	31	27	[Schizosaccharomyces pombe] (AF061282) polyploid protein [Sorghum bicolor]
22344	ENU06138	AN161C9871:	22-41	790-810	NAP		g141051	419	81	6.00E-32	43	53	hypothetical protein in MMSB 3'region (ORF1) [Pseudomonas aeruginosa]
22345	ENU06139	AN161C591:	33-52	644-662	NAP		g497653	70	38	0.058	19	11	(U09782) myosin heavy chain [Argopecten irradians]
22346	ENU06140	AN161C4843:	86-109	514-538	NAP		g1488255	96	75	3.00E-13	26	32	(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
22347	ENU06141	AN161S2985:			NAP		g186396	135	38	0.058	33	15	(M94131) mucin [Homo sapiens]
22348	ENU06142	AN161C8111:	42-61	631-648	NAP		g2494820	1626	125	1.00E-55	85	36	Rhannogalacturonase B precursor (rhannogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus]
22349	ENU06143	AN161C1024:	24-51	806-829	NAP		g1723685	925	180	4.00E-62	56	78	hypothetical 38.3 KD protein in RPL16B-PDC6 intergenic region [Saccharomyces cerevisiae]
22350	ENU06144	AN161S3184:			NAP		g539218	149	41	0.003	25	26	hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []
22351	ENU06145	AN161C2805:	68-87	465-484	NAP		g2131533	167	83	5.00E-16	32	29	hypothetical protein YDR501w - yeast (Saccharomyces cerevisiae)
22352	ENU06146	AN161C8818:	69-88	440-459	NAP		g2492821	330	143	6.00E-34	48	100	[Saccharomyces cerevisiae] Augmenter of liver regeneration (HERV1 protein) [Homo sapiens]
22353	ENU06147	AN161C2583:	118-137	645-663	NAP		g4033486	270	122	2.00E-27	30	58	putative tartrate transporter [Agrobacterium vitis]
22354	ENU06148	AN161C1112:	69-88	765-784	NAP		g2492491	971	167	5.00E-84	86	87	14-3-3 protein homolog (TH1433) [Trichoderma harzianum]
22355	ENU06149	AN161C4678:	67-86	576-596	NAP		g2511761	938	215	4.00E-97	97	23	(AF023156) carnitine acetyl transferase FacC [Emmericella nidulans]
22356	ENU06150	AN161C3182:	27-54	805-829	NAP		g549722	199	51	1.00E-20			DNA-directed RNA polymerase III 25 KD polypeptide (C25) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22357	ENU06151	AN161C7398: 108..485	78-97	445-464	NAP		g3417421	266	126	8.00E-29	52	40	(AL031261) forkhead nuclear signalling domain protein [Schizosaccharomyces pombe]
22358	ENU06152	AN161C476:4 55..1	92-119	330-354	NAP		g4377374	113	43	0.000000	26	35	(AE001684) Adenosylmethionine-8-Amino-7-Oxononanoate Aminotransferase [Chlamydia pneumoniae]
22359	ENU06153	AN161C4149: 592..1281	25-44	581-601	NAP		g2497670	43	49	0.00003	39	15	Homeobox protein LIM-1 [Danio rerio]
22360	ENU06154	AN161C9601: 6926..7975	30-54	620-644	NAP		g2494036	218	60	7.00E-13			D-amino acid oxidase (DAMOX) (DAO) (DAAO) [Trigonopsis variabilis]
22361	ENU06155	AN161C8113: 1170..2314	25-47	657-684	NAP		g729467	564	206	1.00E-52	42	48	purine-cytosine permease (PCP) (cytosine/purine transport protein) [Saccharomyces cerevisiae]
22362	ENU06156	AN161C4412: 5991..4552	59-86	807-829	NAP		g529564	532	115	4.00E-32	36	65	"(L35343) 2,3-butanediol dehydrogenase [Pseudomonas putida]"
22363	ENU06157	AN161C3596: 572..1	102-124	490-515	NAP		g1703372	126	83	1.00E-15	27	35	Probable sterol O-acyltransferase (sterol-ester synthase) [Schizosaccharomyces pombe]
22364	ENU06158	AN161C1165: 1873..10	22-49	786-811	NAP		g1346405	736	181	5.00E-45	34	46	Laccase precursor (benzenediol:oxygen oxidoreductase) (urishiol oxidase) (laccase I) [Emerticella nidulans]
22365	ENU06159	AN161C508:2 561..3516	22-47	806-829	NAP		g2497175	396	92	4.00E-32	39	92	hypothetical 31.1 KD protein in SIP18-SPT21 intergenic region [Saccharomyces cerevisiae]
22366	ENU06160	AN161C6718: 1..527	110-129	477-496	NAP		g1020413	84	55	0.000000	30	22	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
22367	ENU06161	AN161C1080 2:818..1	24-43	684-703	NAP		g1723910	818	321	4.00E-87	66	33	Pre-mRNA splicing factor RNA helicase PRP43 (helicase JA1) [Saccharomyces cerevisiae]
22368	ENU06162	AN161C9004: 1..550	95-114	423-442	NAP		g18343322	347	92	1.00E-29	45	52	(D50661) RNA polymerase II subunit 3 [Schizosaccharomyces pombe]
22369	ENU06163	AN161C4804: 1622..1	22-49	725-749	NAP		g4102636	2457	555	e-159	99	43	(AF014812) G1/S regulator [Emerticella nidulans]
22370	ENU06164	AN161C9461: 1625..2292	38-57	576-603	NAP		g586919	198	80	1.00E-14	37	71	YSA1 protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	5 pos	3 pos	Primer	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22371	ENU06165	ANT61C5506:	27-46	791-816	NAP	NAP	g1723769	261	134	6.00E-31	28	51	51	putative transporter YGR260W [Saccharomyces cerevisiae]
22372	ENU06166	ANT61C8552:	23-46	803-829	NAP	NAP	g2132019	392	70	2.00E-11				hypothetical protein YOL141w - yeast [Saccharomyces cerevisiae]
22373	ENU06167	ANT61C5975:	67-90	554-572	NAP	NAP	g3649751	421	174	5.00E-43	44	54	54	[Saccharomyces cerevisiae] (Z15137) esterase A [Streptomyces chrysomallus]
22374	ENU06168	ANT61C103:1	70-89	562-582	NAP	NAP	g2414601	250	63	3.00E-21	51	20	20	(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
22375	ENU06169	ANT61C5302:	46-66	802-829	NAP	NAP	g465480	283	145	3.00E-34				Dolichyl-diphosphooligosaccharide--protein glycosyltransferase beta subunit precursor [Oligosaccharyl transferase beta subunit] [Saccharomyces cerevisiae]
22376	ENU06170	ANT61C1132:	25-44	776-796	NAP	NAP	g3136056	1918	85	8.00E-16	32	22	22	(AL023592) RanBP7/importin-beta/Cse1p superfamily protein [Schizosaccharomyces pombe]
22377	ENU06171	ANT61C3382:	22-44	711-733	NAP	NAP	g4584836	913	273	3.00E-99	67	37	37	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
22378	ENU06172	ANT61C2441:	39-58	595-614	NAP	NAP	g1723485	403	182	2.00E-45	44	54	54	hypothetical 47.3 KD protein C17G8.13C in chromosome I [Schizosaccharomyces pombe]
22379	ENU06173	ANT61C9052:	122-142	344-363	NAP	NAP	g3581896	89	40	0.000007	34	18	18	(AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
22380	ENU06174	ANT61C3578:	109-128	300-319	NAP	NAP	g3282044	367	159	6.00E-39	66	8	8	(Y13967) alpha-aminoacidipate reductase large subunit [Penicillium chrysogenum]
22381	ENU06175	ANT61C9636:	103-121	521-540	NAP	NAP	g454894	354	148	1.00E-43	45	47	47	(Z29988) Mnt1 protein [Saccharomyces cerevisiae]
22382	ENU06176	ANT61C1147	60-79	805-827	NAP	NAP	g2414593	781	186	2.00E-46	42	52	52	(Z99258) molybdopterin biosynthesis [Schizosaccharomyces pombe]
22383	ENU06177	ANT61C1183:	36-55	449-476	NAP	NAP	g1723514	180	83	9.00E-16	31	100	100	hypothetical 16.7 KD protein C1F12.10C in chromosome I [Schizosaccharomyces pombe]
22384	ENU06178	ANT61C7662:	22-44	628-649	NAP	NAP	g1168807	485	207	5.00E-53	55	32	32	[Schizosaccharomyces pombe] probable protein-tyrosine phosphatase CDC14 [Saccharomyces cerevisiae]
22385	ENU06179	ANT61C6688:	33-60	500-525	NAP	NAP	g476389	55	42	0.003	19	9	9	"myosin heavy chain-B, neuronal - chicken [Gallus gallus]"

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22386	ENU06180	ANI61C8735:	24-50	513-532	NAP		g2224699	197	102	2.00E-21	33	23	(AB002377) KIAA0379 [Homo sapiens]
22387	ENU06181	ANI61C9465:	47-66	776-795	NAP		g3785995	2130	204	6.00E-52	53	18	(AC005499) unknown protein [Arabidopsis thaliana]
22388	ENU06182	ANI61C6501:	93-115	606-625	NAP		g3915154	142	63	1.00E-10	32	42	trichodiene oxygenase (cytochrome P450 58) [Fusarium sporotrichoides]
22389	ENU06183	ANI61C8122:			NAP		g462024	312	91	4.00E-27	42	47	delta(24)-sterol C-methyltransferase [Saccharomyces cerevisiae]
22390	ENU06184	ANI61C6703:	206-229	539-561	NAP		g3695005	350	159	2.00E-38	54	47	(AF038586) pyruvate dehydrogenase kinase isoform 2, PDK2 [Zea mays]
22391	ENU06185	ANI61C4945:	50-73	396-420	NAP		g3282095	199	93	1.00E-18	37	48	(AJ007446) hypothetical protein [Thermotoga neapolitana]
22392	ENU06186	ANI61S920:1.			NAP		g3005587	180	58	0.000000	21	31	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]
22393	ENU06187	ANI61C8511:	64-83	409-429	NAP		g1935000	587	190	5.00E-60	80	75	(Y12314) GTPase [Schizosaccharomyces pombe]
22394	ENU06188	ANI61C7695:	74-93	727-749	NAP		g2094861	234	118	5.00E-26	25	13	(Z95334) rT123.15 protein. [Schizosaccharomyces pombe]
22395	ENU06189	ANI61C7316:	22-47	732-759	NAP		g1666124	417	170	1.00E-41	32	100	(Z82098) hypothetical protein Rv3536c [Mycobacterium tuberculosis]
22396	ENU06190	ANI61C2480:	46-65	781-800	NAP		g1098357	1116	161	4.00E-75	66	43	shk1 gene [Schizosaccharomyces pombe]
22397	ENU06191	ANI61C1054	36-54	804-829	NAP		g1764155	1012	236	1.00E-61	46	46	(U16782) chlorophenol monooxygenase [Ralstonia eutropha]
22398	ENU06192	ANI61S1352:			NAP		g3153821	118	47	0.0001	24	21	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22399	ENU06193	ANI61C5463:	102-126	539-560	NAP		g4107315	225	116	1.00E-25	42	20	(AL035075) conserved hypothetical protein [Schizosaccharomyces pombe]
22400	ENU06194	ANI61C1114			NAP		g1834340	1288	93	2.00E-42	59	15	(Z68904) ATP-binding cassette multidrug transporter [Emmericella nidulans]
22401	ENU06195	ANI61C5207:	37-56	799-818	NAP		g1730102	781	294	6.00E-79	53	84	D-lactate dehydrogenase (D-LDH) [Escherichia coli]
22402	ENU06196	ANI61C7617:	23-44	714-735	NAP		g423973	536	227	7.00E-59	52	36	phenol 2-monooxygenase (EC 1.14.13.7) - jelly fungus (Trichosporon beigeli) []

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22403	ENU06197	ANI61C3223:	102-125	514-536	NAP		g2554598	85	62	0.000000	29	31	(AB000508) poly(3-hydroxybutyrate) depolymerase precursor [Comamonas testosteroni]
22404	ENU06198	ANI61C6564:			NAP		g1351598	408	157	1.00E-37	40	44	hypothetical 59.6 KD protein C4G8.07C in chromosome I [Schizosaccharomyces pombe]
22405	ENU06199	ANI61S826:1.766			NAP		g134769	518	173	1.00E-46	50	59	Stage IV sporulation protein B [Bacillus subtilis]
22406	ENU06200	ANI61C7078:			NAP		g2245428	598	173	5.00E-43	94	15	(U91968) topoisomerase I [Emeticella nidulans]
22407	ENU06201	ANI61C8669:			NAP		g4007795	354	90	3.00E-23			(AL034463) putative nuclear envelope pore membrane protein [Schizosaccharomyces pombe]
22408	ENU06202	ANI61C2274:	100-127	300-327	NAP		g115943	281	128	2.00E-29	51	32	cytochrome C heme lyase (CCHL) (holocytochrome-C synthase) [Neurospora crassa]
22409	ENU06203	ANI61S42:41	48-69	277-303	NAP		g466053	164	95	3.00E-19	38	23	hypothetical 68.7 KD protein ZK757.1 in chromosome III [Caenorhabditis elegans]
22410	ENU06204	ANI61C1077	49-76	807-826	NAP		g1352619	879	146	5.00E-50	73	40	Dihydroliipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex precursor (E2) [Saccharomyces cerevisiae]
22411	ENU06205	ANI61C3628:	72-91	661-680	NAP		g231717	1359	259	1.00E-86	75	36	Minichromosome maintenance protein 5 (cell division control protein 46) [Saccharomyces cerevisiae]
22412	ENU06206	ANI61C2430:	102-127	430-457	NAP		g3261632	375	152	1.00E-36	45	30	(Z79700) accD2 [Mycobacterium tuberculosis]
22413	ENU06207	ANI61C5576:	49-73	809-829	NAP		g3560142	633	109	2.00E-35	34	45	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
22414	ENU06208	ANI61C8479:			NAP		g347455	187	45	0.0003	39	93	(L22030) hydroxyproline-rich glycoprotein [Glycine max]
22415	ENU06209	ANI61C7459:	22-42	528-547	NAP		g4033735	286	156	1.00E-37	50	13	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]
22416	ENU06210	ANI61C1134	46-73	807-829	NAP		g1175452	332	107	1.00E-22	30	25	hypothetical 85.7 KD protein C13G6.03 in chromosome I [Schizosaccharomyces pombe]



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22417	ENU06211	ANI6IS1223:			NAP		g854065	401	49	0.00001	50	26	(X83413) U88 [Human herpesvirus 6]
22418	ENU06212	ANI6IS3220:	157-177	311-331	NAP		g1352438	195	91	5.00E-18	36	38	eukaryotic initiation factor 4A-like protein CIF5.10 [Schizosaccharomyces pombe]
22419	ENU06213	ANI6IC9889:	102-124	366-385	NAP		g112947	150	84	4.00E-16	38	28	AAC-rich MRNA clone AAC3 protein [Dictyostelium discoideum]
22420	ENU06214	ANI6IC8653:			NAP		g4758510	735	195	4.00E-49			H beta 58 homolog [Homo sapiens]
22421	ENU06215	ANI6IC1095	22-48	509-536	NAP		g131782	524	132	1.00E-52	63	13	DNA repair protein RAD50 (153 KD protein) [Saccharomyces cerevisiae]
22422	ENU06216	ANI6IC8033:	22-47	806-829	NAP		g485111	405	159	8.00E-45	42	58	(U00050) similar to enoyl-CoA hydratases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]
22423	ENU06217	ANI6IC9123:	46-65	773-800	NAP		g2493389	136	66	3.00E-10	23	55	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) [Emmericella nidulans]
22424	ENU06218	ANI6IC6123:	22-49	565-585	NAP		g91209	108	43	0.003	38	58	proline-rich protein MP2 - mouse (fragment) []
22425	ENU06219	ANI6IC6470:	22-46	801-828	NAP		g1791305	2018	420	e-143	98	65	(U83489) septin B [Emmericella nidulans]
22426	ENU06220	ANI6IS4337:	36-56	433-452	NAP		g3873862	182	89	2.00E-17	35	30	(Z35595) similar to 4-coumarate-coA ligase; cDNA EST yk455e10.3 comes from this gene; cDNA EST yk455e10.5 comes from this gene; cDNA EST yk286h10.3 comes from this gene; cDNA EST yk286h10.5 comes from this gene [Caenorhabditis ... []
22427	ENU06221	ANI6IS3166:	52-77	481-499	NAP		g3819099	300	127	6.00E-29	51	20	(AJ009825) copper amine oxidase [Cicer arietinum]
22428	ENU06222	ANI6IC1129	37-56	728-749	NAP		g2499576	1347	176	3.00E-89	85	21	protein kinase C-like [Aspergillus niger]
22429	ENU06223	ANI6IC293:1			NAP		g1353167	126	61	0.000000	31	37	hypothetical 30.6 KD protein F52C9.4 in chromosome III [Caenorhabditis elegans]

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22430	ENU06224	ANI61C1386:	42-61	445-464	NAP		g10777342	200	66	1.00E-14	37	54	probable membrane protein YLR284c - yeast (Saccharomyces cerevisiae)
		526..1											[Saccharomyces cerevisiae]
22431	ENU06225	ANI61C1975:	23-42	661-685	NAP		g2342601	1548	166	2.00E-40	36	5	(X89442) peptide synthetase [Metarhizium anisopliae]
		2764..1											[U79756] GTPase cRac1B [Gallus gallus]
22432	ENU06226	ANI61C4494:	54-73	524-546	NAP		g3184512	524	150	8.00E-53	73	77	guanine nucleotide-binding protein alpha-1 subunit (GPI-alpha) [Neurospora crassa]
		772..1419											(AF125451) contains similarity to the NIFR3/SM1 family [Caenorhabditis elegans]
22433	ENU06227	ANI61C3323:	62-89	313-340	NAP		g585175	314	138	2.00E-32	57	33	(AF031194) S276 [Triticum aestivum]
		5084..4724											
22434	ENU06228	ANI61C5753:	202-228	457-482	NAP		g4226107	372	110	7.00E-32	50	27	
		1..504											
22435	ENU06229	ANI61S2462:	24-46	345-372	NAP		g4104056	359	140	6.00E-33	40	38	4-aminobutyrate aminotransferase (gamma-amino-N-butyrate transaminase) (GABA transaminase) (GABA aminotransferase) [Emmericella nidulans]
		1..570											
22436	ENU06230	ANI61C2477:	22-44	799-826	NAP		g120965	2511	473	e-135	99	53	hypothetical LACA/RPIB family protein in SPOIIR-GLYC intergenic region [Bacillus subtilis]
		1677..3344											(AL049608) extensin-like protein [Arabidopsis thaliana]
22437	ENU06231	ANI61S1069:			NAP		g732387	196	77	3.00E-16			"Citrate synthase, mitochondrial precursor [Emmericella nidulans]"
		331..740											hypothetical 49.9 KD protein in SPOI-SIS1 intergenic region [Saccharomyces cerevisiae]
22438	ENU06232	ANI61S769:1.			NAP		g4584539	612			49	36	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
		.859											(Z98762) SPAC4A8.16c, putative nuclear transport protein, len:639aa, similar eg. to YMR309C, NIP1_YEAST, P32497, nuclear transport protein nipl, (812aa), fasta scores, op t:926, E0:0, (34.3% identity in 581 aa overlap), ide... []"
22439	ENU06233	ANI61C6152:	51-69	601-620	NAP		g2493725	869	211	1.00E-84	96	39	
		1..682											
22440	ENU06234	ANI61C6829:	22-43	801-828	NAP		g1730706	583	99	5.00E-20	29	55	
		1799..286											
22441	ENU06235	ANI61C4535:	22-47	782-800	NAP		g1166378	958	114	7.00E-25	32	23	
		2861..1											
22442	ENU06236	ANI61C2280:	24-51	768-795	NAP		g4490654	1064	162	2.00E-72	48	44	
		1536..1											

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22443	ENU06237	ANI61C1032	34-53	561-587	NAP		g1723482	236	125	3.00E-28	37	67	DMA1 protein [Schizosaccharomyces pombe]
22444	ENU06238	ANI61C1064	188-207	624-650	NAP		g1077386	337	82	8.00E-30	40	40	hypothetical protein YLR345w - yeast [Saccharomyces cerevisiae]
22445	ENU06239	ANI61C5085	23-42	716-742	NAP		g730753	1745	249	1.00E-65			[Saccharomyces cerevisiae] chromosome segregation protein SMC2 (DA-BOX protein SMC2) [Saccharomyces cerevisiae]
22446	ENU06240	ANI61C1135	22-48	776-801	NAP		g731834	596	159	2.00E-38	43	60	hypothetical 41.9 KD protein in SDS3-THS1 intergenic region [Saccharomyces cerevisiae]
22447	ENU06241	ANI61C3285	117-136	446-465	NAP		g2623295	174	82	2.00E-16	39	42	(AC002409) hypothetical protein [Arabidopsis thaliana]
22448	ENU06242	ANI61S1082			NAP		g1169440	904	309	7.00E-87	81	5	"dynein heavy chain, cytosolic (DYHC) [Emmericella nidulans]"
22449	ENU06243	ANI61C9181	27-54	728-747	NAP		g2132141	286	80	4.00E-28	43	99	hypothetical protein YOR367w - yeast [Saccharomyces cerevisiae]
22450	ENU06244	ANI61C6586	24-45	723-746	NAP		g2499125	810	150	1.00E-35	28	9	[Saccharomyces cerevisiae] vacuolar protein sorting-associated protein VPS13 [Saccharomyces cerevisiae]
22451	ENU06245	ANI61C1112	32-51	458-481	NAP		g2879853	248	78	1.00E-20	45	36	(AL021815) arginase family protein [Schizosaccharomyces pombe]
22452	ENU06246	ANI61C2339	64-83	301-328	NAP		g1351629	109	90	1.00E-17			hypothetical 18.5 KD protein C12G12.05C in chromosome I [Schizosaccharomyces pombe]
22453	ENU06247	ANI61C4662	109-128	251-278	NAP		g984373	313	134	2.00E-31	65	27	[Schizosaccharomyces pombe] (U32375) tartrate dehydrogenase [Agrobacterium vitis]
22454	ENU06248	ANI61S1794			NAP		g3810866	78	36	0.00006	42	39	(AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
22455	ENU06249	ANI61C9545	100-119	625-644	NAP		g4927212	125	37	0.15			(AF134304) Scar2 [Homo sapiens]
22456	ENU06250	ANI61C9449	25-42	803-823	NAP		g128853	1179	273	4.00E-87	70	62	NADH-ubiquinone oxidoreductase 40 KD subunit precursor (complex I-40KD) (CI-40KD) [Neurospora crassa]
22457	ENU06251	ANI61C1021	22-44	740-767	NAP		g731434	253	126	2.00E-28	37	97	hypothetical 25.1 KD protein in PMID0-PAC2 intergenic region [Saccharomyces cerevisiae]

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22458	ENU06252	ANI61C8628:	102-124	610-637	NAP		g3256848	187	98	8.00E-20	41	78	(AP000002) 219aa long hypothetical protein [Pyrococcus horikoshii]
22459	ENU06253	ANI61C4897:	22-47	636-654	NAP		g1729996	127	62	8.00E-12	32	63	TOXD protein [Cochliobolus carbonum]
22460	ENU06254	ANI61C306:1	22-46	786-810	NAP		g2114323	287	35	0.73	26	32	(D88734) membrane glycoprotein [Equine herpesvirus 1]
22461	ENU06255	ANI61C5208:	31-50	715-738	NAP		g2132688	1499	279	1.00E-74	47	5	probable membrane protein YLR106c - yeast [Saccharomyces cerevisiae]
22462	ENU06256	ANI61C1077	23-42	716-735	NAP		g1945493	1327	109	3.00E-36	44	25	[Saccharomyces cerevisiae] "(U56965) Similar to NAD(P) transhydrogenase, mitochondrial; coded for by C. elegans cDNA yk27c1.5; coded for by C. elegans cDNA yk35b9.5; coded for by C. elegans cDNA yk35b9.3; coded for by C. elegans cDNA yk161c9.3; coded for by C. elegans ... ["] (AL031174) t-complex protein 1 gamma subunit homolog [Schizosaccharomyces pombe] (Z69368) unknown [Schizosaccharomyces pombe] Isoleucyl--TRNA synthetase (isoleucine--TRNA ligase) (ILERS) [Synechocystis sp.] "Ca2+/H+-exchanging protein, vacuolar - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]"
22463	ENU06257	ANI61C8566:	33-60	760-783	NAP		g3393020	965	348	5.00E-95	70	47	(V00618) unidentified reading frame [Escherichia coli] (ACO07584) putative polypeptide [Arabidopsis thaliana] (AC000133) ORF [Emmericella nidulans]
22464	ENU06258	ANI61C9752:	32-59	804-827	NAP		g1182038	583	153	2.00E-36	37	15	probable membrane protein YPR156c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22465	ENU06259	ANI61C7363:	22-46	710-737	NAP		g2501011	986	224	6.00E-58	43	27	
22466	ENU06260	ANI61C1027	22-44	608-630	NAP		g2131201	420	155	3.00E-37	42	55	
22467	ENU06261	ANI61S4372:			NAP		g581280	444	168	5.00E-42	82	85	
22468	ENU06262	ANI61C3636:	22-47	717-744	NAP		g4914370	131	66	1.00E-20			
22469	ENU06263	ANI61C5734:	51-78	696-716	NAP		g1870209	430	59	2.00E-18	34	50	
22470	ENU06264	ANI61C7800:	23-42	714-733	NAP		g2133034	228	95	3.00E-24	31	38	

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22471	ENU06265	ANI6IC2511: 1537..238			NAP		g1351666	1401	129	6.00E-75	66	42	putative ATP-dependent RNA helicase C1F7.02C [Schizosaccharomyces pombe]
22472	ENU06266	ANI6IC6518: 22-49 584..1580		756-782	NAP		g2440082	235	75	9.00E-23	33	31	(Y14849) putative glucose sensor [Kluyveromyces fragilis]
22473	ENU06267	ANI6IC5564: 39-59 137..992		763-782	NAP		g1346390	334	149	2.00E-35	32	31	serine/threonine-protein kinase CLA4 [Saccharomyces cerevisiae]
22474	ENU06268	ANI6IC6853: 120-139 1244..696		496-515	NAP		g1710791	354	118	2.00E-26	48	42	probable mitochondrial 40S ribosomal protein S5 [Schizosaccharomyces pombe]
22475	ENU06269	ANI6IC9440: 50-75 3562..3213		295-314	NAP		g416685	145	61	0.000000	36	36	ATP11 protein precursor [Saccharomyces cerevisiae]
22476	ENU06270	ANI6IC2599: 52-71 580..1		512-531	NAP		g3913432	740	214	5.00E-69	78	25	putative pre-mRNA splicing factor ATP-dependent RNA helicase SPBC16H5.10C [Schizosaccharomyces pombe]
22477	ENU06271	ANI6IC2216: 102-122 1.807		751-777	NAP		g1706440	247	71	1.00E-24	38	39	[Schizosaccharomyces pombe] Spore wall maturation protein DTT1 [Saccharomyces cerevisiae]
22478	ENU06272	ANI6IC6865: 22-49 257..6315		804-827	NAP		g3150262	468	150	2.00E-35	35	80	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
22479	ENU06273	ANI6IC1185: 22-47 3443..1		805-824	NAP		g133356	3156	160	6.00E-75			DNA-directed RNA polymerase III largeST subunit (C160) [Saccharomyces cerevisiae]
22480	ENU06274	ANI6IC4836: 62-81 1040..1		727-749	NAP		g279978	87	80	3.00E-14	24	46	benzoylformate decarboxylase (EC 4.1.1.7) - Pseudomonas putida [ ]
22481	ENU06275	ANI6IC3148: 22-42 1.1073		731-750	NAP		g416574	1638	550	e-156	94	75	probable formate dehydrogenase (NAD-dependent formate dehydrogenase) (FDH) [Emmericella nidulans]
22482	ENU06276	ANI6IC5449: 22-48 1..586		490-517	NAP		g1546072	131	66	2.00E-10	37	5	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22483	ENU06277	ANI6IC8576: 72-91 4984..4375		541-560	NAP		g1705652	369	99	2.00E-34	56	100	20 KD nuclear CAP binding protein (NCBP) (CBP20) [Xenopus laevis]
22484	ENU06278	ANI6IC1081: 22-46 2..1510..3776		763-782	NAP		g1546072	1253	117	8.00E-26	33	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22485	ENU06279	ANI6IC1043: 112-131 8..5637..1		726-749	NAP		g1169440	9561	541	e-153	99	6	"dynein heavy chain, cytosolic (DYHC) [Emmericella nidulans]"

# Database Information

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22486	ENU06280	ANI61C1146:	102-129	636-656	NAP		g1362615	405	204	6.00E-52	43	22	iswi protein - fruit fly (Drosophila melanogaster) [Drosophila melanogaster]
22487	ENU06281	ANI61C9941:	107-127	350-371	NAP		g106185	174	83	1.00E-15	42	53	GTP-binding protein Rab2 - human [Homo sapiens]
22488	ENU06282	ANI61C1081:	30-48	606-625	NAP		g1934645	174	92	3.00E-18	37	97	(U93876) hypothetical protein YrdC [Bacillus subtilis]
22489	ENU06283	ANI61C6360:	115-136	809-828	NAP		g1790870	380	87	2.00E-29	42	97	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni]
22490	ENU06284	ANI61C711:	56-78	373-394	NAP		g2493915	184	90	9.00E-18	41	60	cutinase precursor [Botryotinia fuckeliana]
22491	ENU06285	ANI61S3073:			NAP		g2950476	134	46	0.00009	38	51	(AL022070) vesicle transport v-snare protein [Schizosaccharomyces pombe]
22492	ENU06286	ANI61C2684:	114-133	467-487	NAP		g4506123	243	65	4.00E-21	39	44	pre-mRNA splicing factor similar to S. cerevisiae Prp18 [Homo sapiens]
22493	ENU06287	ANI61C4085:	22-49	809-828	NAP		g2649154	275	123	1.00E-27	31	98	(AE001006) membrane protein [Archaeoglobus fulgidus]
22494	ENU06288	ANI61C861:	22-41	711-730	NAP		g130155	853	162	4.00E-81	56	41	Deoxyribodipyrimidine photolyase (DNA photolyase) (photoreactivating enzyme) [Neurospora crassa]
22495	ENU06289	ANI61C2490:	27-53	807-829	NAP		g3322837	324	51	3.00E-14	31	41	(AE001229) T. pallidum predicted coding region TP0544 [Treponema pallidum]
22496	ENU06290	ANI61C6643:	50-69	802-821	NAP		g2648180	292	98	6.00E-20	34	66	(AE000943) conserved hypothetical protein [Archaeoglobus fulgidus]
22497	ENU06291	ANI61C7691:	22-48	686-708	NAP		g136642	433	131	6.00E-30			Ubiquitin-conjugating enzyme E2-34 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) (cell division control protein 34) [Saccharomyces cerevisiae]
22498	ENU06292	ANI61C6883:	92-111	262-281	NAP		g984373	391	141	2.00E-33	72	31	(U32375) tartrate dehydrogenase [Agrobacterium vitis]
22499	ENU06293	ANI61C4294:	33-52	747-766	NAP		g228477	191			35	50	ECLF2 upstream ORF [saimirine herpesvirus 1]
22500	ENU06294	ANI61C7396:			NAP		g2117306	452	74	1.00E-14	35	39	(Z95620) dna-(apurinic or apyrimidinic site) lyase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22501	ENU06295	AN161C9984: 1..520	126-145	308-330	NAP		g683698	138	74	3.00E-15	29	40	(Z48229) orf1 [Saccharomyces cerevisiae]
22502	ENU06296	AN161C316:5 439..3993	46-65	804-829	NAP		g4499843	327	44	0.001			(AJ011965) oxidoreductase [Claviceps purpurea]
22503	ENU06297	AN161C5121: 1..523	23-50	453-473	NAP		g3891484	142	37	0.0002	35	34	"Chain B, Co-Crystal Structure Of Protein Farnesyltransferase Complexed With A Farnesyl Diphosphate Substrate ["]
22504	ENU06298	AN161C8634: 6707..2925	22-45	796-816	NAP		g538067	2311	123	1.00E-27	33	18	(M77661) putative pol polyprotein [Magnaporthe grisea]
22505	ENU06299	AN161C3333: 1033..1	22-49	705-732	NAP		g3004863	538	113	3.00E-57	50	30	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
22506	ENU06300	AN161C5808: 237..1337	22-46	725-747	NAP		g2209087	897	345	2.00E-94	62	41	(AF000309) putative serine/threonine kinase [Colletotrichum lindemuthianum]
22507	ENU06301	AN161C343:6 77..1	49-76	558-584	NAP		g3914984	143	80	2.00E-14	31	5	Ferrichrome siderophore peptide synthetase [Ustilago maydis]
22508	ENU06302	AN161C1742: 3814..3210	72-93	553-577	NAP		g1652017	201	95	3.00E-19	32	65	(D90901) hypothetical protein [Synechocystis sp.]
22509	ENU06303	AN161C4320: 1455..2587	22-46	805-829	NAP		g1723435	1087	350	6.00E-96	55	18	hypothetical 170.7 KD protein C56F8.02 in chromosome I [Schizosaccharomyces pombe]
22510	ENU06304	AN161C6618: 88..850	49-68	677-699	NAP		g3080522	309	153	1.00E-36	39	36	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
22511	ENU06305	AN161C4435: 20..619	48-69	516-542	NAP		g3913154	319	145	3.00E-34	39	19	beta-galactosidase (lactase) [Enterobacter cloacae]
22512	ENU06306	AN161C8171: 253..1609	23-46	804-828	NAP		g2506360	276	108	5.00E-23	33	34	NPL1 protein (SEC63 protein) [Saccharomyces cerevisiae]
22513	ENU06307	AN161C1086 0:1..554	122-141	500-519	NAP		g729747	411	155	3.00E-37	48	45	Flavohemoprotein (haemoglobin-like protein) (Flavohemoglobin) [Ralstonia eutropha]
22514	ENU06308	AN161C2206: 1..744	222-242	699-719	NAP		g171565	221	113	1.00E-24	35	56	(KO1609) gal10 [Saccharomyces carlsbergensis]
22515	ENU06309	AN161C1729: 1119..1	35-54	730-749	NAP		g1703456	496	128	6.00E-29	43	21	Cation-transporting ATPase PAT1 [Dictyostelium discoideum]
22516	ENU06310	AN161C9369: 2700..1288	22-43	802-820	NAP		g1351635	462	73	4.00E-23	40	70	hypothetical 35.8 KD protein C12G12.12 in chromosome I [Schizosaccharomyces pombe]

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22517	ENU06311	ANI61C8401:	36-55	774-797	NAP		g585255	756	277	7.00E-74	56	49	Histidine biosynthesis bifunctional amidotransferase / cyclase
		355..1384											
22518	ENU06312	ANI61S14:62			NAP		g3114719	542	183	8.00E-57	62	13	[Saccharomyces cerevisiae] (Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
		3..1											
22519	ENU06313	ANI61C6428:	122-141	691-714	NAP		g1345625	322	153	4.00E-46			Biotin--protein ligase (biotin apo-protein ligase) (biotin--[Saccharomyces cerevisiae])
		1..789											
22520	ENU06314	ANI61C8003:			NAP		g140464	594	99	5.00E-20	38	22	hypothetical 107.9 KD protein in POL4-SRD1 intergenic region [Saccharomyces cerevisiae]
		1200..1											
22521	ENU06315	ANI61C1:108			NAP		g1777375	198	92	1.00E-18	46	11	(D78573) aspartate kinase-homoserine dehydrogenase [Oryza sativa]
		2..760											
22522	ENU06316	ANI61C8875:	24-43	809-829	NAP		g2340046	813	334	4.00E-91	51	39	(L48074) secreted dipeptidyl peptidase [Aspergillus fumigatus]
		1..1250											
22523	ENU06317	ANI61C796:1	22-42	709-731	NAP		g406769	921	229	2.00E-59	47	31	(X70694) trehalose-6-phosphate phosphatase [Saccharomyces cerevisiae]
		850..1											
22524	ENU06318	ANI61C8121:	22-47	723-740	NAP		g3121873	483	192	3.00E-48	50	32	Coronin-like protein [Saccharomyces cerevisiae]
		994..1											
22525	ENU06319	ANI61S4368:			NAP		g3687478	213	104	6.00E-22	34	39	(AL031786) putative delta-1-pyrroline-5-carboxylate dehydrogenase [Schizosaccharomyces pombe]
		1..670											
22526	ENU06320	ANI61C7484:	22-42	809-829	NAP		g3879532	213	86	3.00E-16	35	81	(Z49130) cDNA EST EMBL:D74028 comes from this gene; cDNA EST EMBL:D71354 comes from this gene; cDNA EST EMBL:D76320 comes from this gene; cDNA EST yk486c7.3 comes from this gene; cDNA EST yk486c7.5 comes from this gene; cDNA ES... []
		3606..4566											
22527	ENU06321	ANI61C1043	23-50	803-829	NAP		g3560207	234	58	0.000000			(AL031536) fnx1p.
		1:2329..410											[Schizosaccharomyces pombe]
22528	ENU06322	ANI61C4967:	22-48	625-644	NAP		g1389841	559	186	1.00E-58	55	33	(U59303) glucosylase precursor [Aspergillus awamori]
		756..1											
22529	ENU06323	ANI61C1205:	109-128	391-417	NAP		g2956751	205	105	2.00E-22	31	45	(AL022105) hypothetical protein [Schizosaccharomyces pombe]
		513..1											



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22530	ENU06324	ANI61C9687: 69-91		787-808	NAP		g1169870	365	185	3.00E-46	45	56	GCD14 protein [Saccharomyces cerevisiae]
22531	ENU06325	ANI61C8614: 23-48		728-748	NAP		g4557481	325	97	2.00E-23	34	14	Canalicular multispecific organic anion transporter [Homo sapiens] (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]
22532	ENU06326	ANI61C7926: 34-53		808-829	NAP		g932	188	42	0.006			Hypothetical 141.1 KD protein in MET2-SEC2 intergenic region [Saccharomyces cerevisiae]
22533	ENU06327	ANI61C1343: 22-48		755-782	NAP		g1730639	299	136	2.00E-31	31	21	3-phosphatase B precursor (myo-inositol-hexaphosphate 3-phosphohydrolyase B) (3 phytase B) (myo-inositol hexakisphosphate phosphohydrolyase B) [Emericella nidulans]
22534	ENU06328	ANI61C1109 6:561..884	51-70	361-380	NAP		g3914342	175	93	1.00E-18	51	17	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae] (X94769) choline dehydrogenase [Rattus rattus]
22535	ENU06329	ANI61C8939: 22-47		803-829	NAP		g2132443	340	64	0.000000	30	76	hypothetical 72.8 KD protein in AGAI-MTR intergenic region (O678) [Escherichia coli]
22536	ENU06330	ANI61C1065 7:6536..6055	23-42	413-437	NAP		g1154950	153	96	2.00E-19	34	37	"Ankyrin, brain variant 2 (ankyrin B) (ankyrin, nonerythroid) ["] (AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]
22537	ENU06331	ANI61S3435: 38-65		496-518	NAP		g1176816	899	176	1.00E-81	95	28	(U13049) pectate lyase C [Fusarium solani f. sp. pisi]
22538	ENU06332	ANI61C5381: 33-60		709-728	NAP		g231551	262	83	2.00E-28	31	14	hypothetical 20.1 KD protein in RTF1-CSE1 intergenic region [Saccharomyces cerevisiae]
22539	ENU06333	ANI61C6837: 118-136		454-479	NAP		g4007790	151	73	2.00E-13	39	25	putative ATP-dependent RNA helicase C31A2.07C [Schizosaccharomyces pombe]
22540	ENU06334	ANI61C993:8 66..539			NAP		g595570	151	82	2.00E-15	41	54	beta-glucosidase precursor (gentiobiose) (cellobiose) (beta-D-glucoside glucosylhydrolase) [Kluyveromyces marxianus]
22541	ENU06335	ANI61C4542: 23-42		515-534	NAP		g1723978	212	64	1.00E-19			
22542	ENU06336	ANI61C8821: 45-64		747-766	NAP		g1175401	940	371	e-102	66	33	
22543	ENU06337	ANI61C7550: 1..352			NAP		g114971	185	85	2.00E-16	40	13	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22544	ENU06338	ANI61C1577: 1..638	102-126	583-602	NAP	g1169546	177	67	7.00E-13	35	82		putative ER lumen protein retaining receptor C28H8.4 [Caenorhabditis elegans]
22545	ENU06339	ANI61C7523: 3198..2768	65-84	378-397	NAP	g2136261	77	62	0.000000	25	31		tetracycline transporter-like protein - human [Homo sapiens]
22546	ENU06340	ANI61S4287: 259..582	22-48	446-467	NAP	g3941500	153	66	2.00E-10	36	57		(AF062904) putative transcription factor [Arabidopsis thaliana]
22547	ENU06341	ANI61C1023 5:2077..2560	22-45	375-399	NAP	g4539247	196	89	5.00E-19	48	64		(AL049489) putative actin polymerisation complex protein [Schizosaccharomyces pombe]
22548	ENU06342	ANI61C5375: 1536..1	115-134	716-742	NAP	g3929399	896	153	2.00E-36	37	51		proline-specific permease (proline transport protein) [Emericella nidulans]
22549	ENU06343	ANI61C7079: 2167..620			NAP	g549674	832	101	7.00E-42	39	56		hypothetical 49.6 KD protein in ELM1-PR12 intergenic region [Saccharomyces cerevisiae]
22550	ENU06344	ANI61C8750: 1..2178	29-54	790-809	NAP	g3021303	3668	554	e-157	99	12		(Y15996) acetyl-CoA carboxylase [Emericella nidulans]
22551	ENU06345	ANI61C1034 9:5166..8019	22-44	644-663	NAP	g1209391	2070	254	4.00E-67	46	31		(D83659) TPR protein [Schizosaccharomyces pombe]
22552	ENU06346	ANI61C6562: 1021..1			NAP	g3282044	1037	377	e-104	70	19		(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
22553	ENU06347	ANI61C9317: 1151..2158	22-45	803-829	NAP	g4581525	302	117	8.00E-26	34	47		(AL049559) putative short-chain dehydrogenase [Schizosaccharomyces pombe]
22554	ENU06348	ANI61C888:4 328..3784	111-130	412-431	NAP	g3914142	36	38	0.052	25	50		Early nodulin 20 precursor (N-20) [Medicago truncatula]
22555	ENU06349	ANI61C2891: 1..1004			NAP	g2501152	660	222	2.00E-57	53	47		threonine synthase [Schizosaccharomyces pombe]
22556	ENU06350	ANI61C5514: 435..1353	23-42	805-829	NAP	g2956768	664	217	1.00E-55	51	63		(AL022103) transmembrane transporter Itz1p. [Schizosaccharomyces pombe]
22557	ENU06351	ANI61S3594: 561..156			NAP	g2258414	119	52	0.000000	38	54		(AF007873) dolichol monophosphate mannose synthase [Schizosaccharomyces pombe]
22558	ENU06352	ANI61C234:1 575..1	22-42	612-635	NAP	g1077357	1063	124	1.00E-41	61	39		probable membrane protein YLR359w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22559	ENU06353	ANI61C8537: 40-59		712-731	NAP		g409547	239	86	3.00E-20	29	47	(L07492) sugar transport protein [Saccharomyces cerevisiae]
22560	ENU06354	ANI61C5810: 1090..1			NAP		g544232	610	127	9.00E-29	50	59	elongation factor 1-gamma 2 (EF-1-gamma 2) [Saccharomyces cerevisiae]
22561	ENU06355	ANI61C8235: 22-49		786-813	NAP		g731465	818	267	9.00E-83	57	87	putative mitochondrial carrier YER053C [Saccharomyces cerevisiae]
22562	ENU06356	ANI61S1427: 1260..2280			NAP		g110849	161	52	0.000005	31	83	proline-rich protein - mouse [Mus musculus]
22563	ENU06357	ANI61C2541: 1..719	422..1457	741-763	NAP		g2330704	727	249	3.00E-65	49	81	(Z98529) putative transcription initiation factor TFIIIB subunit [Schizosaccharomyces pombe]
22564	ENU06358	ANI61C5404: 1..990		630-650	NAP		g3287946	1040	326	9.00E-89	64	25	putative helicase C6F12.16 in chromosome I [Schizosaccharomyces pombe]
22565	ENU06359	ANI61C8694: 1755..1		639-658	NAP		g3978466	1587	275	2.00E-73	50	37	(AF086822) dihydroxyacetone synthase [Candida boidinii]
22566	ENU06360	ANI61C9257: 1245..1		795-815	NAP		g2414649	827	198	6.00E-50	38	9	(Z99296) hypothetical protein [Schizosaccharomyces pombe]
22567	ENU06361	ANI61C1087 3:876..2793		800-819	NAP		g140474	576	76	4.00E-13			hypothetical 69.2 KD protein in HSP30-PMP1 intergenic region [Schacharomyces cerevisiae]
22568	ENU06362	ANI61C669:1 128..658			NAP		g1722769	225	99	1.00E-20	38	20	Phosphatidylinositol 3-kinase VPS34 (PI3-kinase) (PTDINS-3-kinase) (PI3K) (vacuolar sorting protein 34) [Schizosaccharomyces pombe]
22569	ENU06363	ANI61C1138 6:949..426		477-503	NAP		g4106669	323	120	2.00E-31	56	33	(AL035064) protein kinase skp1p [Schizosaccharomyces pombe]
22570	ENU06364	ANI61C5198: 1013..1		805-825	NAP		g129592	425	188	4.00E-47	45	35	Phenylalanine ammonia-lyase [Rhodotorula mucilaginosa]
22571	ENU06365	ANI61C445:1 ..1246		722-740	NAP		g1708850	684	134	1.00E-49	48	33	probable leukotriene A-4 hydrolase (LTA-4 hydrolase) (leukotriene A(4) hydrolase) [Saccharomyces cerevisiae]
22572	ENU06366	ANI61C7858: 5143..4521		566-585	NAP		g987116	126	52	0.000003	28	99	(X86780) cystathione synthase [Streptomyces hygroscopicus]
22573	ENU06367	ANI61C82:17 60..549		802-829	NAP		g3702638	416	127	1.00E-28	40	61	(AL031825) putative acetylornithine deacetylase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22574	ENU06368	ANI61C1781: 1..537	37-64	400-425	NAP		g1077382	275	133	7.00E-31	41	19	probable membrane protein YLR335w - yeast (Saccharomyces cerevisiae)
22575	ENU06369	ANI61C8774: 290..2421	35-54	802-829	NAP		g3885836	517	45	0.000002			[Saccharomyces cerevisiae]
22576	ENU06370	ANI61C5355: 391..1	40-67	441-468	NAP		g2828151	162	88	5.00E-17	39	41	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
22577	ENU06371	ANI61C1843: 115..525	22-49	458-479	NAP		g3122326	348	163	8.00E-40	50	33	(AF042386) cyclophilin-33B [Homo sapiens]
22578	ENU06372	ANI61C1097 7:4250..5969	27-54	781-806	NAP		g3242972	1836	395	e-109	70	39	LEC14B protein [Lithospermum erythrorhizon]
22579	ENU06373	ANI61C1070 1:1..1037	48-67	791-814	NAP		g4521101	1136	289	e-121	79	75	(AF069523) heat shock protein Hsp88 [Neurospora crassa]
22580	ENU06374	ANI61C1096: 692..161	52-71	464-483	NAP		g1766062	285	125	2.00E-28	42	99	(AB016540) alternative oxidase [Aspergillus niger]
22581	ENU06375	ANI61C9004: 3221..4026	22-41	684-705	NAP		g1077385	325	95	7.00E-19	47	66	(U82218) Ats1 [Schizosaccharomyces pombe]
22582	ENU06376	ANI61C4853: 1709..2856	43-63	782-801	NAP		g522302	1176	360	1.00E-98	63	23	hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae)
22583	ENU06377	ANI61C8573: 7384..7793	37-56	377-399	NAP		g1929333	186	90	1.00E-17	35	66	(L35053) endonuclease [Magnaporthe grisea]
22584	ENU06378	ANI61C9181: 7917..8414	32-51	433-460	NAP		g4115939	407	176	8.00E-44	66	46	(Z93767) ywrf [Bacillus subtilis]
22585	ENU06379	ANI61S1637: 154..690	95-114	296-319	NAP		g1351702	100	61	0.000000	33	31	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850)
22586	ENU06380	ANI61C2866: 491..1	64-82	447-470	NAP		g140371	224	104	4.00E-22	36	29	[Arabidopsis thaliana] hypothetical 61.1 KD protein C11D3.05 in chromosome I
22587	ENU06381	ANI61C1059 9:1..477	22-44	431-452	NAP		g4263825	301	130	5.00E-30	42	12	[Schizosaccharomyces pombe] hypothetical 58.8 KD protein in GLK1-SRO9 intergenic region
22588	ENU06382	ANI61C5967: 8462..9284	22-46	690-717	NAP		g585175	452	104	2.00E-43	47	60	[Saccharomyces cerevisiae] (AC006067) hypothetical protein [Arabidopsis thaliana] guanine nucleotide-binding protein alpha-1 subunit (GPI-alpha) [Neurospora crassa]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22589	ENU06383	AN161C1050 1:1298..7124			NAP		g1491929	10043	316	e-126	98	13	"(U51272) 1,3-beta-D-glucan synthase catalytic subunit [Emmericella nidulans]"
22590	ENU06384	AN161C7768: 29-48 3164..3929		633-652	NAP		g3135013	507	136	1.00E-45	51	26	(AJ005963) 100 kDa protein [Ajellomyces capsulatus]
22591	ENU06385	AN161C1085 3:4930..4464	40-64	422-445	NAP		g1834342	444	175	1.00E-43	60	9	(Z68905) ATP-binding cassette multidrug transporter [Emmericella nidulans]
22592	ENU06386	AN161C2190: 62-81 2788..1		722-741	NAP		g1351615	1732	235	3.00E-61	41	23	hypothetical protein C23D3.15 in chromosome I [Schizosaccharomyces pombe]
22593	ENU06387	AN161C5726: 22-48 1..959		728-749	NAP		g3298291	535	229	9.00E-61	46	52	(AB010389) ALK2 [Yarrowia lipolytica]
22594	ENU06388	AN161C1262: 45-66 524..1		446-465	NAP		g2625138	275	122	2.00E-27	39	10	(AF032443) ABC1 transporter, ABC-type ATPase [Magnaporthe grisea]
22595	ENU06389	AN161C8354: 22-44 1077..1		723-743	NAP		g3861449	420	108	7.00E-23	25	26	(Z98596) SMC-family protein [Schizosaccharomyces pombe]
22596	ENU06390	AN161C5304: 22-49 1..1908		762-780	NAP		g2660670	680	135	4.00E-31	36	22	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
22597	ENU06391	AN161C8656: 22-45 1944..2456		470-492	NAP		g4769004	415	74	5.00E-36			(AF140598) ring-box protein 1 [Homo sapiens]
22598	ENU06392	AN161C3866: 87-105 497..962		439-458	NAP		g1352994	132	78	2.00E-16			hypothetical 30.6 KD protein in SCP160-SMC3 intergenic region precursor [Saccharomyces cerevisiae]
22599	ENU06393	AN161C3152: 185..3464			NAP		g4539277	2340	127	1.00E-28	27	18	(AL049498) myosin II [Schizosaccharomyces pombe]
22600	ENU06394	AN161C6685: 38-57 1..938		717-735	NAP		g3219947	566	244	5.00E-64	52	45	hypothetical 61.8 KD protein C16E8.13 in chromosome I [Schizosaccharomyces pombe]
22601	ENU06395	AN161C1464: 83-108 1183..1		735-762	NAP		g3219304	443	185	4.00E-46	40	30	(AB009461) MUS38 [Neurospora crassa]
22602	ENU06396	AN161C8385: 26-45 1400..3387		771-790	NAP		g1351714	483	83	2.00E-15	33	44	putative transporter C11D3.18C [Schizosaccharomyces pombe]
22603	ENU06397	AN161C1122 5:1..442	22-41	395-421	NAP		g2462931	228	100	5.00E-21	42	20	(Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]
22604	ENU06398	AN161C85:71 4..1	27-46	591-613	NAP		g136753	726	303	1.00E-81			"glycogen (starch) synthase, isoform 1 [Saccharomyces cerevisiae]"

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22605	ENU06399	ANT61C5996: 24-45		791-816	NAP		g4126481	196	100	1.00E-20	29	98	(AB015352) <i>Akt2</i> [ <i>Alternaria alternata</i> ]
22606	ENU06400	5587..4751 ANT61C1158: 63-82		802-829	NAP		g127277	841	254	1.00E-69			mitochondrial phosphate carrier protein (phosphate transport protein) (mitochondrial import receptor) (P32) [ <i>Saccharomyces cerevisiae</i> ]
22607	ENU06401	4:7772..8074 ANT61C1029: 22-41		413-432	NAP		g4468224	84	48	0.00004	21	33	(Y14855) tropomyosin [ <i>Helix aspersa</i> ]
22608	ENU06402	1..970 ANT61C8089: 31-53		767-784	NAP		g117178	147	86	3.00E-16	24	41	benzoate 4-monooxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) [ <i>Aspergillus niger</i> ]
22609	ENU06403	3623..1 ANT61C5229: 22-42		725-744	NAP		g1351684	914	87	2.00E-16			hypothetical 420.8 KD protein CIF5.11C in chromosome I [ <i>Schizosaccharomyces pombe</i> ]
22610	ENU06404	2415..1768 ANT61C1135: 53-72		596-615	NAP		g586531	379	140	1.00E-32	46	98	hypothetical 21.1 KD protein in YMC2-CMD1 intergenic region [ <i>Saccharomyces cerevisiae</i> ]
22611	ENU06405	209..1 ANT61C100: 1 22-48		802-829	NAP		g4388818	256	157	7.00E-38			(AC006528) putative pol polyprotein with a Zn-finger CCHC type domain (prosite:QDOC50158) and a DDE integrase signature motif [ <i>Arabidopsis thaliana</i> ]
22612	ENU06406	7631..6374 ANT61C7675: 24-43		809-829	NAP		g120593	192	57	0.000000			L-fucose permease [ <i>Escherichia coli</i> ]
22613	ENU06407	3..1 ANT61C29: 98 38-57		714-733	NAP		g2132238	370	151	7.00E-36	39	21	hypothetical protein YPL226w - yeast [ <i>Saccharomyces cerevisiae</i> ]
22614	ENU06408	4995..4254 ANT61C7767: 22-46		694-712	NAP		g129072	68	49	0.00003	30	57	pyruvate dehydrogenase protein X component precursor [ <i>Saccharomyces cerevisiae</i> ]
22615	ENU06409	158..1950 ANT61C6108: 22-46		780-799	NAP		g2342601	656	100	2.00E-20	25	5	(X89442) peptidase synthetase [ <i>Metarhizium anisopliae</i> ]
22616	ENU06410	1..2627 ANT61C4919: 59-86		628-648	NAP		g586461	272	112	3.00E-24	32	29	hypothetical 104.7 KD protein in PKC1-RTG3 intergenic region [ <i>Saccharomyces cerevisiae</i> ]
22617	ENU06411	8:402..1302 ANT61C1116: 22-48		793-820	NAP		g1279693	740	287	6.00E-77	70	19	(X92971) translocation elongation factor [ <i>Saccharomyces cerevisiae</i> ]

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22618	ENU06412	ANI61C2633:	66-85	343-362	NAP		g1332941	348	151	3.00E-36	53	36	"branched-chain amino acid aminotransferase, cytosolic (BCAT) (TWT2 protein) [Saccharomyces cerevisiae]"
22619	ENU06413	ANI61C1352:	24-44	298-320	NAP		g1176707	81	52	0.000003	28	51	hypothetical 33.0 KD protein in PROB-PROA intergenic region [Corynebacterium glutamicum]
22620	ENU06414	ANI61C8273:	22-46	804-829	NAP		g1399532	2420	113	2.00E-42	41	24	"(U51118) Neurospora crassa NUC-2 (Nuc-2) gene, complete cds. [Neurospora crassa]"
22621	ENU06415	ANI61C8911:	22-48	641-660	NAP		g3288709	506	193	1.00E-48	46	16	(AB010442) PMR1 [Penicillium digitatum]
22622	ENU06416	ANI61S1445:			NAP		g730030	141	63	0.000000	16	44	micronuclear linker histone polypeptide (MLH) [Tetrahymena thermophila]
22623	ENU06417	ANI61C7533:	22-42	800-827	NAP		g418391	823	328	2.00E-89	56	75	ZRT1 protein [Saccharomyces cerevisiae]
22624	ENU06418	ANI61C9971:	25-43	292-310	NAP		g1655675	73	67	7.00E-11	33	32	(Z81368) hlpK [Mycobacterium tuberculosis]
22625	ENU06419	ANI61C1064	39-66	557-581	NAP		g4176535	417	122	2.00E-38	41	66	(AL035263) putative TFIIF subunit (transcription-repair fac tor) [Schizosaccharomyces pombe]
22626	ENU06420	ANI61C3805:	102-129	413-437	NAP		g1834342	447	186	7.00E-47	53	10	(Z68905) ATP-binding cassette multidrug transporter [Emmentella nidulans]
22627	ENU06421	ANI61C3317:	56-75	397-418	NAP		g3702646	59	41	0.0009	29	27	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
22628	ENU06422	ANI61C6551:	22-46	723-749	NAP		g3834294	156	55	0.000000			(U80846) No definition line found [Caenorhabditis elegans]
22629	ENU06423	ANI61C9287:	30-49	802-829	NAP		g1546072	1848	103	1.00E-21			(U68040) polyketide synthase [Cochliobolus heterostrophus]
22630	ENU06424	ANI61C8021:	51-70	805-829	NAP		g3885836	510	125	4.00E-28	30	43	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
22631	ENU06425	ANI61S2328:	33-52	505-527	NAP		g2497183	573	131	2.00E-60	57	17	hypothetical 126.6 KD protein in RPL39-VTI1 intergenic region [Saccharomyces cerevisiae]
22632	ENU06426	ANI61C5663:	22-46	805-828	NAP		g3395556	131	43	0.000001	31	72	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]

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22633	ENU06427	AN161C7197:	23-46	781-808	NAP		g1170186	1129	316	2.00E-85	53	36	probable ATP-dependent RNA helicase DBP4 (helicase CA4) (helicase UFI1) [Saccharomyces cerevisiae]
		1..1163											
22634	ENU06428	AN161C6444:	24-51	752-775	NAP		g3668171	894	313	1.00E-95	66	22	(AB006052) RNA polymerase I second-largest subunit [Neurospora crassa]
		1..819											
22635	ENU06429	AN161C362:1	22-44	801-828	NAP		g2330871	430	174	2.00E-48	41	29	(Z98603) hypothetical protein [Schizosaccharomyces pombe]
		..1628											
22636	ENU06430	AN161C1027	67-88	727-746	NAP		g1711561	256	50	0.00002			sugar transporter STL1 [Saccharomyces cerevisiae]
		5:2528..4163											
22637	ENU06431	AN161C7202:			NAP		g1709181	680	192	3.00E-48	47	46	high affinity methionine permease [Saccharomyces cerevisiae]
		1217..1											
22638	ENU06432	AN161C3971:	34-53	726-749	NAP		g3150253	605	178	6.00E-44	39	23	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
		1149..1											
22639	ENU06433	AN161C2161:	30-49	802-829	NAP		g3730	1119	197	3.00E-75	54	47	(X53424) glycolipid-anchored surface protein [Saccharomyces cerevisiae]
		3504..5047											
22640	ENU06434	AN161C1116	27-46	728-747	NAP		g131768	541	136	2.00E-31	34	46	quinate permease (quinate transporter) [Emicella nidulans]
		4:1595..1											
22641	ENU06435	AN161C4297:			NAP		g553045	65	47	0.00009	32	64	(M28651) chloroperoxidase [Caldariomyces funago]
		1275..1678											
22642	ENU06436	AN161C1263:	22-49	696-723	NAP		g3810839	375	150	1.00E-35	41	44	(AL032684) conserved hypothetical zinc-finger protein [Schizosaccharomyces pombe]
		1..745											
22643	ENU06437	AN161C8233:	24-43	750-774	NAP		g3947877	540	91	1.00E-54	53	100	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]
		1688..894											
22644	ENU06438	AN161C3897:			NAP		g1799532	211	59	7.00E-17	30	66	(AB000564) salicylate hydroxylase [Sphingomonas sp.]
		1212..2040											
22645	ENU06439	AN161C2901:	22-47	411-433	NAP		g3342802	197	87	5.00E-17	30	31	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]
		1060..607											
22646	ENU06440	AN161C8881:	22-49	725-749	NAP		g2494411	100	37	0.21	28	16	3-(3-hydroxy-phenyl)propionate hydroxylase [Escherichia coli]
		1327..1											
22647	ENU06441	AN161S4274:	35-62	494-519	NAP		g4733982	693	173	3.00E-61			(AC007268) hypothetical protein [Arabidopsis thaliana]
		1..635											
22648	ENU06442	AN161C8550:	51-78	802-821	NAP		g1166378	743	132	2.00E-30	32	25	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
		1..2571											



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22649	ENU06443	ANI61C9556: 7386..8061	36-55	632-651	NAP		g4106657	653	118	5.00E-61	79	50	(AL035064) activator 1 subunit (replication factor subunit) [Schizosaccharomyces pombe]
22650	ENU06444	ANI61C8783: 1.601	122-141	519-538	NAP		g1176982	71	59	0.000000	29	41	hypothetical metabolite transport protein in HTPG-IOLR intergenic region []
22651	ENU06445	ANI61C4477: 1..757	103-130	659-684	NAP		g3702635	288	135	3.00E-31	32	61	(AL031825) hypothetical protein [Schizosaccharomyces pombe]
22652	ENU06446	ANI61C1099: 9:5329..6029	33-52	616-633	NAP		g78100	336	113	2.00E-24	33	37	cyclohexanone monooxygenase (EC 1.14.13.22) - Acinetobacter sp []
22653	ENU06447	ANI61C3891: 1..526	22-45	456-476	NAP		g3183364	236	94	6.00E-19	34	30	putative transporter C1B3.16C [Schizosaccharomyces pombe]
22654	ENU06448	ANI61S2827: 1..628			NAP		g3808062	134	57	0.000000	20	25	(AB019195) PV100 [Cucurbita maxima]
22655	ENU06449	ANI61C6432: 8274..9352	23-45	721-741	NAP		g3928166	346	149	3.00E-35	35	42	(AJ010317) Sand [Fugu rubripes]
22656	ENU06450	ANI61C6774: 1..1713	36-55	789-806	NAP		g461623	350	47	2.00E-10	36	21	beta-galactosidase precursor (lactase) [Aspergillus niger]
22657	ENU06451	ANI61S4263: 1..838			NAP		g4218005	300	45	0.0006	29	38	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
22658	ENU06452	ANI61C1061: 2:790..184	112-131	535-555	NAP		g4049341	99	35	0.52	38	34	(AL034567) putative protein [Arabidopsis thaliana]
22659	ENU06453	ANI61C3499: 2369..2795	22-41	460-479	NAP		g585899	97	56	0.000000	37	100	mitochondrial 60S ribosomal protein L37 precursor (YML37) [Saccharomyces cerevisiae]
22660	ENU06454	ANI61C4192: 4222..3816	153-178	360-386	NAP		g3913969	146	59	2.00E-11	37	28	kynureninase (L-kynurenine hydrolase) [Rattus norvegicus]
22661	ENU06455	ANI61C1912: 1325..348	30-49	785-804	NAP		g1723076	270	80	2.00E-21	35	48	hypothetical 57.3 KD protein GMC-type oxidoreductase CY50.03C [Mycobacterium tuberculosis]
22662	ENU06456	ANI61S1424: 1..649			NAP		g228937	211	37	0.11	34	64	Hyp-rich glycoprotein [Zea mays]
22663	ENU06457	ANI61C3442: 740..2427	50-69	657-675	NAP		g400924	349	101	7.00E-21	24	26	DNA repair protein RAD3 [Schizosaccharomyces pombe]
22664	ENU06458	ANI61C9247: 1..1208	22-41	808-829	NAP		g3139137	592	111	8.00E-24	36	31	(AF063864) essential nuclear protein Mem3p [Schizosaccharomyces pombe]

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22665	ENU06459	ANI61C1877: 1629..1	31-51	716-738	NAP		g3288709	1663	267	8.00E-71	54	17	(AB010442) PMR1 [Penicillium digitatum]
22666	ENU06460	ANI61C1878: 1..362	59-82	314-341	NAP		g3041855	180	85	1.00E-16	34	29	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]
22667	ENU06461	ANI61C7121: 1363..958	35-61	451-478	NAP		g1850540	183	56	0.000000	45	99	(U87806) ribosomal P2 phosphoprotein [Alternaria alternata]
22668	ENU06462	ANI61C1054: 832..1	28-49	700-719	NAP		g3183342	235	73	6.00E-28	38	54	hypothetical 44.5 KD protein C14C4.09 in chromosome I [Schizosaccharomyces pombe]
22669	ENU06463	ANI61C8705: 1..943			NAP		g2213552	369	163	1.00E-39	35	44	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
22670	ENU06464	ANI61C4350: 1..602			NAP		g1174862	141	52	4.00E-14	41	33	putative ubiquitin carboxyl-terminal hydrolase C13A11.04C (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
22671	ENU06465	ANI61C7356: 418..2288	22-48	803-828	NAP		g231993	2396	388	e-107			succinate dehydrogenase (ubiquinone) flavoprotein subunit precursor (FP) (flavoprotein subunit of complex II) [Saccharomyces cerevisiae]
22672	ENU06466	ANI61C2512: 1..919			NAP		g2492798	485	179	9.00E-47	48	62	aryl-alcohol dehydrogenase (NADP+) (AAD) [Phanerochaete chrysosporium]
22673	ENU06467	ANI61S1309: 653..1			NAP		g2959371	670	265	4.00E-72	64	38	(AL022117) asparagine synthetase [Schizosaccharomyces pombe]
22674	ENU06468	ANI61S3208: 594..267	120-141	284-304	NAP		g117820	515	132	4.00E-42	96	50	cytochrome B6 [Spinacia oleracea]
22675	ENU06469	ANI61S3578: 1..612			NAP		g1131489	72	45	0.0005	25	58	"(U42580) Pro-rich protein; PAPK (24X); similar to Triticum PK-rich protein, corresponds to GenBank Accession Number X52472 [Paramecium bursaria Chlorella virus 1]"
22676	ENU06470	ANI61S1366: 1..686			NAP		g283032	153	60	0.000000	33	64	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]

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22677	ENU06471	ANI61C1037	22-48	549-576	NAP		g3914384	686	189	3.00E-71	84	100	probable peroxisomal membrane protein PMP20 (allergen ASP F 3)
		7:1768..1143											[Aspergillus fumigatus]
22678	ENU06472	ANI61C5116:	22-45	640-660	NAP		g117619	121	50	5.00E-10	27	28	choline transport protein
		780..1											[Saccharomyces cerevisiae]
22679	ENU06473	ANI61C1063	136-160	541-560	NAP		g3219959	290	87	1.00E-16	39	34	probable zinc metalloproteinase C17A5.04C precursor
		9:622..1											[Schizosaccharomyces pombe]
22680	ENU06474	ANI61C1118	89-108	730-749	NAP		g2146836	1134	270	7.00E-72	56	32	hypothetical protein YCL054w - yeast
		7:5234..6480											[Saccharomyces cerevisiae]
22681	ENU06475	ANI61C7956:	22-46	617-644	NAP		g3929357	223	87	2.00E-16	37	34	O-methylsterigmatocystin oxidoreductase (OMST)
		752..1											[Saccharomyces cerevisiae]
22682	ENU06476	ANI61C8967:	22-48	802-829	NAP		g1168351	414	76	2.00E-13	38	71	oxidoreductase (cytochrome P450 64)
		4367..3128											[Aspergillus parasiticus]
22683	ENU06477	ANI61S4000:	214-231	401-420	NAP		g1723751	446	80	4.00E-28	72	42	alcohol dehydrogenase (ADH)
		472..1											[Bacillus stearothermophilus]
22684	ENU06478	ANI61C6670:	87-106	380-398	NAP		g4760344	167	49	0.00002			hypothetical 34.9 KD protein in SMI1-PHO81 intergenic region
		1400..1791											[Saccharomyces cerevisiae]
22685	ENU06479	ANI61C2264:	49-68	760-780	NAP		g409547	261	56	2.00E-16	29	47	(AL049769) mitochondrial 60s ribosomal protein 110 precursor
		1412..43											[Schizosaccharomyces pombe]
22686	ENU06480	ANI61C4164:	52-71	662-683	NAP		g1770212	175	81	1.00E-21	29	59	(L07492) sugar transport protein
		1348..2131											[Saccharomyces cerevisiae]
22687	ENU06481	ANI61C1984:			NAP		g3776152	873	195	2.00E-84	62	55	(X99340) nucleic acid binding protein
		1..1014											[Drosophila melanogaster]
22688	ENU06482	ANI61C5698:	189-210	786-813	NAP		g3006179	436	139	2.00E-32	45	32	(AB018537) elongation factor 3
		925..1											[Yarrowia lipolytica]
22689	ENU06483	ANI61C6002:	111-130	295-314	NAP		g118678	462	132	4.00E-46			(AL022304) putative long-chain-fatty-acid--coa ligase [Schizosaccharomyces pombe]
		1831..1443											
22690	ENU06484	ANI61S2737:			NAP		g4836896	198	63	0.000000			dihydroliipoamide dehydrogenase precursor [Saccharomyces cerevisiae]
		1..928											(AC007369) Similar to RNA helicases
22691	ENU06485	ANI61S4388:	64-83	296-315	NAP		g2497956	114	71	4.00E-12	27	40	[Arabidopsis thaliana]
		470..1											molybdopterin biosynthesis MOEA protein [Synechococcus sp.]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22692	ENU06486	ANT61C1404: 1463..496	22-48	629-647	NAP	g729296	180	76	2.00E-13	31	76	76	dihydropicolinate synthase (DHDPS) [Corynebacterium glutamicum]
22693	ENU06487	ANT61C4023: 1..1098	37-56	621-640	NAP	g1352956	1303	381	e-105	68	43	43	hypothetical 75.5 KD protein in CCT3-CCT8 intergenic region [Saccharomyces cerevisiae]
22694	ENU06488	ANT61S3272: 1..462	40-67	391-415	NAP	g2257528	597	209	4.00E-55	70	26	26	(AB004537) methionyl-tRNA synthetase [Schizosaccharomyces pombe]
22695	ENU06489	ANT61C6841: 2213..1178	22-46	803-829	NAP	g231361	910	308	4.00E-83	58	81	81	L-aminocyclopropane-L-carboxylate deaminase (ACC deaminase) [Pseudomonas sp.]
22696	ENU06490	ANT61S2126: 533..63	195-220	405-431	NAP	g1706695	96	34	0.48	26	31	31	phosphomevalonate kinase [Saccharomyces cerevisiae]
22697	ENU06491	ANT61C7863: 2642..1821	107-126	725-744	NAP	g1175491	570	129	4.00E-58	51	82	82	hypothetical 33.9 KD protein C16C9.02C in chromosome I [Schizosaccharomyces pombe]
22698	ENU06492	ANT61C1117: 8..1.497	22-43	360-379	NAP	g1546072	289	118	3.00E-26	40	6	6	(U68040) polyketide synthase [Cochliobolus heterotrophus]
22699	ENU06493	ANT61C9611: 1087..189	22-47	777-804	NAP	g2623175	982	226	2.00E-98	65	67	67	(AF030425) pyruvate dehydrogenase E1 component alpha subunit [Pichia stipitis]
22700	ENU06494	ANT61C4200: 632..1	22-45	508-531	NAP	g3560136	534	138	4.00E-53	54	32	32	(AL031534) 2-isopropylmalate synthase. [Schizosaccharomyces pombe]
22701	ENU06495	ANT61C8517: 541..1	89-108	412-432	NAP	g128862	354	154	4.00E-37	51	55	55	NADH-ubiquinone oxidoreductase 30.4 KD subunit precursor (complex I-30KD) (CI-31KD) []
22702	ENU06496	ANT61C2596: 1435..1	22-44	724-748	NAP	g2388993	693	129	3.00E-29	34	14	14	(Z98981) putative sodium channel [Schizosaccharomyces pombe]
22703	ENU06497	ANT61S3056: 1..536			NAP	g228937	164	53	0.000001	34	53	53	Hyp-rich glycoprotein [Zea mays]
22704	ENU06498	ANT61C2202: 1..1020	57-76	770-789	NAP	g3122099	1167	433	e-121	72	81	81	farnesyl pyrophosphate synthetase (FPP synthetase) (FPPS) (farnesyl diphosphate synthetase) (dimethylallyltransferase / geranyltransferase [Gibberella fujikuroi] (U73900) 2-hydroxybiphenyl-3-monooxygenase [Pseudomonas azelaica]
22705	ENU06499	ANT61C7060: 1..456	43-62	412-435	NAP	g2098616	210	100	7.00E-21	38	25	25	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22706	ENU06500	ANI61C6470:	40-64	801-824	NAP		g2497989	681	212	4.00E-54	49	65	putative mitochondrial carrier YMR166C [Saccharomyces cerevisiae]
22707	ENU06501	ANI61C4397:	45-66	799-818	NAP		g2408036	655	211	5.00E-54	43	67	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
22708	ENU06502	ANI61C7311:	31-52	795-822	NAP		g1345823	910	202	3.00E-51	47	52	nitrate transporter (nitrate permease) [Emmericella nidulans]
22709	ENU06503	ANI61C294:4	28-48	808-827	NAP		g225924	273	51	7.00E-14			uracil transport protein [Saccharomyces cerevisiae]
22710	ENU06504	ANI61C7960:	22-45	780-799	LINAP		g728904	1577	261	3.00E-69	50	22	calcium-transporting ATPase 2 (vacuolar CA2+-ATPase) ; Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae) ; (U03060) calcium ATPase [Saccharomyces cerevisiae] ; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
22711	ENU06505	ANI61C7336:	22-44	790-809	LINAP		g3915140	201	113	2.00E-24	32	45	isotrichoderm C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichoderm C-15 hydroxylase [Fusarium sporotrichoides]
22712	ENU06506	ANI61C3911:	42-61	750-770	LINAP		g464369	220	64	5.00E-16	31	37	phenol 2-monooxygenase (phenol hydroxylase) ; (L04488) phenol hydroxylase [Trichosporon cutaneum]
22713	ENU06507	ANI61C7950:	22-48	680-699	LINAP		g3925779	125	70	1.00E-11	22	41	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
22714	ENU06508	ANI61C9771:	24-45	451-471	LINAP		g549594	41	54	0.000000	33	15	hypothetical 102.5 KD protein in YPT52-DBP7 intergenic region ; hypothetical protein YKR021w - yeast (Saccharomyces cerevisiae) ; (Z28246) ORF YKR021w [Saccharomyces cerevisiae]
22715	ENU06509	ANI61C3160:	22-48	562-581	LINAP		g1582765	59	36	0.31	36	24	YFW1 gene [Saccharomyces cerevisiae]
22716	ENU06510	ANI61C6787:	23-42	671-690	LINAP		g3116145	494	208	3.00E-53	43	41	(AL023290) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	5 pos	Primer 3 pos	Primer	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22717	ENU06511	ANI6IC7358:	30-49	705-730	LINAP	LINAP	g124211	772	34	0.98				translation initiation factor IF-2; (M36878) translational initiation factor IF2 [Streptococcus faecium]
22718	ENU06512	ANI6IC801:8	22-47	752-773	LINAP	LINAP	g4522004	367	164	5.00E-40	37	46		"(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]"
22719	ENU06513	ANI6IC3916:	22-46	776-795	LINAP	LINAP	g2662028	577	166	2.00E-40	35	32		(Z99296) beta-transducin [Schizosaccharomyces pombe]
22720	ENU06514	ANI6IC6734:	23-45	439-458	LINAP	LINAP	g4464201	120	66	2.00E-10	30	24		(AL031587) dJ1039K5.2 (similar to monocarboxylate transporter (MCT3)) [Homo sapiens]
22721	ENU06515	ANI6IC7353:	50-69	790-809	LINAP	LINAP	g3184110	716	87	2.00E-16				(AL023780) putative mma stability protein [Schizosaccharomyces pombe]
22722	ENU06516	ANI6IC9768:	30-57	713-735	LINAP	LINAP	g4249705	449	215	4.00E-55	38	48		(AF101074) step II splicing factor SLU7 [Homo sapiens]
22723	ENU06517	ANI6IC3176:	32-55	781-800	LINAP	LINAP	g4107314	191	61	8.00E-18	29	52		(AL035075) conserved hypothetical SH3 domain-containing protein [Schizosaccharomyces pombe]
22724	ENU06518	ANI6IC7404:	114-133	709-730	LINAP	LINAP	g2388993	644	143	2.00E-33	29	15		(Z98981) putative sodium channel [Schizosaccharomyces pombe]
22725	ENU06519	ANI6IC3918:	28-47	803-829	LINAP	LINAP	g4033414	905	110	1.00E-23	31	24		putative importin beta-4 subunit (karyopherin beta-4 subunit); (AL023780) putative importin beta-4 subunit [Schizosaccharomyces pombe]
22726	ENU06520	ANI6IC6734:	22-48	632-654	LINAP	LINAP	g284667	111	46	0.0002				neurofilament triplet H1 protein - rabbit (fragment); (M94315) neurofilament-H [Oryctolagus cuniculus]
22727	ENU06521	ANI6IC3180:	50-69	798-817	LINAP	LINAP	g2262189	91	64	0.000000				(U56098) FacB [Aspergillus oryzae]
22728	ENU06522	ANI6IC6786:	22-45	314-340	LINAP	LINAP	g2132273	99	59	0.000000				hypothetical protein YPR090w - yeast (Saccharomyces cerevisiae); (U51033) P9513.3 gene product [Saccharomyces cerevisiae]
22729	ENU06523	ANI6IC7390:	31-50	809-828	LINAP	LINAP	g2388994	1466	235	2.00E-62	54	46		(Z98981) hypothetical gtp-binding protein associated [Schizosaccharomyces pombe]
22730	ENU06524	ANI6IC8005:	66-85	791-810	LINAP	LINAP	g2465159	1080	231	6.00E-60	46	38		[Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22731	ENU06525	ANI61C378:4	22-46	550-569	LINAP		g2271503	90	57	0.000000	26	46	(AF009672) unknown [Acinetobacter sp. ADP1]
22732	ENU06526	ANI61C6790:567..5166			LINAP		g2688966	748	275	2.00E-73	51	46	(AF027979) carnitine acetyl transferase [Magnaporthe grisea]
22733	ENU06527	ANI61C7416:1..979	38-57	805-829	LINAP		g728850	107	53	0.000003			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] "
22734	ENU06528	ANI61C7393:4538..3586	22-46	785-804	LINAP		g547769	561	177	7.00E-44	44	54	KES1 protein ; KES1 protein - yeast (Saccharomyces cerevisiae) ; (U03913) Kes1p [Saccharomyces cerevisiae] ; (U43703) Kes1p [Saccharomyces cerevisiae] ; (Z73501) ORF YPL145c [Saccharomyces cerevisiae] ; (X96770) P2614 product [Saccharomyces cerevisiae]
22735	ENU06529	ANI61C9798:2257..1	22-45	734-761	LINAP		g522302	1289	182	3.00E-45	40	23	(L35053) endonuclease [Magnaporthe grisea]
22736	ENU06530	ANI61C3204:1281..1	22-42	679-706	LINAP		g1169871	1040	120	4.00E-65	65	29	GCN20 protein ; GCN20 protein - yeast (Saccharomyces cerevisiae) ; (U19971) Gen20p [Saccharomyces cerevisiae] ; (D50617) YFR009W [Saccharomyces cerevisiae]
22737	ENU06531	ANI61C6807:364..1149	22-45	727-748	LINAP		g4499840	209	93	2.00E-18	33	7	(AJ011964) d-lysergyl-peptide-synthetase [Claviceps purpurea]
22738	ENU06532	ANI61C9792:1991..1121	22-45	762-781	LINAP		g3738149	190	36	0.27			(AL031852) conserved protein-PHD-finger family [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat ncbi gi	Score 68	Blast Score 51	Blast Prob 0.000007	% id	% cvrg	Description
22739	ENU06533	ANI61C6772:	54-73	627-647	LINAP		g3877858	68	51	0.000007			(Z34801) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans]; (Z66514) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans] (AB010810) phospholipase D [Candida albicans] (U89352) lysophospholipase I [Mus musculus]; (U97148) calcium-independent phospholipase A2 isoform 2 [Oryctolagus cuniculus] hypothetical 30.9 KD protein K07C11.7 in chromosome V; (U53336) coded for by C. elegans cDNA cm12g2; coded for by C. elegans cDNA yk56a6.5; coded for by C. elegans cDNA yk70a12.5; coded for by C. elegans cDNA cm11d9; coded for by C. elegans cDNA yk102d1.5; coded for by C. elegans cDNA yk102d1.3;...
22740	ENU06534	ANI61C8028:	113-132	569-588	LINAP		g3413518	711	291	4.00E-78	68	11	
22741	ENU06535	ANI61C8042:	23-42	775-794	LINAP		g1864159	214	85	7.00E-19	33	91	
22742	ENU06536	ANI61C3954:	102-128	421-440	LINAP		g3025256	118	67	1.00E-10	37	39	
22743	ENU06537	ANI61C8012:	48-67	456-479	LINAP		g3650394	77	52	0.000003	30	61	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe] (Z99165) protein kinase [Schizosaccharomyces pombe] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe] (U23517) similar to ubiquitin conjugating enzyme [Caenorhabditis elegans]
22744	ENU06538	ANI61C7420:	22-49	773-796	LINAP		g2408067	860	280	8.00E-75	50	44	(AL035076) putative allantoinase [Schizosaccharomyces pombe]
22745	ENU06539	ANI61C805:8	22-42	803-829	LINAP		g2462679	138	66	4.00E-10	24	26	
22746	ENU06540	ANI61C7418:	105-124	363-381	LINAP		g746510	310	144	3.00E-34	48	48	
22747	ENU06541	ANI61C3955:	27-46	519-538	LINAP		g4107287	320	85	5.00E-36	43	39	



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22748	ENU06542	ANI61C7422:	25-44	486-508	LINAP		g731584	125	41	0.007			hypothetical 17.1 KD protein in PUR5 3region ; hypothetical protein YHR217c - yeast (Saccharomyces cerevisiae) ; (U00029) Yhr217cp [Saccharomyces cerevisiae] (Z95397) unknown
22749	ENU06543	ANI61C3946:	24-51	803-829	LINAP		g2104460	359	124	7.00E-28	34	25	[Schizosaccharomyces pombe] (U95159) gelsolin-related protein GRP125 [Dictyostelium discoideum] (AF091042) putative cercosporin transporter [Cercospora kikuchii] (U74380) cholinesterase 1 [Branchiostoma floridae] (U78523) histidine secretory acid phosphatase [Leishmania donovani] (AB010810) phospholipase D [Candida albicans]
22750	ENU06544	ANI61C9800:	41-68	648-669	LINAP		g4100186	110	43	0.002			probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emmericella nidulans]
22751	ENU06545	ANI61C3970:	34-61	722-744	LINAP		g3885836	333	156	2.00E-37	36	45	sperm histone P2 precursor (protamine P2) ; protamine P2 - rhesus macaque ; (X71338) Protamine P2 [Macaca mulatta] (AF055904) acetylornithine deacetylase; ArgE [Myxococcus xanthus]
22752	ENU06546	ANI61C3143:	35-54	810-829	LINAP		g3435078	362	154	8.00E-43	40	46	amino-acid permease INDA1 ; INDA1 protein - fungus (Trichoderma harzianum) ; (Z22594) INDA1 [Trichoderma harzianum]
22753	ENU06547	ANI61C3210:	22-46	516-543	LINAP		g2058526	63	40	0.009			probable oxygenase - Streptomyces fradiae ; (X87093) putative oxygenase [Streptomyces fradiae]
22754	ENU06548	ANI61C8088:	108-127	801-820	LINAP		g3413518	467	94	2.00E-35	38	14	
22755	ENU06549	ANI61C7429:	31-49	465-485	LINAP		g2493391	303	145	2.00E-34	43	38	
22756	ENU06550	ANI61C397:1	22-48	739-758	LINAP		g462350	324	33	2.3			
22757	ENU06551	ANI61C3228:	50-69	492-512	LINAP		g3044087	217	94	1.00E-18			
22758	ENU06552	ANI61C9804:	41-60	417-438	LINAP		g462414	320	135	2.00E-31	52	23	
22759	ENU06553	ANI61C7396:	22-44	806-827	LINAP		g1076090	349	139	2.00E-32	33	54	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22760	ENU06554	ANI61C3230:	69-87	625-649	LINAP		g1730591	132	76	2.00E-13			hypothetical 41.1 KD protein ON CDC91-PAU4 intergenic region ; hypothetical protein YLR460c - yeast (Saccharomyces cerevisiae) ; (U22383) Ylr460cp [Saccharomyces cerevisiae] hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
22761	ENU06555	ANI61C9803:	22-49	806-829	LINAP		g586486	328	71	2.00E-26	32	38	"(AL031540) internalin - related, Leucine rich repeat containing protein [Schizosaccharomyces pombe] " (AB010466) multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1) [Rattus norvegicus] ; (U73038) multidrug resistance-associated protein 6 [Rattus norvegicus]
22762	ENU06556	ANI61C3999:	122-141	264-289	LINAP		g3581887	70	48	0.00002			(AL035637) glycoprotein endopeptidase-like protein. [Schizosaccharomyces pombe] (AL031179) importin beta subunit [Schizosaccharomyces pombe]
22763	ENU06557	ANI61C3208:	22-47	794-813	LINAP		g3242458	382	111	2.00E-36	38	15	cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]
22764	ENU06558	ANI61C9820:			LINAP		g4481949	149	63	7.00E-11	44	33	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
22765	ENU06559	ANI61C7446:	27-54	650-669	LINAP		g3395584	843	229	2.00E-59	42	25	
22766	ENU06560	ANI61C318:5	23-50	792-819	LINAP		g1706177	210	110	1.00E-23	26	28	
22767	ENU06561	ANI61C9777:	22-46	810-829	LINAP		g2507070	253	51	0.000009			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22768	ENU06562	ANI61C7436: 458..1	125-152	437-464	LINAP		g2499507	211	46	0.000000	32	28	"6-phosphofructo-2-kinase / fructose-2,6-bisphosphatase liver isozyme (6PF-2-K/FRU-2,6-P2ASE) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46) - chicken ; (S54076) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase [chickens, liver, Peptide, 469 aa] [Gallus gallus] "
22769	ENU06563	ANI61C318:3 444..2978	50-77	454-479	LINAP		g2764632	651	233	8.00E-61	73	73	(AJ001520) 19.3kD iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]
22770	ENU06564	ANI61C9796: 7361..6942	22-48	453-472	LINAP		g2149953	141	56	9.00E-18	39	10	(U97066) sulfonyleurea receptor 2B [Mus musculus]
22771	ENU06565	ANI61C3216: 1375..803	28-47	515-534	LINAP		g2894086	118	65	5.00E-10	38	36	(Y11395) seven transmembrane-domain protein [Homo sapiens]
22772	ENU06566	ANI61C4015: 1923..1370	64-83	494-513	LINAP		g2414599	74	52	0.000004	32	38	(Z99295) dihydrofolate reductase [Schizosaccharomyces pombe]
22773	ENU06567	ANI61C7419: 2705..1866	22-44	783-810	LINAP		g133323	68	63	0.000000	003		DNA-directed RNA polymerase II largest subunit (RPB1) ; DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - Chinese hamster (fragment) ; (M19538) RNA polymerase II largest subunit [Cricetus griseus]
22774	ENU06568	ANI61C7451: 1913..2465			LINAP		g2347100	423	136	3.00E-33	40	50	(U76846) ubiquitin-specific protease [Arabidopsis thaliana] ; (AC007168) putative ubiquitin-specific protease [Arabidopsis thaliana]
22775	ENU06569	ANI61C3238: 942..1	81-100	715-737	LINAP		g1077530	263	96	4.00E-24	32	48	hypothetical protein YDR132c - yeast (Saccharomyces cerevisiae) ; (Z48179) unknown [Saccharomyces cerevisiae]
22776	ENU06570	ANI61C3257: 1104..339	53-72	715-734	LINAP		g3914096	214	116	2.00E-25	38	24	NA(+)/H(+)-antiporter 2 : (AB010106) Zsod22p [Zygosaccharomyces rouxii]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22777	ENU06571	ANI61C7427: 5672..3569	41-60	769-788	LINAP		g549627	997	127	1.00E-28	39	37	hypothetical 83.6 KD protein in CCP1-MET1 intergenic region ; hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae) ; (Z28292) ORF YKR067w [Saccharomyces cerevisiae]
22778	ENU06572	ANI61C4052: 1755..251	26-46	802-829	LINAP		g1351681	479	141	5.00E-33	36	31	heat shock protein 70 homolog precursor ; (Z68136) unknown [Schizosaccharomyces pombe]
22779	ENU06573	ANI61C8108: 3842..3264	102-127	532-558	LINAP		g2924313	226	124	5.00E-28	35	18	"(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]"
22780	ENU06574	ANI61C4051: 326..1	37-63	453-475	LINAP		g3915154	70	47	0.00007			trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4-fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
22781	ENU06575	ANI61C3252: 2449..1630	32-51	765-792	LINAP		g3093476	306	157	7.00E-38	33	31	(AF008915) EVI-5 homolog [Homo sapiens]
22782	ENU06576	ANI61C7454: 2674..2011	22-48	617-642	LINAP		g2981475	108	74	1.00E-15	31	60	(AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica]
22783	ENU06577	ANI61C7447: 1052..2869	22-46	809-829	LINAP		g549738	610	158	4.00E-38	33	45	hypothetical amino-acid permease in STE3-GIN10 intergenic region ; probable transport protein YKL174c - yeast (Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28174) ORF YKL174c [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
22784	ENU06578	ANI61C4067: 17..1066	24-43	803-829	LINAP		g3116134	379	141	6.00E-33	36	10	(AL023288) hypothetical protein [Schizosaccharomyces pombe]
22785	ENU06579	ANI61C3274: 1629..2588	35-55	801-820	LINAP		g3006175	524	196	2.00E-49	39	53	(AL022305) putative transcription factor [Schizosaccharomyces pombe]
22786	ENU06580	ANI61C4055: 308..670	66-85	454-473	LINAP		g1073049	70	69	1.00E-11	28	36	salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida ; (X83926) salicylate 1-monoxygenase [Pseudomonas putida]
22787	ENU06581	ANI61C3287: 865..1187	22-48	459-478	LINAP		g4581773	111	62	0.000000	32	24	(AF110766) transcription factor AFLR [Aspergillus parasiticus]

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22788	ENU06582	ANI6IC815:1	22-49	776-802	LINAP		g2497523	820	260	1.00E-68	50	16	kinesin-like protein KIF1A (axonal transporter of synaptic vesicles) ; (X90840) axonal transporter of synaptic vesicles [Homo sapiens] (AB017641) polyketide synthase [Micromonospora griseorubida] (AL035161) putative secreted peptidase [Streptomyces coelicolor] probable phosphatidylinositol-4-phosphate 5-kinase FAB1 (1-phosphatidylinositol-4-phosphate kinase) (P1P5K) (PTDINS(4)P-5-kinase) (diphosphoinositide kinase) ; (U01017) Fab1p [Saccharomyces cerevisiae]
22789	ENU06583	ANI6IC4055: 25-48		724-747	LINAP		g4586928	757	263	9.00E-70	43	6	(AL033534) serine-rich protein [Schizosaccharomyces pombe] (U97191) similar to nucleoporins [Caenorhabditis elegans] "(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus] " (M63836) beta-glucuronidase [Mus musculus]
22790	ENU06584	ANI6IC8073: 32-58		552-572	LINAP		g4154074	76	56	0.000000	36	27	(U89492) arylsulfatase [Neurospora crassa] (AF033013) Notch homolog [Bombyx mori] (AF116463) unknown [Streptomyces lincolnensis] (AF027979) carnitine acetyl transferase [Magnaporthe grisea] (AL035075) putative transcription factor tftiib component [Schizosaccharomyces pombe] erythrocyte ankyrin [Homo sapiens]
22791	ENU06585	ANI6IC3281: 40-59		811-829	LINAP		g462047	759	225	4.00E-58	36	12	(AC006284) putative ankyrin [Arabidopsis thaliana]
22792	ENU06586	ANI6IC7469: 102-127		415-441	LINAP		g3873550	95	41	0.004			
22793	ENU06587	ANI6IC4090: 69-87		500-519	LINAP		g1943773	94	47	0.00008	34	22	
22794	ENU06588	ANI6IC814: 67-86		740-759	LINAP		g2246532	148	60	0.000000	20	24	
22795	ENU06589	ANI6IC329:1			LINAP		g193723	458	59	2.00E-21	33	41	
22796	ENU06590	ANI6IC7490: 27-54		729-749	LINAP		g2873363	841	237	8.00E-62	47	39	
22797	ENU06591	ANI6IC817:1	22-45	459-478	LINAP		g2654086	167	57	0.000000			
22798	ENU06592	ANI6IC409:4	117-135	517-536	LINAP		g4455041	77	33	1.4			
22799	ENU06593	ANI6IC8142: 22-41		463-485	LINAP		g2688966	449	130	8.00E-30	68	24	
22800	ENU06594	ANI6IC7484: 116-135		379-402	LINAP		g4107317	222	104	4.00E-22	38	27	
22801	ENU06595	ANI6IC814:1			LINAP		g226788	86	64	3.00E-10	41	5	
22802	ENU06596	ANI6IC411:6			LINAP		g4335756	99	65	3.00E-10	30	66	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat ncbi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
22803	ENU06597	ANI61C814:5	23-50	796-823	LINAP	g2342601	805	100	3.00E-34	33	5		(X89442) peptide synthetase [Metarhizium anisopliae]
22804	ENU06598	ANI61C4133: 1..502	92-111	456-479	LINAP	g557084	78	56	0.000000	32	10		(L35601) ankyrin [Drosophila melanogaster] ; ankyrin [Drosophila melanogaster]
22805	ENU06599	ANI61C7512: 1..828	48-74	770-789	LINAP	g3859678	398	185	3.00E-46	36	30		(AL033503) conserved hypothetical protein [Candida albicans]
22806	ENU06600	ANI61C3310: 1328..712	22-43	541-560	LINAP	g2791489	156	70	1.00E-14	38	36		(AL021246) hypothetical protein Rv2449c [Mycobacterium tuberculosis]
22807	ENU06601	ANI61C3306: 1895..310	22-48	806-829	LINAP	g1546072	714	129	2.00E-50	45	10		(U68040) polyketide synthase [Cochliobolus heterostrophus]
22808	ENU06602	ANI61C4133: 2028..1713			LINAP	g730197	54	43	0.0005	31	18		protein N-terminal amidase (NT-amidase) ; amino-terminal amidase NTA1 - yeast (Saccharomyces cerevisiae) ; (L35564) N-terminal amidase [Saccharomyces cerevisiae] ; (Z49562) ORF YJR062c [Saccharomyces cerevisiae] ; (L47993) ORF YJR062c [Saccharomyces cerevisiae]
22809	ENU06603	ANI61C8187: 409..1	29-48	460-479	LINAP	g2497685	51	55	0.000000		2		platelet-activating factor acetylhydrolase precursor (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetylgllyceroph... ; (U34246) plasma PAF acetylhydrolase [Canis familiaris] ; platelet-activating factor acetylhydrolase [Canis familiaris]
22810	ENU06604	ANI61C413:1 205..1889	49-68	612-631	LINAP	g3153851	236	94	1.00E-27	41	38		(AF064524) carboxylesterase [Anisopteromalus calandrae]
22811	ENU06605	ANI61C8185: 1..715	107-126	672-693	LINAP	g1352321	561	137	9.00E-32	45	57		ubiquitin-like protein DSK2 ; (L40587) ubiquitin-like protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22812	ENU06606	ANT61C8180:	25-51	805-827	LINAP		g4522026	74	40	0.018			"(AC004886) C-terminus matches KIAA0559, N-terminus similar to Basoon protein; match to P1D:g3043642; similar to P1D:g3413810 [Homo sapiens]" unknown ; (AF072250) methyl-CpG binding protein MBD4 [Homo sapiens] ; (AF114784) methyl-CpG binding endonuclease [Homo sapiens] probable membrane protein YPR022c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] putative polypeptide hydroxylase
22813	ENU06607	ANT61C7516:	24-51	427-447	LINAP		g4505121	160	78	1.00E-15	39	22	
22814	ENU06608	ANT61C4132:	37-56	671-690	LINAP		g1084945	282	99	1.00E-28	35	19	
22815	ENU06609	ANT61C7536:	43-62	380-399	LINAP		g729786	170	89	2.00E-17	31	28	(AL031907) putative cystine-rich transcriptional regulator [Schizosaccharomyces pombe]
22816	ENU06610	ANT61C8186:	22-47	589-614	LINAP		g3766365	454	212	3.00E-54	44	20	(AL035592) hypothetical protein [Schizosaccharomyces pombe]
22817	ENU06611	ANT61C7535:	44-62	566-591	LINAP		g4538674	132	70	2.00E-13	34	81	hypothetical 78.3 KD protein in R1P1-URA3 intergenic region ; hypothetical protein YEL023c - yeast (Saccharomyces cerevisiae) ; (U18530) Yel023cp [Saccharomyces cerevisiae]
22818	ENU06612	ANT61C4134:	51-70	790-815	LINAP		g731409	264	124	6.00E-28	39	36	sexual differentiation process protein ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe) ; (D14064) ORF [Schizosaccharomyces pombe]
22819	ENU06613	ANT61C8218:	34-53	447-466	LINAP		g729862	120	64	3.00E-10	32	27	homolog of yeast Rael (Bharathi) mRNA-associated protein of 41 kDa (Kraemer) ; MRNA-associated protein MRNP41 (RAE1 protein homolog) ; (U84720) mRNA export protein [Homo sapiens]
22820	ENU06614	ANT61C4168:	38-58	429-449	LINAP		g4506399	222	32	3.4			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22821	ENU06615	ANI61C7519:	23-44	802-829	LINAP		g2132156	336	150	2.00E-35	36	45	hypothetical protein YPL030w - yeast (Saccharomyces cerevisiae) ; (U36624)
		6109..4986											Lpb1p [Saccharomyces cerevisiae] (AJ005273) Kin17 [Homo sapiens]
22822	ENU06616	ANI61C4155:	22-47	804-829	LINAP		g3850704	443	94	1.00E-40	44	59	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] ; (U39847) AO66 ankyrin [Caenorhabditis elegans]
22823	ENU06617	ANI61C7554:	102-128	458-477	LINAP		g1208874	66	57	0.000000	33	8	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] ; (U39847) AO66 ankyrin [Caenorhabditis elegans]
		1674..2564											(AL031349) zinc-finger protein [Schizosaccharomyces pombe]
		53..499											(AB014768) chitinase [Aeromonas sp. 10S-24]
22824	ENU06618	ANI61C8221:	33-53	426-445	LINAP		g3451460	72	48	0.000002	26	25	hypothetical 83.0 KD protein in ATP1-ROX3 intergenic region ; hypothetical protein YBL097w - yeast (Saccharomyces cerevisiae) ; (X79489) C-728 protein [Saccharomyces cerevisiae] ; (Z35858) ORF YBL097w [Saccharomyces cerevisiae]
22825	ENU06619	ANI61C8238:	22-48	809-829	LINAP		g4115619	254	32	5.3			(AJ011964) d-lysergyl-peptide-synthetase [Claviceps purpurea] (U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans]
		1..1254											(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
22826	ENU06620	ANI61C412:5	24-48	808-828	LINAP		g586455	784	73	3.00E-12	37	15	"(AL031525) RNA binding protein, puntilio-family [Schizosaccharomyces pombe]"
		746..3420											probable chitin biosynthesis protein C6G9.12 (CHS5 homolog) ; (Z81317) yeast chs5 homolog [Schizosaccharomyces pombe]
22827	ENU06621	ANI61C4161:	29-48	799-823	LINAP		g4499840	1058	109	3.00E-23	35	8	
		1..2181											
22828	ENU06622	ANI61C8239:	22-44	745-765	LINAP		g1086900	178	86	2.00E-21	37	72	
		1534..748											
22829	ENU06623	ANI61C4153:	24-51	441-460	LINAP		g3551484	107	38	0.046			
		1988..2361											
22830	ENU06624	ANI61C4153:	56-75	765-784	LINAP		g4539278	117	82	5.00E-15	24	20	
		3043..4469											
22831	ENU06625	ANI61C825:1	22-47	726-745	LINAP		g3560162	674	276	1.00E-73	54	34	
		714..2502											
22832	ENU06626	ANI61C8266:	59-78	795-814	LINAP		g2842702	544	228	4.00E-59	44	45	
		10..898											



# Sequence Alignment

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22833	ENU06627	ANI61C4186:	119-138	452-473	LINAP		g1175456	119	78	3.00E-14	34	29	hypothetical 60.5 KD protein C13G6.08 in chromosome I ;
		448..1											hypothetical protein SPAC13G6.08 - fission yeast (Schizosaccharomyces pombe) ; (Z54308) putative cdc protein [Schizosaccharomyces pombe] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum] "
22834	ENU06628	ANI61C4107:	25-46	796-817	LINAP		g2924313	956	107	1.00E-29	49	18	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ;
		1..1585											probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22835	ENU06629	ANI61C8222:	22-46	805-829	LINAP		g1723918	178	62	1.00E-10	30	20	(L42758) proteinase [Streptomyces lividans] ; (AL035636) proteinase [Streptomyces coelicolor]
		3752..4677											(Z83857) ppsc [Mycobacterium tuberculosis]
22836	ENU06630	ANI61C8252:	23-44	661-680	LINAP		g940303	309	111	5.00E-24	29	51	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium ; (D83643) polyketide synthase [Colletotrichum lagenarium] (AB018274) KIAA0731 protein [Homo sapiens]
		1012..1											(U97407) strong similarity to the ATP-binding transport protein family (ABC transporters) [Caenorhabditis elegans] (AC004561) putative glutathione S-transferase [Arabidopsis thaliana]
22839	ENU06633	ANI61C8283:	68-87	231-250	LINAP		g3882183	89	66	1.00E-10	35	9	suppressor of RNA polymerase B SRB4 ; RNA polymerase II suppressor protein SRB4 - yeast (Saccharomyces cerevisiae) ; (L12026) SRB4 [Saccharomyces cerevisiae] ; (U18778) Srb4p: transcription factor [Saccharomyces cerevisiae]
		1208..897											(Z99162) hypothetical protein [Schizosaccharomyces pombe]
22840	ENU06634	ANI61C4234:	122-147	308-330	LINAP		g1943844	201	101	3.00E-21	50	8	
		1..351											
22841	ENU06635	ANI61C4240:	72-91	423-441	LINAP		g3980387	59	57	0.000000			
		2166..1839								1			
22842	ENU06636	ANI61C4216:	22-42	484-509	LINAP		g417806	107	66	2.00E-10	28	22	
		4493..5022											
22843	ENU06637	ANI61C8298:			LINAP		g2408014	288	68	3.00E-11	40	22	
		941..481											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22844	ENU06638	ANI61C4252:	26-53	416-443	LINAP		g3688380	379	147	5.00E-35	51	26	(AJ006267) ClpX-like protein [Homo sapiens]
22845	ENU06639	1694..2273 ANI61C8280:	26-45	603-622	LINAP		g3953466	201	73	3.00E-27	34	28	(AC002328) F20N2.11 [Arabidopsis thaliana]
22846	ENU06640	2187..1518 ANI61C4233:	47-66	803-829	LINAP		g3004489	351	100	1.00E-34	43	75	(AJ223304) geranylgeranyl transferase type I [Schizosaccharomyces pombe]
22847	ENU06641	2205..1278 ANI61C4220:	22-42	806-829	LINAP		g1351690	216	104	8.00E-22	24	47	hypothetical 63.5 KD protein C3H1.06C in chromosome I ; (Z68144) putative major facilitator superfamily transporter [Schizosaccharomyces pombe]
22848	ENU06642	5089..6046 ANI61C8282:	67-86	772-795	LINAP		g3451312	1627	126	3.00E-42	45	17	(AL031324) membrane atpase [Schizosaccharomyces pombe]
22849	ENU06643	3721..358 ANI61C8303:	41-60	414-438	LINAP		g3879389	147	78	3.00E-14	50	9	(Z83123) Similarity to S.pombe ATP-dependent DNA helicase (SW:Q09811); cDNA EST EMBL:DJ27628 comes from this gene; cDNA EST CEMSC83FB comes from this gene; cDNA EST EMBL:D35012 comes from this gene; cDNA EST yk398a1.3 comes from...
22850	ENU06644	1..1707 ANI61C4272:	36-55	796-813	LINAP		g4007734	256	44	0.001			(AL034447) putative transmembrane protein [Streptomyces coelicolor]
22851	ENU06645	2006..2485 ANI61C8296:			LINAP		g88462	162	37	0.00001	31	70	"proline-rich phosphoprotein (gene PRH1, Db allele) - human "
22852	ENU06646	3055..2585 ANI61C4276:	46-65	414-433	LINAP		g4505829	108	76	2.00E-13	32	21	gene from NF2/meningioma region of 22q12 ; gene anonymous protein - human ; (L18972) anonymous [Homo sapiens]
22853	ENU06647	1038..686 ANI61C8291:	23-42	457-479	LINAP		g116415	147	79	2.00E-14	37	8	Cubitus interruptus dominant protein ; DNA-binding protein ci (D) - fruit fly (Drosophila melanogaster) ; (X54360) cld product [Drosophila melanogaster]
22854	ENU06648	802..489 ANI61C4283:	37-56	454-473	LINAP		g4507069	143	42	0.000000			"SW/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 ; SNF2alpha protein - human ; (D26155) hSNF2a [Homo sapiens] "

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22855	ENU06649	ANT61C8302: 2038..668	24-43	810-829	LINAP		g2342601	375	95	5.00E-19	27	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22856	ENU06650	ANT61C8316: 932..1611	23-44	627-646	LINAP		g1730692	54	49	0.00003			putative transcriptional regulatory protein in BIO3-HXT17 intergenic region ; probable membrane protein YNR063w - yeast (Saccharomyces cerevisiae) ; (Z71678) ORF YNR063w [Saccharomyces cerevisiae] (AL034490) pseudouridylyl synthase [Schizosaccharomyces pombe]
22857	ENU06651	ANT61C4300: 1208..773	42-69	460-479	LINAP		g4008551	647	144	4.00E-40	52	28	RHO-type GTPase activating protein RGA1/DBM1 ; DBM1 protein - yeast (Saccharomyces cerevisiae) ; (U07421) Dbm1p [Saccharomyces cerevisiae] ; (X90518) ORF O3290 [Saccharomyces cerevisiae] ; (X94335) YOR3290w [Saccharomyces cerevisiae] ; (Z75035) ORF YOR127w [Saccharomyces cerevisiae] ; GTPase-activating protein [Saccharomyces cerevisiae]
22858	ENU06652	ANT61C8320: 2159..1676	24-51	422-449	LINAP		g729298	231	107	6.00E-23			cytochrome P450 4F5 (CYP4F5) ; cytochrome P450 4F5 protein - rat ; (U39207) cytochrome P450 4F5 [Rattus norvegicus]
22859	ENU06653	ANT61C8338: 335..752	22-43	404-428	LINAP		g1706094	122	76	9.00E-15	34	31	mucin 5AC (clone JER58) - human (fragment) ; (Z34278) mucin [Homo sapiens]
22860	ENU06654	ANT61C8332: 2196..1878	22-48	271-290	LINAP		g1082604	106	42	0.002			TRNA nucleotidyltransferase precursor (TRNA adenylyltransferase) (TRNA CCA-pyrophosphorylase) (CCA-adding enzyme) ; tRNA nucleotidyltransferase - yeast (Saccharomyces cerevisiae) ; (M59870) transfer RNA nucleotidyltransferase [Saccharomyces cerevisiae] ; (U18922) Ccalp: tRNA nucleotidyltransferase(tRNA CCA-pyrophosphorylase) [Saccharomyces cerevisiae]
22861	ENU06655	ANT61C8344: 1..905	48-70	787-814	LINAP		g135969	619	274	6.00E-73			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22862	ENU06656	ANI61C8337: 1..1325	22-46	807-826	LINAP	g3810845	686	243	1.00E-63	46	53	(AL032684) possible ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]
22863	ENU06657	ANI61C8362: 962..260	31-53	480-499	LINAP	g3746895	258	98	8.00E-20	36	30	(AF088906) clock-controlled gene-9 protein [Neurospora crassa]
22864	ENU06658	ANI61C8308: 4900..4412	22-48	452-479	LINAP	g729853	62	45	0.0003	29	50	protein-tyrosine-phosphatase precursor ; dual specificity phosphatase (EC 3.1.3.-) IphP - Nostoc commune ; (L11392) protein tyrosine/serine phosphatase [Nostoc commune]
22865	ENU06659	ANI61C8356: 2099..837	50-69	785-804	LINAP	g728850	78	54	0.000001			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosylhydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diasticus] "
22866	ENU06660	ANI61C1000 3:978..1837	22-48	803-822	LINAP	g2132941	157	57	3.00E-18	29	57	probable membrane protein YOR301w - yeast (Saccharomyces cerevisiae) ; (Z75209) ORF YOR301w [Saccharomyces cerevisiae]
22867	ENU06661	ANI61C1002 2:2945..2086	22-49	802-829	LINAP	g2497214	508	114	5.00E-45	44	27	hypothetical 107.7 KD protein in TSP3-IPP2 intergenic region ; probable membrane protein YMR266w - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae]
22868	ENU06662	ANI61C1000 4:2709..669	24-43	792-811	LINAP	g2498597	699	206	1.00E-52	42	27	MRNA transport regulator MTR10 ; MTR10 protein - yeast (Saccharomyces cerevisiae) ; (U55020) Mtr10p [Saccharomyces cerevisiae] ; (Z75068) ORF YOR160w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvg	Description
22869	ENU06663	ANT61C1004	22-41	805-829	LINAP		g731872	777	99	3.00E-20	34	26	"putative 108.8 KD transcriptional regulatory protein in FKH1-STH1 intergenic region ; probable membrane protein YIL130w - yeast (Saccharomyces cerevisiae) ; (Z38059)orf, len: 964, CAI: 0.15, possible regulatory protein [Saccharomyces cerevisiae] "
22870	ENU06664	ANT61C1006	24-45	713-737	LINAP		g2924771	181	64	0.000000			(AC002334) putative dimethylaniline monooxygenase [Arabidopsis thaliana]
22871	ENU06665	ANT61C1005	39-58	449-476	LINAP		g1723454	219	55	0.000000	33	25	hypothetical 43.9 KD protein C13G7.10 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69729) hypothetical protein [Schizosaccharomyces pombe] (AC006248) putative copia polyprotein [Arabidopsis thaliana]
22872	ENU06666	ANT61C1008	208-229	388-411	LINAP		g4335736	44	64	5.00E-10			hypothetical 63.9 KD protein C1F12.09 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (D90903) esterase [Synecocystis sp.]
22873	ENU06667	ANT61C1009	22-48	777-800	LINAP		g1723513	250	64	0.000000	31	49	hypothetical 63.9 KD protein C1F12.09 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (D90903) esterase [Synecocystis sp.]
22874	ENU06668	ANT61C1010	22-44	456-479	LINAP		g1652216	93	68	3.00E-11			(AC006248) putative copia polyprotein [Arabidopsis thaliana]
22875	ENU06669	ANT61C1008	28-55	502-521	LINAP		g4335736	166	85	1.00E-18	32	14	proline transport protein - Emericella nidulans
22876	ENU06670	ANT61C1012	102-121	449-476	LINAP		g630383	178	85	3.00E-16	40	25	"putative 40S ribosomal protein YJR113C ; probable ribosomal protein S7, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49613) ORF YJR113c [Saccharomyces cerevisiae] "
22877	ENU06671	ANT61C1010	112-139	450-477	LINAP		g1352914	132	63	0.000000	37	40	(AF079900) tetracycline efflux protein [Streptomyces rimosus]
22878	ENU06672	ANT61C1015	22-42	279-299	LINAP		g3617954	105	65	4.00E-10			(AF076848) trihydroxytoluene oxygenase [Burkholderia cepacia]
22879	ENU06673	ANT61C1016	54-77	328-350	LINAP		g3746666	91	57	0.000000	42	30	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat nchi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
22880	ENU06674	ANI61C1011	26-53	457-477	LINAP	g4107286	50	59	0.000000	03			(AL035076) putative zinc-finger protein [Schizosaccharomyces pombe]
22881	ENU06675	ANI61C1017	66-85	456-478	LINAP	g1877327	162	96	1.00E-19				(Z92771) hypothetical protein Rv3272 [Mycobacterium tuberculosis]
22882	ENU06676	ANI61C1018	22-41	452-472	LINAP	g47149	90	62	0.000000	003			(X67953) carboxyphosphoenolpyruvate mutase [Streptomyces hygroscopicus]
22883	ENU06677	ANI61C1020	42-61	311-332	LINAP	g1942321	69	59	0.000000	01	29	13	"Bacterial Chitinase Complexed With Chitinase (Dinag) ; Bacterial Chitinase, Glycosyl Hydrolase Family 20"
22884	ENU06678	ANI61C1019	122-149	635-658	LINAP	g2498702	138	55	9.00E-14	35	35		sterigmatocystin 7-O-methyltransferase precursor ; (L25835) O-methyltransferase [Aspergillus flavus] ; (L25834) O-methyltransferase [Aspergillus parasiticus] ; (L22091) O-methyltransferase [Aspergillus parasiticus]
22885	ENU06679	ANI61C1022	36-61	802-829	LINAP	g1709181	283	78	6.00E-14	28	46		"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
22886	ENU06680	ANI61C1023	64-83	461-480	LINAP	g2501427	152	66	9.00E-19	45	24		tyrosinase (monophenol monooxygenase) ; (U66807) tyrosinase [Podospira anserinal] ; (U66808) tyrosinase [Podospira anserinal] (AL033388) leucine-rich repeat protein - weak similarity to adenylate cyclase [Schizosaccharomyces pombe]
22887	ENU06681	ANI61C1062	41-60	576-594	LINAP	g3850105	179	65	3.00E-15	38	17		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22888	ENU06682	ANI61C1024	22-49	367-386	LINAP		g1172542	267	88	3.00E-27	60	14	dolichyl'-phosphate-mannose--protein mannosyltransferase 4 ; dolichyl-phosphate-mannose--protein mannosyltransferase (EC 2.4.1.109)
		0:1709..2074											PMT4 - yeast (Saccharomyces cerevisiae) ; (X83798) PMT4 [Saccharomyces cerevisiae] ; (Z49643) ORF YJR143c [Saccharomyces cerevisiae]
22889	ENU06683	ANI61C1065	41-62	619-639	LINAP		g4584202	123	42	0.000000	29	45	(AJ000394) chromate transport protein [Bacillus cereus]
		1:812..1496								06			(AL023594) protein complex assembly protein [Schizosaccharomyces pombe]
22890	ENU06684	ANI61C1058	22-47	805-829	LINAP		g3150136	460	90	1.00E-18	33	38	regulatory protein algr3 - Pseudomonas aeruginosa (U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
22891	ENU06685	ANI61C1058	22-44	503-528	LINAP		g94816	98	42	0.002			(AL023518) hypothetical protein [Schizosaccharomyces pombe]
		9:9595..10143											(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana] (Z99168) putative heat shock transcription factor [Schizosaccharomyces pombe]
22892	ENU06686	ANI61C1024	23-46	657-681	LINAP		g2673951	324	140	8.00E-33	36	17	(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
		3:722..1											(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
22893	ENU06687	ANI61C1058	100-119	713-732	LINAP		g3130045	203	89	3.00E-17	31	17	(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
		9:10697..1163											(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
22894	ENU06688	ANI61C4949:	22-48	756-780	LINAP		g3080393	1399	118	1.00E-34	39	50	(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
		640..2097											(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
22895	ENU06689	ANI61C4971:	22-46	421-442	LINAP		g3327019	80	63	0.000000			(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
		681..319								001			(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
22896	ENU06690	ANI61C4972:	22-49	614-633	LINAP		g3184059	536	96	4.00E-48	65	39	(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
		739..1406											(AL023776) prephenate dehydrogenase [Schizosaccharomyces pombe]
22897	ENU06691	ANI61C4990:	119-144	486-505	LINAP		g1345955	106	46	3.00E-12	31	40	(L33464) alcohol dehydrogenase 3 [Methylobacter marinus]
		809..255											(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
22898	ENU06692	ANI61C1067	51-70	767-786	LINAP		g3282044	216	99	3.00E-20	35	17	(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
		2:1359..546											(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22899	ENU06693	ANI61C4929: 2226..1582	52-71	585-603	LINAP		g125727	291	76	5.00E-29			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactic) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactic] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactic] ; (X01095) URF2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactic]
22900	ENU06694	ANI61C4929: 5034..5547	25-44	469-493	LINAP		g584748	53	52	0.000004			autolysin (N'-acetylmuramoyl-L-alanine amidase) ; autolysin - Enterococcus faecalis ; (M58002) bacterial cell wall hydrolase [Streptococcus faecalis]
22901	ENU06695	ANI61C1068 1:1252..1586	79-98	360-380	LINAP		g113517	95	72	3.00E-12			alpha-glucosidase precursor (maltase) ; alpha-glucosidase (EC 3.2.1.20) - yeast (Candida tsukubaensis) ; (X56024) alpha-glucosidase [Pseudozyma tsukubaensis]
22902	ENU06696	ANI61C5004: 495..903	58-77	455-476	LINAP		g1077401	477	151	3.00E-36	49	18	probable membrane protein YLR277c - yeast (Saccharomyces cerevisiae) ; (U17245) Ysh1p: subunit of polyadenylation factor I (PF I) [Saccharomyces cerevisiae]
22903	ENU06697	ANI61C1069 8:1..499	36-59	442-461	LINAP		g2507475	87	57	0.000000	27	9	paired amphipathic helix protein ; regulatory protein SIN3 - yeast (Saccharomyces cerevisiae) ; (Z74746) ORF YOL004w [Saccharomyces cerevisiae]
22904	ENU06698	ANI61C1068 7:2970..2166	22-48	758-784	LINAP		g2618766	327	153	7.00E-38	39	46	(U94362) glycogenin-2 alpha [Homo sapiens]
22905	ENU06699	ANI61C5009: 1519..964	61-80	515-534	LINAP		g1469400	50	34	0.6			(U44088) TDA G51 [Mus musculus]
22906	ENU06700	ANI61C1025 1:1382..3059	22-45	802-829	LINAP		g125935	418	118	6.00E-26	29	44	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactic) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactic]



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22907	ENU06701	ANI61C1027	22-48	804-824	LINAP		g3559970	656	66	8.00E-24	37	28	(AL031514) putative beta-mannosidase [Streptomyces coelicolor]
22908	ENU06702	ANI61C8537	52-71	765-789	LINAP		g121087	162	56	3.00E-18			GCY protein ; GCY1 protein - yeast (Saccharomyces cerevisiae) ; (X13228) GCY protein (AA 1-312) [Saccharomyces cerevisiae] ; (X90518) ORF O31567 [Saccharomyces cerevisiae] ; (X94335) YOR3269w [Saccharomyces cerevisiae] ; (X96740) GCY protein [Saccharomyces cerevisiae] ; (Z75028) ORF YOR120w [Saccharomyces cerevisiae] (AL031155) putative amidase [Streptomyces coelicolor]
22909	ENU06703	ANI61C5049	102-121	539-558	LINAP		g3367750	322	81	2.00E-28	46	34	hypothetical 36.9 KD protein C21E11.07 in chromosome I ; hypothetical protein SPAC21E11.07 - fission yeast (Schizosaccharomyces pombe) ; (Z67999) hypothetical protein [Schizosaccharomyces pombe] (AJ000482) Hormone-sensitive lipase [Sus scrofa] ; (AJ000483) hormone-sensitive lipase [Sus scrofa] (Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22912	ENU06706	ANI61C1070	25-44	726-753	LINAP		g2104438	429	138	2.00E-43	50	22	(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22913	ENU06707	ANI61C1027	44-71	472-499	LINAP		g2494132	74	70	9.00E-12			(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22914	ENU06708	ANI61C8658	41-68	802-829	LINAP		g2239203	431	89	2.00E-36	39	92	(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22915	ENU06709	ANI61C5032	22-49	809-828	LINAP		g2134102	564	198	6.00E-50	48	19	(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22916	ENU06710	ANI61C1024	48-67	537-555	LINAP		g168849	114	77	6.00E-15	33	13	(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]
22917	ENU06711	ANI61C1024	22-43	803-825	LINAP		g2731377	988	175	3.00E-43	32	29	(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe] (AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana] (Z97209) aldolase reductase [Schizosaccharomyces pombe] [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22918	ENU06712	ANI61C507.2	89-116	453-479	LINAP		g3080535	391	177	4.00E-44	57	7	(AL022600) RNA helicase [Schizosaccharomyces pombe]
22919	ENU06713	ANI61C1024	22-42	453-479	LINAP		g2495215	184	94	8.00E-19	39	67	hypothetical 20.9 KD protein in ROX1-SPE3 intergenic region ; hypothetical protein YPR067w - yeast (Saccharomyces cerevisiae) ; (Z49219) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
22920	ENU06714	ANI61C1073	42-61	644-671	LINAP		g1351612	256	90	3.00E-29	39	64	hypothetical oxidoreductase C23D3.11 in chromosome I ; hypothetical protein SPAC23D3.11 - fission yeast (Schizosaccharomyces pombe)
22921	ENU06715	ANI61C507.3	32-52	481-502	LINAP		g2135950	122	39	0.017			PQ-rich protein - human ; (Z50194) PQ-rich protein [Homo sapiens]
22922	ENU06716	ANI61C1028	23-46	678-700	LINAP		g1175484	276	110	2.00E-28	41	15	ATP-dependent DNA helicase HUS2 ; hypothetical protein SPAC2G11.12 - fission yeast (Schizosaccharomyces pombe) ; (Z54354) atp-dependent dna helicase hus2 [Schizosaccharomyces pombe] ; (Y09426) DNA-helicase [Schizosaccharomyces pombe]
22923	ENU06717	ANI61C5107	22-46	455-479	LINAP		g1077552	286	135	2.00E-31	40	49	hypothetical protein YDR051c - yeast (Saccharomyces cerevisiae) ; (Z49209) unknown [Saccharomyces cerevisiae] ; (Z74347) ORF YDR051c [Saccharomyces cerevisiae]
22924	ENU06718	ANI61C505.1	34-53	810-828	LINAP		g2114323	106	41	0.011	21	32	(D88734) membrane glycoprotein [Equine herpesvirus 1]
22925	ENU06719	ANI61C1028	47-66	365-388	LINAP		g115918	128	63	1.00E-17			cell division control protein 2 cognate ; protein kinase (EC 2.7.1.37) cdc2 homolog C - fruit fly (Drosophila sp.) ; (X57486) p34-cdc2 homologue [Drosophila melanogaster]

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22926	ENU06720	ANI61C1074	22-45	773-790	LINAP		g1351636	860	292	2.00E-78	49	22	hypothetical 143.3 KD TRP-ASP repeats containing protein
		7:1714..362											CI2G12.13C in chromosome I ; hypothetical protein SPAC12G12.13c - fission yeast (Schizosaccharomyces pombe)
22927	ENU06721	ANI61C1028	35-58	785-812	LINAP		g112713	184	63	0.000000			"1-aminocyclopropane-1-carboxylate synthase CMW33 (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase) ; 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14), wound-induced - winter squash ; (D01032) 1-aminocyclopropane-1-carboxylate synthase [Cucurbita maxima] ; aminocyclopropane carboxylate synthase [Cucurbita maxima] ; aminocyclopropane carboxylate synthase:ISOtype=wound-induced [Cucurbita maxima] "
22928	ENU06722	ANI61C1027	31-50	419-438	LINAP		g586486	90	57	0.000000			hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
22929	ENU06723	ANI61C8691	69-87	492-516	LINAP		g729562	442	160	2.00E-44	60	23	UDP-glucose 4-epimerase (galactowaldenase) / aldose 1-epimerase (mutarotase) ; UDPglucose 4-epimerase (EC 5.1.3.2) - yeast (Pachysolen tannophilus) ; (X68593) UDP-galactose-4-epimerase [Pachysolen tannophilus]
22930	ENU06724	ANI61C8668	22-45	520-539	LINAP		g2147899	275	77	2.00E-21	40	32	phosphate transporter - Glomus versiforme ; (U38650) phosphate transporter [Glomus versiforme] ; phosphate transporter [Glomus versiforme]

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22931	ENU06725	ANI61C8674: 2419..1690	32-51	673-692	LINAP		g1730741	143	51	0.000000	002		hypothetical 65.3 KD protein in SUN4-MASS5 intergenic region ; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae) ; (U12141)
22932	ENU06726	ANI61C5139: 980..303	211-230	628-647	LINAP		g500628	280	120	1.00E-26	37	37	membrane protein [Saccharomyces cerevisiae] ; (Z71341) ORF YNL065w [Saccharomyces cerevisiae] (U05211) Ttp1p [Saccharomyces cerevisiae]
22933	ENU06727	ANI61C1070 6:6562..5865	22-44	638-657	LINAP		g3219924	276	112	2.00E-24	36	43	hypothetical 57.6 KD protein C30D10.15 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] (AL035216) probable involvement in ergosterol biosynthesis [Schizosaccharomyces pombe] (AF038585) pyruvate dehydrogenase kinase isoform 1; [PDK1 [Zea mays] (X97119) pectate lyase [Erwinia chrysanthemi] cyclosporin synthetase - Tolypocladium inflatum ; (Z28383) cyclosporine synthetase [Tolypocladium inflatum] putative 89.3 KD transcriptional regulatory protein C1F7.11C ; (AL021837) histone promoter control 2 protein [Schizosaccharomyces pombe] ; (Z67998) unknown [Schizosaccharomyces pombe] (S58126) Unknown [Saccharomyces cerevisiae] (AL049497) hypothetical protein [Streptomyces coelicolor] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum] "
22934	ENU06728	ANI61C8669: 627..1	46-65	542-561	LINAP		g4160344	171	88	6.00E-17	51	23	
22935	ENU06729	ANI61C5129: 1253..1604	24-50	446-471	LINAP		g3746431	244	62	0.000000	44	24	
22936	ENU06730	ANI61C1027 8:4789..5584	22-41	748-775	LINAP		g1765918	190	61	0.000000	34	57	
22937	ENU06731	ANI61C1067 7:1299..1	22-41	719-743	LINAP		g1083855	388	131	9.00E-30	35	1	
22938	ENU06732	ANI61C5136: 1914..1594	22-44	457-476	LINAP		g1351672	63	38	0.061	21	20	
22939	ENU06733	ANI61C1030 5:277..769	22-44	458-479	LINAP		g2894295	162	90	6.00E-18	40	39	
22940	ENU06734	ANI61C1067 7:3220..1716	36-55	805-828	LINAP		g2342601	571	140	1.00E-32	32	5	
22941	ENU06735	ANI61C8697: 1460..1832	46-70	295-314	LINAP		g4261597	79	55	0.000000	30	11	
22942	ENU06736	ANI61C5133: 2148..974	39-58	807-829	LINAP		g4539214	817	177	1.00E-43	52	64	
22943	ENU06737	ANI61C1077 0:1696..2012	22-43	454-473	LINAP		g2924313	109	64	6.00E-10	27	15	

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22944	ENU06738	ANT61C8696:	43-63	628-647	LINAP		g2499841	1691	315	3.00E-85	54	31	26S proteasome regulatory subunit MTS4 (19S regulatory CAP region of 26S protease subunit 2) ; (Y09819) 19S regulatory cap region of 26S protease subunit 2 [Schizosaccharomyces pombe]
22945	ENU06739	ANT61C506:1	121-140	307-326	LINAP		g3550985	194	63	8.00E-10	35	34	(AB010740) OsSSa [Oryza sativa]
22946	ENU06740	ANT61C8681:	..420		LINAP		g1293655	407	107	1.00E-22	35	35	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
22947	ENU06741	ANT61C1079:	26-46	452-479	LINAP		g3550283	80	55	0.000000	31	40	(AJ007590) XRP2 protein [Homo sapiens]
22948	ENU06742	ANT61C5149:	109-129	571-590	LINAP		g133322	78	49	0.00003			DNA-directed RNA polymerase II largest subunit ; DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - Caenorhabditis elegans ; (M29235) RNA polymerase II [Caenorhabditis elegans]
22949	ENU06743	ANT61C1032	3:115..1300		LINAP		g1805251	275	92	6.00E-18	30	51	(U58946) transposase [Aspergillus awamori]
22950	ENU06744	ANT61C1077	41-59	262-285	LINAP		g479395	77	51	0.000005	34	6	probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
22951	ENU06745	ANT61C1031	29-48	459-479	LINAP		g2224683	121	68	6.00E-11	28	10	(AB002369) KIAA0371 [Homo sapiens]
22952	ENU06746	ANT61C1078	25-46	536-558	LINAP		g4503247	126	55	0.000000	33	29	novel nuclear protein 1 ; NNP-1 (D21S2056E) ; (U79775) NNP-1 [Homo sapiens]
22953	ENU06747	ANT61C1032	34-53	459-479	LINAP		g2950464	185	75	4.00E-17	55	17	(AL022071) hypothetical protein [Schizosaccharomyces pombe]
22954	ENU06748	ANT61C1032	24-51	453-479	LINAP		g3136055	76	57	0.000000	24	27	(AL023592) betaine-aldehyde dehydrogenaseprecursor [Schizosaccharomyces pombe]
22955	ENU06749	ANT61C8702:	32-51	710-730	LINAP		g1546072	925	108	7.00E-23	32	10	(U68040) polyketide synthase [Cochliobolus heterotrophus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22956	ENU06750	ANI61C8694:	53-72	803-821	LINAP		g481230	566	104	4.00E-30	41	63	L-idiol 2-dehydrogenase (EC 1.1.1.14) precursor - rat ; (X74593) L-idiol 2-dehydrogenase [Rattus norvegicus] (X75561) GTPase activating protein [Saccharomyces cerevisiae] (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana]
22957	ENU06751	ANI61C5154:	22-49	782-802	LINAP		g414689	329	146	1.00E-34	30	30	
22958	ENU06752	ANI61C1078	27-46	653-674	LINAP		g3600039	103	59	1.00E-10	25	31	
22959	ENU06753	ANI61C8703:	27-46	459-478	LINAP		g2132846	139	73	2.00E-12			probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae] (Z99295) phosphatidyl synthase [Schizosaccharomyces pombe] putative transporter C1B3.16C ; (Z98598) putative transporter [Schizosaccharomyces pombe] (AL023634) hypothetical protein [Schizosaccharomyces pombe] "hypothetical 32.9 KD protein in NFO-FRUA intergenic region ; (U00007) yeiN [Escherichia coli] ; (AE000306) orf, hypothetical protein [Escherichia coli] ; yeiN gene [Escherichia coli] " exocyst complex component SEC3 (PSL1 protein) ; PSL1 protein - yeast (Saccharomyces cerevisiae) ; (L22204) Psl1p [Saccharomyces cerevisiae] ; (U18778) Sec3p [Saccharomyces cerevisiae] (AL031107) putative secreted glucosidase [Streptomyces coelicolor]
22960	ENU06754	ANI61C1079	22-43	804-829	LINAP		g2414601	414	149	3.00E-35	39	43	
22961	ENU06755	ANI61C8703:	66-93	572-591	LINAP		g3183364	178	100	1.00E-20	33	30	
22962	ENU06756	ANI61C1033	116-143	450-473	LINAP		g3150252	62	50	0.00001	38	6	
22963	ENU06757	ANI61C1145	34-54	754-780	LINAP		g465602	389	70	2.00E-11			
22964	ENU06758	ANI61C5147:	22-42	598-625	LINAP		g464482	235	100	1.00E-20	42	11	
22965	ENU06759	ANI61C1081	22-47	804-823	LINAP		g3334796	373	154	1.00E-45	41	55	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22966	ENU06760	ANI61C1147	22-44	452-479	LINAP		g127992	117	31	6			"beta-(1->2)glucan export ATP-binding protein NDVA ; beta-1,2-glucan export protein ndvA - Rhizobium meliloti ; (M20726) ndvA peptide (put.); putative [Rhizobium meliloti]"
22967	ENU06761	ANI61C8695: 663..1023	22-44	460-479	LINAP		g1799532	77	59	0.000000	33	38	(AB000564) salicylate hydroxylase [Sphingomonas sp.]
22968	ENU06762	ANI61C5176: 827..1444	40-59	572-591	LINAP		g2193933	66	46	0.0002			(Z96800) hypothetical protein Rv0312 [Mycobacterium tuberculosis]
22969	ENU06763	ANI61C1079 7:258..1799	27-46	767-786	LINAP		g1020413	464	143	2.00E-33	34	50	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
22970	ENU06764	ANI61C1032 9:5912..4715	22-49	807-829	LINAP		g3023956	787	256	2.00E-67	51	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
22971	ENU06765	ANI61C8710: 2634..2074			LINAP		g3367797	472	208	2.00E-53	55	22	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
22972	ENU06766	ANI61C5177: 357..1	108-127	454-477	LINAP		g4191793	71	40	0.000000			(AC005917) putative zinc finger protein [Arabidopsis thaliana]
22973	ENU06767	ANI61C1079 7:4799..5578	22-43	732-751	LINAP		g4455664	347	166	2.00E-40	37	13	(AL035480) putative polyketide synthase [Mycobacterium leprae]
22974	ENU06768	ANI61C1032 4:7594..8132	40-59	490-508	LINAP		g2582351	370	164	4.00E-40	43	40	(AF018639) unknown [Dictyostelium discoideum]
22975	ENU06769	ANI61C5177: 1806..1464	22-49	456-479	LINAP		g1703534	68	67	7.00E-11	43	29	(U80030) short region of weak similarity to rat dihydroxypolyphenylbenzoate methyltransferase (GI:457372) [Caenorhabditis elegans]
22976	ENU06770	ANI61C1082 0:1054..1	36-55	648-669	LINAP		g3023956	801	243	6.00E-69	51	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
22977	ENU06771	ANI61C1034 3:1453..323	25-44	802-829	LINAP		g1352911	983	112	2.00E-35	41	38	hypothetical 80.2 KD protein in CPA2-NNF1 intergenic region ; hypothetical protein YJR110w - yeast (Saccharomyces cerevisiae) ; (Z49610) ORF YJR110w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22978	ENU06772	ANI6IC1147	22-47	809-829	LINAP		g1708195	190	66	5.00E-11			HFM1 protein ; (U22156) Hfm1p [Saccharomyces cerevisiae]
22979	ENU06773	6:3430..2272	22-47	805-829	LINAP		g538067	461	141	6.00E-33	34	18	(M77661) putative pol polyprotein [Magnaporthe grisea]
22980	ENU06774	9:2123..721	22-46	805-824	LINAP		g1723769	247	55	0.000000			putative transporter YGR260W ; probable membrane protein YGR260w - yeast [Saccharomyces cerevisiae]
		1:652..2179							5				(Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
22981	ENU06775	ANI6IC1081	22-41	495-518	LINAP		g127060	184	77	4.00E-24	40	92	zinc finger protein MFG-1 (zinc finger protein 58) ; finger protein mfg1 - mouse (fragment) ; (M28513) zinc finger protein mfg1 mRNA (put.) ; putative [Mus musculus]
22982	ENU06776	ANI6IC1034	22-46	779-806	LINAP		g1706591	412	175	3.00E-43	48	23	elongation factor 3B (EF-3B) ; probable membrane protein YNL014w - yeast [Saccharomyces cerevisiae] ; (Z71290) ORF YNL014w [Saccharomyces cerevisiae]
22983	ENU06777	ANI6IC1030	43-62	807-826	LINAP		g1169645	227	32	5.3			"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) alpha chain - yeast (Candida albicans) ; (L29063) fatty acid synthase alpha subunit [Candida albicans] " (AJ011849) fengycin synthetase [Bacillus subtilis]
22984	ENU06778	ANI6IC5932:	22-41	771-791	LINAP		g3724089	212	58	4.00E-16	35	8	(AF000149) ATP-binding cassette transporter [Mus musculus]
22985	ENU06779	9680..11615	22-46	798-825	LINAP		g2547314	466	192	3.00E-48	40	12	(AL033389) putative antioxidant protein [Schizosaccharomyces pombe]
22986	ENU06780	ANI6IC5187:	22-44	454-477	LINAP		g3850080	120	58	3.00E-14			sepB protein - Emericella nidulans ; sepB protein - Emericella nidulans ; (X86399) sepB [Emericella nidulans]
22987	ENU06781	ANI6IC1148	25-46	737-755	LINAP		g1078634	2239	323	e-127	97	35	



Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	aat ncbi gi	Score	Blast Score	Blast Prob	% id	% cvrg	Description
22988	ENU06782	ANI61C6060:	58-83	482-501	LINAP		g549628	413	171	4.00E-43	57	90	hypothetical 22.1 KD protein in CCP1-MET1 intergenic region ; hypothetical protein YKRO68c - yeast
		1366..2025											(Saccharomyces cerevisiae) ; (Z28293) ORF YKRO68c [Saccharomyces cerevisiae]
22989	ENU06783	ANI61C1080	53-72	807-829	LINAP		g125727	533	90	8.00E-35			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URF2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis]
		7:3996..5261											(AL031532) sap2 family putative cell cycle dependent phosphatase associated protein [Schizosaccharomyces pombe] (AJ224865) IgE-binding protein [Aspergillus fumigatus]
22990	ENU06784	ANI61C6076:	27-46	802-829	LINAP		g3560253	470	139	7.00E-37	50	39	alpha-glucosidase precursor (malase) ; (D45356) alpha-glucosidase [Aspergillus niger]
		359..1325											(Y12527) HMWP1 protein [Yersinia enterocolitica]
22991	ENU06785	ANI61C1148	22-47	423-448	LINAP		g2980819	135	88	5.00E-17			(AF030886) telomere-associated recQ-like helicase [Ustilago maydis]
22992	ENU06786	ANI61C8728:	29-51	805-827	LINAP		g3023267	950	209	8.00E-58	45	26	HST1 protein (homologous TO SIR2 protein 1) ; HST1 protein - yeast (Saccharomyces cerevisiae) ; (U47120)
		1012..2089											homolog of SIR2; transcribed ORF flanked by NUF2 (X72225) and RTG1 (M97690) [Saccharomyces cerevisiae] ; (U39041) Hst1p [Saccharomyces cerevisiae] ; (Z74810) ORF YOL068c [Saccharomyces cerevisiae]
22993	ENU06787	ANI61C6090:	63-80	308-327	LINAP		g2765195	79	58	0.000000			
		1..364									03		
22994	ENU06788	ANI61C1163:	72-92	469-488	LINAP		g2642224	61	57	0.000000	26	16	
		1..518									07		
22995	ENU06789	ANI61C1084	49-67	766-785	LINAP		g1708325	638	137	9.00E-32	45	46	
		6:668..1854											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22996	ENU06790	ANI61C8729: 5126..5536			LINAP		g1731071	66	72	2.00E-12	30	35	hypothetical 47.0 KD protein in GLNQ-ANSR intergenic region ; (D84432) Y qjH [Bacillus subtilis] ; (Z99116) similar to DNA-damage repair protein [Bacillus subtilis] (AF024496) contains similarity to Plasmodium falciparum glycophorin-binding protein homolog 2 (GB:X69769) [Caenorhabditis elegans] (AB002377) KIAA0379 [Homo sapiens]
22997	ENU06791	ANI61C5223: 23-44 2348..825		805-827	LINAP		g2394451	212	59	0.000000 04	31	18	(M74066) Major body wall myosin [Onchocerca volvulus] (AP000003) 348aa long hypothetical dehydrogenase [Pyrococcus horikoshii] regulatory protein CYS-3 ; regulatory protein cys-3 - Neurospora crassa ; (M26008) cys-3 [Neurospora crassa] (AL034563) putative yeast CF Ib (RNA3' Cleavage factor Ib) homolog; ribonucleoprotein [Schizosaccharomyces pombe]
22998	ENU06792	ANI61C1086 1:302..1	97-117	432-451	LINAP		g2224699	117	80	1.00E-14	31	18	cell cycle protein kinase CDC5/MSD2 ; protein kinase CDC5 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (M84220) PKX2 protein kinase [Saccharomyces cerevisiae] ; (Z48613) Cdc5p [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]
22999	ENU06793	ANI61C1036 5:1658..1991	30-49	364-385	LINAP		g159893	80	52	0.000004			(AL049559) protein kinase cek1 [Schizosaccharomyces pombe]
23000	ENU06794	ANI61C5213: 1108..1539			LINAP		g3257063	123	45	1.00E-10			Leucine rich repeat containing protein [Schizosaccharomyces pombe] " (AE001017) conserved hypothetical protein [Archaeoglobus fulgidus]
23001	ENU06795	ANI61C1085 6:2845..2191	22-48	593-620	LINAP		g118126	226	71	9.00E-12	33	91	UV-endonuclease - Neurospora crassa
23002	ENU06796	ANI61C1034 9:3166..4194	44-64	797-816	LINAP		g4049514	642	153	2.00E-45	49	53	
23003	ENU06797	ANI61C1178: 1625..2522	22-49	772-799	LINAP		g416768	438	203	1.00E-51	41	36	
23004	ENU06798	ANI61C8746: 619..1315	39-58	639-658	LINAP		g4499843	203	74	9.00E-13	37	40	
23005	ENU06799	ANI61C5230: 25-52 2738..464	25-52	806-829	LINAP		g4581521	696	240	7.00E-63	68	12	
23006	ENU06800	ANI61C1085 8:3973..4384	22-45	263-289	LINAP		g3581887	234	92	2.00E-18	34	15	
23007	ENU06801	ANI61C1086 0:2530..2876	22-45	437-458	LINAP		g2649315	98	63	0.000000 001	29	65	
23008	ENU06802	ANI61C1037 8:900..1809	22-48	803-827	LINAP		g1362529	1047	391	e-108	69	40	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23009	ENU06803	ANT61C1037	22-49	805-824	LINAP		g2655202	1286	206	3.00E-70	56	32	(AF026402) U5 snRNP 100 kD protein [Homo sapiens]
23010	ENU06804	ANT61C9209: 6:2137..433	22-44	522-541	LINAP		g3914934	129	99	2.00E-20			probable RNA 3'-terminal phosphate cyclase (RNA-3'-phosphate cyclase) (RNA cyclase) ; (AP000006) 369aa long hypothetical phosphate cyclase [Pyrococcus horikoshii]
23011	ENU06805	ANT61C9263: 1380..883	22-43	441-460	LINAP		g2414601	235	106	8.00E-23	43	28	(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
23012	ENU06806	ANT61C5998: 10102..10727	135-158	484-503	LINAP		g3123165	372	167	7.00E-41	42	57	zinc finger protein 183 ; (X98253) ZNF183 [Homo sapiens] ; (AC002477) zinc-finger protein [Homo sapiens] (AB004535) ATP-dependent RNA helicase MSS116 precursor [Schizosaccharomyces pombe]
23013	ENU06807	ANT61C9250: 3162..4281	37-56	798-825	LINAP		g2257514	480	182	2.00E-45	39	49	regulatory protein GAL4 ; regulatory protein GAL4 - yeast (Saccharomyces cerevisiae) ; (K01486) GAL4 protein [Saccharomyces cerevisiae] ; (Z67751) GAL4 [Saccharomyces cerevisiae] ; (Z73604) ORF YPL248c [Saccharomyces cerevisiae]
23014	ENU06808	ANT61C8731: 4890..3869	59-78	807-829	LINAP		g1169823	219	109	2.00E-23	28	28	lactose permease ; lactose permease - yeast (Kluveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluveromyces lactis] "succinyl-CoA ligase (GDP-forming), beta-chain precursor (succinyl-CoA synthetase, beta chain) (SCS-beta) ; beta-succinyl CoA synthetase - rumen fungus (Neocallimastix frontalis) ; (X84222) beta-succinyl CoA synthetase [Neocallimastix frontalis] " (U58946) transposase [Aspergillus awamori]
23015	ENU06809	ANT61C5930: 388..933	175-195	499-518	LINAP		g125935	56	45	0.0004	24	24	(AL031764) putative FAD synthetase [Schizosaccharomyces pombe]
23016	ENU06810	ANT61C120:1 015..1	30-57	797-824	LINAP		g1711577	697	222	2.00E-68	53	61	(AL033534) serine-rich protein [Schizosaccharomyces pombe]
23017	ENU06811	ANT61C5930: 3180..1803	24-43	803-822	LINAP		g1805251	1122	289	1.00E-77	50	50	
23018	ENU06812	ANT61C5245: 452..1	104-127	451-477	LINAP		g3668151	111	59	0.000000	32	52	
23019	ENU06813	ANT61C9251: 295..851	23-47	513-536	LINAP		g3873550	105	50	0.00002	28	34	

# Genomic Information

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23020	ENU06814	ANI61C8754:	23-48	783-810	LINAP		g138350	121	57	0.000000			glycoprotein X precursor ; glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p) ; (M86664) membrane glycoprotein [Equine herpesvirus 1] "(AJ223012) rifamycin polypeptide synthase, type 1 [Amycolatopsis mediterranei] ; (AF040570) polypeptide synthase [Amycolatopsis mediterranei]
		1291..2226								1			
23021	ENU06815	ANI61C6099:	22-46	575-602	LINAP		g2764761	51	34	0.0006			"
		1..625											
23022	ENU06816	ANI61C1086	22-46	780-806	LINAP		g1353088	176	89	4.00E-17	32	69	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50.19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37711); cDNA EST EMBL:TD1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene;
		0:4578..3752											
23023	ENU06817	ANI61C1159:	27-46	616-640	LINAP		g1703266	249	109	2.00E-23	41	43	
		11409..12069											
23024	ENU06818	ANI61C6067:			LINAP		g3879121	265	128	4.00E-29			
		2562..1697											
23025	ENU06819	ANI61C5243:	109-132	364-391	LINAP		g1711534	261	112	1.00E-24	47	37	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50.19C ; (Z77137) amiB2 [Mycobacterium tuberculosis] (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37711); cDNA EST EMBL:TD1923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene;
		1..423											

# Genomic Data

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23026	ENU06820	ANI61C1160:	22-45	663-690	LINAP		g119164	271	134	5.00E-31	40	48	elongation factor 1-gamma (EF-1-gamma) ; translation elongation factor eEF-1 gamma chain - brine shrimp ; (M28020) elongation factor 1-gamma [Artemia sp.]
23027	ENU06821	ANI61C9253:			LINAP		g2494878	828	319	1.00E-89	90	55	guanine nucleotide-binding protein alpha subunit ; (U49917) Fada [Emeticella nidulans]
23028	ENU06822	ANI61C8748:	22-45	654-679	LINAP		g1172741	337	111	1.00E-37	40	36	peptide transporter PTR2 ; (U09781) peptide transporter [Candida albicans]
23029	ENU06823	ANI61C9281:	48-67	769-789	LINAP		g4164426	403	159	2.00E-38	42	29	(AL035247) putative spindle pole body-associating protein [Schizosaccharomyces pombe]
23030	ENU06824	ANI61C8743:	23-50	570-589	LINAP		g1729825	101	47	6.00E-10	31	57	transaldolase ; transaldolase (EC 2.2.1.2) - yeast (Saccharomyces cerevisiae) ; (U19102) Tal1p: Transaldolase [Saccharomyces cerevisiae]
23031	ENU06825	ANI61C5255:	22-46	451-478	LINAP		g1176486	114	80	1.00E-14	34	25	hypothetical 63.9 KD protein in IME2-MEF2 intergenic region ; protein YKR029c homolog YJL105w - yeast (Saccharomyces cerevisiae) ; (X85021) YKR029c homologue [Saccharomyces cerevisiae] ; (Z49380) ORF YJL105w [Saccharomyces cerevisiae]
23032	ENU06826	ANI61C1084	22-45	572-592	LINAP		g2493399	74	77	1.00E-13			putative cytochrome P450 T10B9.5 in chromosome II ; (Z48717) similar to cytochrome P450 [Caenorhabditis elegans]
23033	ENU06827	ANI61C9282:	22-43	449-468	LINAP		g731628	436	167	2.00E-44	59	44	putative mitochondrial carrier YHR002W ; hypothetical protein YHR002w - yeast (Saccharomyces cerevisiae) ; (U10555) Yhr002wp [Saccharomyces cerevisiae]

# Sequence Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23034	ENU06828	ANI6IC8744:	39-58	803-822	LINAP		g1175977	738	185	3.00E-58	47	48	hypothetical 61.8 KD peptidase in MPRI-GCN20 intergenic region ; probable membrane protein YFR006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR006W [Saccharomyces cerevisiae]
23035	ENU06829	ANI6IC6078:	23-43	446-473	LINAP		g284667	100	36	0.13			neurofilament triplet H1 protein - rabbit (fragment) ; (M94315) neurofilament-H [Oryctolagus cuniculus]
23036	ENU06830	ANI6IC5244:	26-46	562-584	LINAP		g586937	171	34	0.66			zinc-finger protein 2 (zinc-finger homeodomain protein 2) ; homeotic protein zfh-2 - fruit fly (Drosophila melanogaster) ; (M63450) zinc-finger homeodomain protein 2 [Drosophila melanogaster]
23037	ENU06831	ANI6IC1088	22-47	656-675	LINAP		g2492758	123	38	2.00E-10	34	66	probable short-chain type dehydrogenase/reductase VDL C
23038	ENU06832	ANI6IC8753:	52-71	807-829	LINAP		g114967	244	71	2.00E-17	35	30	beta-glucosidase (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) ; beta-glucosidase (EC 3.2.1.21) - Agrobacterium tumefaciens ; (M59852) beta-D-glucosidase [Agrobacterium tumefaciens]
23039	ENU06833	ANI6IC527:1	25-44	306-325	LINAP		g4587324	142	39	0.011			(AB025420) Family 19 chitinase (PRYA1 ORF) [Aeromonas sp. 10S-24]
23040	ENU06834	ANI6IC1187:	54-73	459-478	LINAP		g1652749	201	117	4.00E-26	45	65	(D90908) hypothetical protein [Synechocystis sp.]
23041	ENU06835	ANI6IC1089	38-59	781-800	LINAP		g4107289	654	94	2.00E-18	32	47	(AL035076) putative carboxylesterase-lipase family member [Schizosaccharomyces pombe]
23042	ENU06836	ANI6IC1090	22-47	464-483	LINAP		g1945094	145	48	0.00004	31	51	(D88802) ydhJ [Bacillus subtilis] ; (Z99107) similar to hypothetical proteins [Bacillus subtilis]
23043	ENU06837	ANI6IC6147:	45-64	801-820	LINAP		g1346290	423	137	1.00E-31	33	45	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23044	ENU06838	ANI61C9285: 1551..941	58-77	568-590	LINAP	g10882283	125	34	0.78				protein kinase (EC 2.7.1.37) cdc2-related PITS/LRE alpha 2-1 - human (X91243) XrpFbeta1 [Xenopus laevis]
23045	ENU06839	ANI61C8762: 2587..2010	25-52	530-557	LINAP	g992626	64	49	0.00003	29	35		(AF026032) ATRX protein [Mus musculus]
23046	ENU06840	ANI61C6148: 536..1492			LINAP	g3002558	72	57	0.000000	26	9		hypothetical 73.8 KD protein in SPC98-TOM70 intergenic region ; probable membrane protein YNL125c - yeast (Saccharomyces cerevisiae) ; (Z46843) orf23 [Saccharomyces cerevisiae] ; (Z69382) Identical to putative protein ESBP6 [Saccharomyces cerevisiae] ; (Z71401) ORF YNL125c [Saccharomyces cerevisiae]
23047	ENU06841	ANI61C1210: 4317..3508	47-73	740-759	LINAP	g1730773	211	103	2.00E-21				(D89164) unnamed protein product [Schizosaccharomyces pombe]
23048	ENU06842	ANI61C9292: 2016..1490	23-50	480-506	LINAP	g1749536	235	103	8.00E-22	45	44		"epoxide hydrolase (microsomal epoxide hydrolase) (epoxide hydratase) ; epoxide hydrolase (EC 3.3.2.3), microsomal - rabbit ; (M21496) microsomal epoxide hydrolase (EC 3.3.2.3) [Oryctolagus cuniculus]" (AC002294) Similar to transcription factor gblZ46606 1658307 and others [Arabidopsis thaliana]
23049	ENU06843	ANI61C8740: 2899..2451	64-83	459-478	LINAP	g123927	84	54	1.00E-12				"(Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]" (AF052435) odd-paired-like [Danio rerio]
23050	ENU06844	ANI61C6153: 1472..1033			LINAP	g2443887	166	61	0.000000	29	11		(M77661) putative pol polypeptide [Magnaporthe grisea]
23051	ENU06845	ANI61C5274: 1181..611	53-74	528-549	LINAP	g3850821	247	33	1.8	45	26		(U58946) transposase [Aspergillus awamori]
23052	ENU06846	ANI61C1214: 3821..4206	22-44	364-391	LINAP	g3283028	182	53	8.00E-17	40	30		
23053	ENU06847	ANI61C9286: 2977..4449	22-45	775-795	LINAP	g538067	718	270	7.00E-72	47	20		
23054	ENU06848	ANI61C876: 037..324			LINAP	g1805251	475	190	8.00E-48	42	42		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23055	ENU06849	ANI61C526:1	25-45	662-689	LINAP		g3219917	167	89	3.00E-17	31	85	hypothetical 27.4 KD protein C30D10.14 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
23056	ENU06850	ANI61C1092			LINAP		g493955	223	71	1.00E-11	35	38	Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase) ; Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase) (AB002377) KIAA0379 [Homo sapiens]
23057	ENU06851	ANI61C9299:1..642	105-124	597-616	LINAP		g2224699	133	49	2.00E-13	32	23	hypothetical 55.5 KD GTP-binding protein in CDC23-DBP8 intergenic region ; probable purine nucleotide-binding protein YHR168w - yeast (Saccharomyces cerevisiae) ; (U00027) Yhr168wp [Saccharomyces cerevisiae]
23058	ENU06852	ANI61C122:3	22-49	278-304	LINAP		g731739	188	92	1.00E-18	50	19	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
23059	ENU06853	ANI61C8758:2220..998	22-47	807-827	LINAP		g3367789	530	109	2.00E-23	48	50	(U13646) homeotic region most like HMPB_DROME: homeotic proboscipedia protein [Caenorhabditis elegans]
23060	ENU06854	ANI61C6155:917..201	22-41	629-647	LINAP		g532113	77	41	0.01			probable membrane protein YPR157w - yeast (Saccharomyces cerevisiae) ; (U28371) P9584.4 gene product [Saccharomyces cerevisiae]
23061	ENU06855	ANI61C5259:3275..2159	33-54	809-828	LINAP		g2133035	226	82	8.00E-30	36	51	(X89442) peptide synthetase [Metarhizium anisopliae]
23062	ENU06856	ANI61C9288:2693..896	27-53	801-828	LINAP		g2342601	408	101	9.00E-21	29	5	TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
23063	ENU06857	ANI61C8774:3868..3465	22-48	272-291	LINAP		g1729996	69	54	0.000000	29	51	(AL021428) hypothetical protein Rv0063 [Mycobacterium tuberculosis]
23064	ENU06858	ANI61C6159:2762..3303	54-73	477-494	LINAP		g2808720	152	55	0.000000	32	27	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti]
23065	ENU06859	ANI61C5247:1364..936	30-50	454-476	LINAP		g1353088	151	75	3.00E-13	34	37	



# Sequence Alignment

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23066	ENU06860	ANT61C1092	22-42	529-552	LINAP		g3023677	67	50	0.00001			probable translation initiation factor EIF-2B gamma subunit (EIF-2B GDP-GTP exchange factor) ; (Z98602)
		9:1120..1693											translation initiation factor eif-2b gamma subunit [Schizosaccharomyces pombe]
23067	ENU06861	ANT61C8761:			LINAP		g3080535	4244	395	e-109	67	14	(AL022600) RNA helicase [Schizosaccharomyces pombe]
		4912..402											D-3-phosphoglycerate dehydrogenase (PGDH) ; phosphoglycerate dehydrogenase (EC 1.1.1.95) -
23068	ENU06862	ANT61C6176:	45-63	753-779	LINAP		g3122874	354	105	2.00E-35	37	50	Methanococcus jannaschii ; (U67544) phosphoglycerate dehydrogenase (serA) [Methanococcus jannaschii]
		800..1											

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23070	ENU06864	AN161C9267: 22-47	416-435		LINAP		g1706177	147	48	0.00004	38	15	cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisil]
23071	ENU06865	AN161C8784: 28-53	762-781		LINAP		g2781417	162	109	3.00E-23	25	15	(AF081920) polyketide synthase type I; PtC [Pseudomonas fluorescens]
23072	ENU06866	AN161C6188: 93-113	678-700		LINAP		g4102999	440	168	3.00E-41	46	64	(AF019630) pathogenicity protein [Magnaporthe grisea]
23073	ENU06867	AN161C5275: 40-59	756-783		LINAP		g1176583	924	162	3.00E-61	49	28	hypothetical 102.5 KD protein in KRE1-HXT14 intergenic region ; probable membrane protein YNL321w - yeast (Saccharomyces cerevisiae) ; (Z46259) NO339 [Saccharomyces cerevisiae] ; (Z71597) ORF YNL321w [Saccharomyces cerevisiae] (Z99163) similar to nitrogen permease regulator. [Schizosaccharomyces pombe]
23074	ENU06868	AN161C1191: 45-68	784-808		LINAP		g2832742	576	199	3.00E-50	42	59	(AF111179) G-septin alpha [Rattus norvegicus]
23075	ENU06869	AN161C8791: 22-48	331-352		LINAP		g4455009	91	60	0.000000			(AB010442) PMR1 [Penicillium digitatum]
23076	ENU06870	AN161C6183: 45-72	742-767		LINAP		g3288709	997	139	2.00E-62	50	18	hypothetical 98.1 KD TRP-ASP repeats containing protein in PAF1-MRP127 intergenic region ; hypothetical protein YBR281c - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2018-ORF [Saccharomyces cerevisiae] ; (Z36150) ORF YBR281c [Saccharomyces cerevisiae] ; ORF YBR2018 [Saccharomyces cerevisiae]
23077	ENU06871	AN161C1191: 22-48	730-749		LINAP		g586394	369	100	9.00E-23			(U35779) 1-aminocyclopropane-1-carboxylate synthase [Triticum aestivum]
23078	ENU06872	AN161C8759: 52-71	779-798		LINAP		g1173638	301	144	7.00E-34	30	75	

# Sequence Alignment

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23079	ENU06873	ANI61C5284:	82-101	712-732	LINAP		g1168817	847	136	1.00E-48	52	20	(Schizosaccharomyces pombe) ; cell division control protein 7 ; protein kinase cdc7 - fission yeast
		1696..245											
23080	ENU06874	ANI61C1093:	61-87	587-614	LINAP		g1397341	85	44	7.00E-10	35	23	[Schizosaccharomyces pombe] (U61955) Similar to kinesin-like protein; coded for by C. elegans cDNA yk184h5.3; coded for by C. elegans cDNA yk184h5.5; coded for by C. elegans cDNA yk13d7.3; coded for by C. elegans cDNA yk13d7.5; coded for by C. elegans cDNA yk31e1.5; co... ; (AF057567) kinesin-like protein ZEN-4a [Caenorhabditis elegans] proline utilization trans-activator ; transcription activator PUT3 - yeast (Saccharomyces cerevisiae) ; (X55384) proline utilization trans-activator [Saccharomyces cerevisiae] ; (X74152) orf5; homologous to S.cerevisiae PUT3 gene [Saccharomyces cerevisiae] ; (Z28015) ORF YKL015w [Saccharomyces cerevisiae] PIM1 protein ; pim1 hypothetical protein - fission yeast (Schizosaccharomyces pombe) (AF041382) microtubule binding protein D-CLRP-190 [Drosophila melanogaster] (AL049608) putative protein [Arabidopsis thaliana] cell-cycle nuclear autoantigen SG2NA (S/G2 nuclear antigen) ; nuclear autoantigen - human ; (U17989) GS2NA [Homo sapiens]
		1275..602											
23081	ENU06875	ANI61C1212:	22-48	503-528	LINAP		g131653	62	45	0.000008			
		11259..10711											
23082	ENU06876	ANI61C5251:	49-68	433-452	LINAP		g132172	108	63	0.000000	26	28	
		5260..4784								001			
23083	ENU06877	ANI61C1095	22-47	565-584	LINAP		g2773363	85	52	0.000002	26	11	
		6:243..861											
23084	ENU06878	ANI61C6137:	22-45	599-618	LINAP		g4584545	125	84	7.00E-16	35	55	
		937..280											
23085	ENU06879	ANI61C2185:	71-90	455-476	LINAP		g3122872	177	65	3.00E-11	31	20	
		438..805											

# Sequence Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23086	ENU06880	ANI61C1239:	98-118	456-474	LINAP		g547902	89	35	0.37			putative nucin core protein precursor 24 (multi-glycosylated core protein 24) (MGC-24) (MUC-24) (CD164 antigen) ; core protein MGC-24 - human ; (D14043) MGC-24 precursor [Homo sapiens]
23087	ENU06881	ANI61C2134:	24-51	506-529	LINAP		g559044	160	68	4.00E-11	26	27	(L29296) alpha-adducin [Homo sapiens]
23088	ENU06882	ANI61C8786:	22-48	609-629	LINAP		g559964	145	52	4.00E-15	40	68	(J05282) insect-type dehydrogenase [Pseudomonas cepacia]
23089	ENU06883	ANI61C6181:	22-49	803-828	LINAP		g2842510	423	96	2.00E-19	26	30	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
23090	ENU06884	ANI61C5251:	24-45	741-765	LINAP		g1076802	106	64	0.000000	34	11	extensin-like protein - maize ; (Z34465) extensin-like protein [Zea mays] ; extensin-like domain [Zea mays]
23091	ENU06885	ANI61C1216:	22-48	806-829	LINAP		g538067	2006	169	2.00E-41	38	19	(M77661) putative pol polypeptide [Magnaporthe grisea]
23092	ENU06886	ANI61C8786:	22-49	675-693	LINAP		g1709181	249	42	0.000000	36	40	"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae]"
23093	ENU06887	ANI61C1216:	28-47	804-829	LINAP		g2132868	160	34	1.4			probable membrane protein YOR053w - yeast (Saccharomyces cerevisiae) ; (Z74961) ORF YOR053w [Saccharomyces cerevisiae] ; (Z70678) YOR29-04 [Saccharomyces cerevisiae] (AF074951) cellobiose dehydrogenase [Thielavia heterothallica]
23094	ENU06888	ANI61C1096	22-47	586-605	LINAP		g3319315	340	150	1.00E-35	38	26	cytochrome P450 3A2 (CYP3A2) (P450-PCN2) ; cytochrome P450 3A2 - rat ; (M13646) cytochrome P450 [Rattus norvegicus]
23095	ENU06889	ANI61C2160:	102-126	447-474	LINAP		g117154	113	66	1.00E-10	34	23	cyclosporin synthetase - Tolypocladium inflatum ; (Z28383) cyclosporine synthetase [Tolypocladium inflatum]
23096	ENU06890	ANI61C9256:	23-42	805-829	LINAP		g1083855	340	96	2.00E-19	25	1	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23097	ENU06891	ANT61C8777: 22-48		804-829	LINAP		g1491795	672	248	4.00E-65	47	28	"(U39812) beta-1,4-mannanase [Callicellulosinriptor saccharolyticus]"
23098	ENU06892	2603..1599 ANT61C6218: 37-57		809-828	LINAP		g4522004	160	94	9.00E-19	31	38	"(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana]"
23099	ENU06893	ANT61C5291: 22-44		615-638	LINAP		g3850084	85	83	1.00E-15	37	62	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
23100	ENU06894	1929..1250 ANT61C9272: 83-102		603-625	LINAP		g2773203	545	224	8.00E-61	51	43	(AF039713) Similar to phosphoglycerate mutase, coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk387c10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cm10f9; coded for by C. elegans cDNA cm18g...
23101	ENU06895	ANT61C8802: 22-46		793-812	LINAP		g3395351	350	79	3.00E-14	29	25	(AB012696) DNA polymerase V [Schizosaccharomyces pombe]; (AL022305) DNA polymerase V [Schizosaccharomyces pombe]
23102	ENU06896	ANT61C5300: 22-41		453-473	LINAP		g2120949	87	77	9.00E-14	37	28	lipase-like enzyme - Alcaligenes eutrophus; (L36817) lipase-like enzyme [Alcaligenes eutrophus]; ORF 8 [Ralstonia eutropha]
23103	ENU06897	ANT61C1095 0:1..423	72-95	376-400	LINAP		g1181493	97	61	0.000000	33	21	"(U42580) 4 ankyrin repeats; similar to Drosophila melanogaster ankyrin, encoded by GenBank Accession Number L35601 [Paramecium bursaria Chlorella virus 1]"
23104	ENU06898	ANT61C219:1 677..2320	22-48	595-615	LINAP		g3757521	302	121	4.00E-27	40	17	(AC005167) unknown protein [Arabidopsis thaliana]
23105	ENU06899	ANT61C9301: 23-46		414-432	LINAP		g2673951	172	50	4.00E-14	31	11	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
23106	ENU06900	ANT61C8766: 590..2566	34-53	802-821	LINAP		g2494692	999	118	6.00E-26	36	22	White collar 1 protein (WC1); (X94300) wc-1 [Neurospora crassa]
23107	ENU06901	ANT61C219:3 639..4561	22-47	781-800	LINAP		g4539260	123	53	0.000003			(AL049495) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23108	ENU06902	ANI61C8806: 1480..1947	29-50	444-463	LINAP		g1723291	489	150	6.00E-36	47	69	hypothetical 26.3 KD protein C13D6.03C in chromosome I ; (Z69725) unknown [Schizosaccharomyces pombe]
23109	ENU06903	ANI61C625: 70..1414	39-58	626-643	LINAP		g464347	135	82	3.00E-15	29	17	peroxisome biosynthesis protein PASS (peroxin-6) ; (Z22556) PASS [Pichia pastoris] (Z95334) unknown [Schizosaccharomyces pombe]
23110	ENU06904	ANI61C5296: 1627..3637	53-80	724-746	LINAP		g2094857	599	108	5.00E-23	42	32	(Z95334) unknown [Schizosaccharomyces pombe]
23111	ENU06905	ANI61C1098: 2023..2692	22-44	627-649	LINAP		g3980042	135	85	6.00E-16			(AL033514) similar to ABC transporters ; ABC transporter transmembrane region. [Caenorhabditis elegans] (AC005275) predicted protein of unknown function [Arabidopsis thaliana] (Z98981) putative sodium channel [Schizosaccharomyces pombe] putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emericella nidulans] hypothetical 126.9 KD protein C22G7.04 in chromosome I ; hypothetical protein SPAC22G7.04 - fission yeast (Schizosaccharomyces pombe) ; (Z54328) putative poly(a)-specific ribonuclease subunit [Schizosaccharomyces pombe] fibrillarin (nucleolar protein 1) ; nucleolar protein NOP1 - yeast (Saccharomyces cerevisiae) ; (J05230) fibrillarin [Saccharomyces cerevisiae] ; (Z48432) nucleolar protein NOP1 (J05230) [Saccharomyces cerevisiae] ; (Z74062) ORF YDL014w [Saccharomyces cerevisiae] (D85895) diacylglycerol lipase [Aspergillus oryzae]
23112	ENU06906	ANI61C8822: 2014..319	31-50	778-804	LINAP		g4262148	772	190	1.00E-47	40	35	
23113	ENU06907	ANI61C6255: 642..1	143-170	592-612	LINAP		g2388993	392	98	1.00E-35	49	10	
23114	ENU06908	ANI61C5309: 1418..1978	52-71	489-510	LINAP		g2498971	131	64	0.000000	37	26	
23115	ENU06909	ANI61C8764: 920..4304	23-48	809-828	LINAP		g1175466	1302	215	2.00E-55	43	23	
23116	ENU06910	ANI61C6247: 1889..2799	65-84	803-829	LINAP		g119857	1026	309	2.00E-83	72	80	
23117	ENU06911	ANI61C5311: 797..89			LINAP		g1772352	181	106	1.00E-22	34	52	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23118	ENU06912	ANI61C1099	107-132	254-273	LINAP		g3122326	90	59	0.000000	43	17	LEC14B protein ; (D83074) LEC14B protein [Lithospermum erythrorhizon]
23119	ENU06913	ANI61C817	41-60	454-473	LINAP			85		008	29		
23120	ENU06914	ANI61C1099	34-53	731-755	LINAP		g1175399	288	89	4.00E-17			hypothetical 180.2 KD protein C31A2.05C in chromosome I ; hypothetical protein SPAC31A2.05c - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe] ; (AB016866) Mis4 [Schizosaccharomyces pombe]
23121	ENU06915	ANI61C930	1 29-51	796-815	LINAP		g4154078	472	98	9.00E-30	37	29	[Schizosaccharomyces pombe] (AL035161) putative efflux protein [Streptomyces coelicolor]
23122	ENU06916	ANI61C6811	122-142	427-446	LINAP		g1171755	279	82	3.00E-23	54	36	"neutral protease II precursor (deuterolysin) (NPII) ; neutral proteinase II - Aspergillus oryzae ; (S53810) neutral protease II, NPII [Aspergillus oryzae, Peptide, 352 aa] [Aspergillus oryzae] ; neutral protease II [Aspergillus oryzae] "
23123	ENU06917	ANI61C2244	22-41	460-479	LINAP		g549706	183	68	4.00E-11	38	35	KTII2 protein ; KTII2 protein - yeast (Saccharomyces cerevisiae) ; (Z28110) ORF YKL110c [Saccharomyces cerevisiae] ; (X77511) KTII2 [Saccharomyces cerevisiae] (AL031515) hypothetical protein SC5C7.08 [Streptomyces coelicolor] (AF016585) polyketide synthase module 3 [Streptomyces caelestis]
23124	ENU06918	ANI61C6808	22-45	613-633	LINAP		g3559998	312	116	2.00E-27	37	62	hypothetical 84.5 KD protein C24H6.09 in chromosome I ; hypothetical protein SPAC24H6.09 - fission yeast (Schizosaccharomyces pombe) ; (Z54142) putative guanine nucleotide exchange factor [Schizosaccharomyces pombe]
23125	ENU06919	ANI61C8823	43-63	808-829	LINAP		g2558839	204	118	5.00E-26	34	14	
23126	ENU06920	ANI61C6788	108-127	749-766	LINAP		g1175438	223	100	2.00E-20	27	34	



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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23127	ENU06921	ANI61C6265: 909..1657	50-69	693-712	LINAP		g2275336	263	44	0.001			(AF001978) differentially expressed in relation to the extent of cell elongation [Candida albicans]
23128	ENU06922	ANI61C931:1..598	102-125	552-573	LINAP		g4490644	155	66	2.00E-10	36	18	"(Z98762) SPAC4A8.06c, unknown, len:578aa, some similarity eg. to BAH_STRHY, Q01109, acetyl-hydrolase, (Z99aa), fasta sco res, opt:259, E0:8.2e-17, (35.6% identity in 118 aa over lap) [Schizosaccharomyces pombe]"
23129	ENU06923	ANI61C8833: 1833..609	22-42	810-829	LINAP		g4096660	376	104	1.00E-27			(U34807) extracellular lipase [Candida albicans]
23130	ENU06924	ANI61C6788: 3962..4460	22-49	451-478	LINAP		g2257504	171	90	1.00E-17	37	39	(AB004535) similar to S.pombe unknown protein : DDBJ ACC# D89156 [Schizosaccharomyces pombe] (U72998) ErpM [Borrelia burgdorferi]
23131	ENU06925	ANI61C6269: 1..1100	35-54	810-829	LINAP		g2627268	71	36	0.35	28	57	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
23132	ENU06926	ANI61C1209: 7140..6797	23-47	428-455	LINAP		g3367791	149	65	4.00E-10	31	26	(Y10491) putative cytochrome P450 [Glycine max]
23133	ENU06927	ANI61C9291: 1094..432	48-67	608-627	LINAP		g3334663	59	38	0.000003	31	21	(AF069442) putative polypeptide of LTR transposon [Arabidopsis thaliana]
23134	ENU06928	ANI61C6814: 1..341	67-86	299-320	LINAP		g3924609	91	34	0.38			(AF016449) Similar to cytochrome P450 [Caenorhabditis elegans]
23135	ENU06929	ANI61C6274: 607..1048	22-44	420-439	LINAP		g2315475	59	52	0.000002			regulatory protein MSR1 - yeast (Saccharomyces cerevisiae) ; (Z70202) unknown [Saccharomyces cerevisiae]
23136	ENU06930	ANI61C1259: 967..385			LINAP		g2133082	128	79	3.00E-14	38	29	(AF009672) unknown [Acinetobacter sp. ADP1]
23137	ENU06931	ANI61C1098: 1..5200..5803	22-49	559-580	LINAP		g2271503	156	45	0.0006	26	51	(AL031740) dna ligase protein [Schizosaccharomyces pombe]
23138	ENU06932	ANI61C9265: 11512..10812	122-144	657-680	LINAP		g3650376	283	122	3.00E-27	37	24	(U88309) T23B3.5 gene product [Caenorhabditis elegans]
23139	ENU06933	ANI61C8847: 740..1109	22-47	452-479	LINAP		g1825739	123	39	0.016	24	59	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23140	ENU06934	ANI61C5355: 105-124	648-666		LINAP		g2257531	155	68	4.00E-19	34	15	[Schizosaccharomyces pombe] ; (AB004537) WEB1 protein
		1074..1826											[Schizosaccharomyces pombe] ; (AL022072) web1 homolog: protein transport protein; WD-repeat protein [Schizosaccharomyces pombe]
23141	ENU06935	ANI61C1208: 25-43	452-472		LINAP		g3123302	150	81	6.00E-15	31	24	hypothetical 75.1 KD protein
		1785..2107											C22E12.19 in chromosome I
23142	ENU06936	ANI61C6833: 22-48	433-452		LINAP		g1351664	310	78	9.00E-24	43	28	hypothetical 59.0 KD protein
		3809..4322											C30D11.14 in chromosome I ; hypothetical protein SPAC30D11.14 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe]
23143	ENU06937	ANI61C6224: 22-48	802-829		LINAP		g1168457	782	130	1.00E-29	29	15	Ankyrin ; ankyrin - mouse ; (M84756) ankyrin [Mus musculus]
23144	ENU06938	ANI61C2250: 315..754			LINAP		g1172906	165	60	7.00E-11	31	24	cell division cycle related-protein RES2/PCT1 ; cell cycle regulator res2 - fission yeast (Schizosaccharomyces pombe) ; RES2 protein - fission yeast (Schizosaccharomyces pombe) ; (D17761) cell cycle regulator Res2 [Schizosaccharomyces pombe] ; (Z54285) Res2 [Schizosaccharomyces pombe]
23145	ENU06939	ANI61C932: 8 09..1	44-63	682-701	LINAP		g731024	711	259	2.00E-68	62	59	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) ; TWT1 protein - yeast (Saccharomyces cerevisiae) ; (U00029) Balp: Branched-Chain Amino Acid Transaminase [Saccharomyces cerevisiae] ; (X78961) TWT1 [Saccharomyces cerevisiae] "
23146	ENU06940	ANI61C628: 3 84..1	106-128	444-471	LINAP		g2117302	710	173	7.00E-43	49	48	(Z95620) putative ribose-phosphate pyrophosphokinase [Schizosaccharomyces pombe]
23147	ENU06941	ANI61C5335: 22-46	799-818		LINAP		g1749560	134	41	0.00003			(D89176) unnamed protein product [Schizosaccharomyces pombe]

# Sequence Alignment

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23148	ENU06942	ANI61C1273:	69-88	260-282	LINAP		g547991	62	57	0.000000	25	35	NA(+)/H(+) antiporter ; Na+/H+-exchanging protein - fission yeast (Schizosaccharomyces pombe) ; (Z11736) putative sodium/proton antiporter [Schizosaccharomyces pombe]
		1086..712								1			
23149	ENU06943	ANI61C1100:	22-48	481-500	LINAP		g2497628	114	65	4.00E-10	38	62	microsomal SIGNAL peptidase 21.3 KD subunit ; probable membrane protein YLR066w - yeast (Saccharomyces cerevisiae) ; (X94607) L2186 [Saccharomyces cerevisiae] ; (Z73238) ORF YLR066w [Saccharomyces cerevisiae] ; (U92975) signal peptidase subunit [Saccharomyces cerevisiae] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]
23150	ENU06944	ANI61C2231:	22-40	502-521	LINAP		g2462679	56	58	0.000000	25	22	
		637..1								07			
23151	ENU06945	ANI61C932:1	33-52	762-783	LINAP		g1711351	585	83	2.00E-15			SCY1 protein ; SCY1 protein - yeast (Saccharomyces cerevisiae) ; (X97305) suppressor of GTPase mutant [Saccharomyces cerevisiae] ; (Z72605) ORF YGL083w [Saccharomyces cerevisiae]
		682..3727											
23152	ENU06946	ANI61C6847:	23-42	767-793	LINAP		g1175418	1174	229	2.00E-59	43	21	hypothetical 147.4 KD protein C12C2.02C in chromosome II ; (Z54140) conserved hypothetical protein [Schizosaccharomyces pombe] ; (AJ223984) Ste20 protein [Schizosaccharomyces pombe]
		1662..4157											
23153	ENU06947	ANI61C6256:	28-47	590-609	LINAP		g548757	202	106	2.00E-22	33	83	50S ribosomal protein L1 ; (M94319) ribosomal protein L1 [Citrus greening disease-associated bacterium-like organism] ; ribosomal protein L1 [Citrus greening disease-associated bacterium]
		4907..4259											
23154	ENU06948	ANI61C1100	22-45	773-800	LINAP		g1946288	442	200	9.00E-51	46	55	(Y11520) vanillin dehydrogenase [Pseudomonas sp.]
		7:1209..2066											

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23155	ENU06949	ANI61C2241: 1732..719	33-51	808-827	LINAP	g131777	746	247	2.00E-77	53	25		DNA repair protein RAD13 ; excision repair protein - fission yeast (Schizosaccharomyces pombe) ; (X66795) excision repair protein [Schizosaccharomyces pombe]
23156	ENU06950	ANI61C9340: 1050..1515	30-57	446-473	LINAP	g117090	259	80	9.00E-25				cytochrome C oxidase polypeptide IV precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - yeast (Saccharomyces cerevisiae) ; (X01418) cytochrome c oxidase subunit IV precursor [Saccharomyces cerevisiae] ; (X91489) cytochrome C oxidase chain IV precursor [Saccharomyces cerevisiae] ; (Z712709) ORF YGL187c [Saccharomyces cerevisiae]
23157	ENU06951	ANI61C8861: 2192..2787	22-45	548-575	LINAP	g417762	227	114	5.00E-25	30	18		exocyst complex component SEC8 ; SEC8 protein - yeast (Saccharomyces cerevisiae) ; (X64693) SEC8 [Saccharomyces cerevisiae] ; (Z49219) Sec8p [Saccharomyces cerevisiae] ; (Z71255) Sec8p [Saccharomyces cerevisiae]
23158	ENU06952	ANI61C1098: 2..1.1262	56-75	780-799	LINAP	g4107287	474	83	6.00E-24				(AL035076) putative allantoin permease [Schizosaccharomyces pombe]
23159	ENU06953	ANI61C2241: 1676..2069	40-59	429-448	LINAP	g2606019	84	38	0.061				(AF030027) 71 [Equine herpesvirus 4]
23160	ENU06954	ANI61C1098: 2..2486..3656	44-63	771-790	LINAP	g128340	262	120	1.00E-26	30	29		nitrogen assimilation transcription factor NIRA ; nitrate assimilation regulatory protein nira - Emericella nidulans ; (M68900) NIRA protein [Emericella nidulans]
23161	ENU06955	ANI61C8867: 2241..2737..2018	22-41	675-694	LINAP	g448109	160	82	6.00E-15	33	34		6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
23162	ENU06956	ANI61C1230: 7214..8025	32-51	636-655	LINAP	g2132661	378	180	1.00E-44	42	45		probable membrane protein YLR020c - yeast (Saccharomyces cerevisiae) ; (Z73192) ORF YLR020c [Saccharomyces cerevisiae]

# Sequence Summary

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23163	ENU06957	ANI61C6860:	31-50	720-746	LINAP		g464912	1190	256	1.00E-68	47	19	helicase SGS1 (helicase TPS1) ; DNA helicase TPS1 - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (L07870) bps. 390..881 = homology to E.coli recQ; bps. 414..430 = ATP binding site [ <i>Saccharomyces cerevisiae</i> ] ; (Z47815) Tps1p [ <i>Saccharomyces cerevisiae</i> ] ; (U22341) Sgs1p [ <i>Saccharomyces cerevisiae</i> ] (AF042799) suppressor of white apricot homolog 2 [ <i>Mus musculus</i> ] (AL031013) putative secreted protein [ <i>Streptomyces coelicolor</i> ] hypothetical 37.6 KD protein in GNTR-HTPG intergenic region ; (AB005554) see SWISS_PROT ACC#: P42106 [ <i>Bacillus subtilis</i> ] ; (Z99124) yxaG [ <i>Bacillus subtilis</i> ] (Z99113) polyketide synthase [ <i>Bacillus subtilis</i> ] cutinase transcription factor I beta ; (U51672) cutinase transcription factor I [ <i>Fusarium solani</i> f. sp. pisi] interleukin enhancer-binding factor 1 (cellular transcription factor ILF-1) ; (U58196) interleukin enhancer binding factor 1 [ <i>Homo sapiens</i> ] hypothetical 44.8 KD protein C57A10.01 in chromosome I GAM1 gene [ <i>Saccharomyces cerevisiae</i> ] probable membrane protein YDR109c - yeast ( <i>Saccharomyces cerevisiae</i> ) ; (Z48758) unknown [ <i>Saccharomyces cerevisiae</i> ] (D64006) Ap-4-A phosphorylase II [ <i>Synechocystis</i> sp.]
23164	ENU06958	ANI61C9827:	41-60	810-829	LINAP		g3941324	65	38	0.092			
23165	ENU06959	ANI61C9347:	33-54	633-659	LINAP		g3288616	100	53	0.000001			
23166	ENU06960	ANI61C6815:	22-48	448-475	LINAP		g1176967	105	42	0.000000	30	43	
23167	ENU06961	ANI61C9346:			LINAP		g2634103	157	80	1.00E-14	29	4	
23168	ENU06962	ANI61C2233:	22-46	767-790	LINAP		g1706177	322	109	3.00E-23	32	27	
23169	ENU06963	ANI61C8870:	22-42	455-479	LINAP		g3183529	60	64	6.00E-10			
23170	ENU06964	ANI61C6839:	22-43	378-398	LINAP		g3287948	152	82	2.00E-15	34	32	
23171	ENU06965	ANI61C6278:	41-60	781-800	LINAP		g228213	2404	265	4.00E-70	56	16	
23172	ENU06966	ANI61C2238:	29-54	767-786	LINAP		g1077569	996	255	2.00E-67	47	39	
23173	ENU06967	ANI61C9335:	24-47	437-456	LINAP		g1001338	62	63	0.000000			

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23174	ENU06968	ANI61C6798:	23-42	802-829	LINAP		g1708909	356	62	1.00E-19	27	56	malic acid transport protein (malate permease) ; C4-dicarboxylate transport protein mae1 - fission yeast (Schizosaccharomyces pombe) ; (U21002) malic acid transport protein [Schizosaccharomyces pombe]
23175	ENU06969	ANI61C1229:	50-69	460-479	LINAP		g2146829	173	91	5.00E-18	43	54	"hypothetical protein YCL010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL010c, len:146 [Saccharomyces cerevisiae] "
23176	ENU06970	ANI61C9328:	28-47	776-794	LINAP		g2342601	1390	166	1.00E-40	35	5	(X89442) peptide synthetase [Metarhizium anisopliae]
23177	ENU06971	ANI61C6798:	22-44	453-479	LINAP		g4160354	125	69	1.00E-11	47	28	(Z64354) unknown [Schizosaccharomyces pombe]
23178	ENU06972	ANI61C2212:			LINAP		g3549891	170	75	7.00E-17	33	34	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi]
23179	ENU06973	ANI61C9349:	24-51	787-809	LINAP		g2144467	1068	159	1.00E-54	44	42	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae)
23180	ENU06974	ANI61C6835:	158-179	476-499	LINAP		g3395590	193	90	1.00E-17	37	56	(AL031179) hypothetical protein [Schizosaccharomyces pombe]
23181	ENU06975	ANI61C6308:	48-67	527-549	LINAP		g3702642	398	98	7.00E-42	56	41	(AL031825) ma binding protein - putative pre mna splicing factor [Schizosaccharomyces pombe]
23182	ENU06976	ANI61C1322:	22-42	777-797	LINAP		g125731	162	75	1.00E-16	30	32	"ATP-dependent DNA helicase II, 86 KD subunit (Iupus KU autoantigen protein P86) (86 KD subunit of KU antigen) (thyroid-lupus autoantigen) (TLAA) (CTC BOX binding factor 85 KD subunit) (CTCBF) (CTC85) (nuclear factor IV) (...; Ku antigen 80K chain - human ; (J04977) Ku antigen [Homo sapiens] ; (M30938) Ku (p70/p80) subunit [Homo sapiens] "
23183	ENU06977	ANI61C2259:	36-55	442-467	LINAP		g3123282	98	56	0.000000	20	7	TRNA-splicing endonuclease positive effector ; SEN1 protein - yeast (Saccharomyces cerevisiae) ; (U20939) Sen1p [Saccharomyces cerevisiae]
23184	ENU06978	ANI61C9795:	22-49	804-829	LINAP		g4589488	54	75	9.00E-13	24	11	(AB023145) KIAA0928 protein [Homo sapiens]

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23185	ENU06979	ANI6IC8837:	22-46	795-822	LINAP	g3122656	1264	161	2.00E-61	57	50	amidophosphoribosyltransferase (glutamine phosphoribosylpyrophosphate amidotransferase) (ATASE) ; (U32992) glutamine phosphoribosylpyrophosphate amidotransferase [Saccharomyces kluyveri]
23186	ENU06980	ANI6IC5401:	22-48	380-398	LINAP	g1438949	60	53	0.000001			(U61841) cutinase G-box binding protein [Fusarium solani f. sp. pisi]
23187	ENU06981	ANI6IC227:1	22-48	806-825	LINAP	g2764761	171	104	6.00E-22	30	5	"(AJ223012) rifamycin polyketide synthase, type 1 [Amycolatopsis mediterranei] ; (AF040570) polyketide synthase [Amycolatopsis mediterranei]"
23188	ENU06982	ANI6IC8882:	22-43	736-761	LINAP	g2497111	304	123	2.00E-27	30	35	hypothetical 84.6 KD protein in GLO1-YPT7 intergenic region ; probable membrane protein YML002w - yeast (Saccharomyces cerevisiae)
23189	ENU06983	ANI6IC5382:	22-45	476-495	LINAP	g2494239	241	100	3.00E-24	37	52	probable peroxisomal enoyl-CoA hydratase ; peroxisomal enoyl hydratase-like protein - rat ; (U08976) peroxisomal enoyl hydratase-like protein [Rattus norvegicus]
23190	ENU06984	ANI6IC2257:	22-43	434-453	LINAP	g4581525	170	75	4.00E-13	34	27	(AL049559) putative short-chain dehydrogenase [Schizosaccharomyces pombe]
23191	ENU06985	ANI6IC8894:	22-44	794-817	LINAP	g1168817	418	143	6.00E-35	37	24	cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035537) cell division control protein 7
23192	ENU06986	ANI6IC6882:	36-60	587-610	LINAP	g4507075	250	122	2.00E-27	40	17	[Schizosaccharomyces pombe] "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 ; (AB010882) hSNF2H [Homo sapiens]"

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23193	ENU06987	ANI61C5397: 22-46	2937..2595	414-434	LINAP		g2499778	176	41	0.007			cell binding factor 2 precursor (antigen PEB4A) ; cell binding factor 2 - Campylobacter jejuni ; (X84703) cell binding factor 2 [Campylobacter jejuni]
23194	ENU06988	ANI61C1337: 24-43	405..1105	566-585	LINAP		g3122986	160	110	1.00E-23	33	42	beta-TRCP (beta-transducin repeat-containing protein) (BTRCP) ; beta-transducin repeat-containing protein - African clawed frog ; (M98268) beta-TRCP [Xenopus laevis] "(AE000314) orf, hypothetical protein [Escherichia coli]"
23195	ENU06989	ANI61C5418: 24-45	929..1313	443-466	LINAP		g1788578	90	63	0.000000			thyroid receptor interacting protein 12 (TRIP12) (KIAA0045) ; (D28476)
23196	ENU06990	ANI61C1329: 34-53	1267..2834	810-829	LINAP		g2499839	331	94	2.00E-18			KIAA0045 [Homo sapiens]
23197	ENU06991	ANI61C2215: 31-50	2977..4211	777-796	LINAP		g3183326	351	151	5.00E-36	31	31	hypothetical 93.2 KD TRP-ASP repeats containing protein C4F8.11 in chromosome I ; (Z98530) beta-transducin [Schizosaccharomyces pombe]
23198	ENU06992	ANI61C1330: 22-45	1244..274	782-801	LINAP		g2656001	294	109	2.00E-23	35	31	(Z98977) hypothetical protein [Schizosaccharomyces pombe]
23199	ENU06993	ANI61C8878: 25-45	4372..5020	559-586	LINAP		g2132218	263	139	2.00E-32	42	32	hypothetical protein YPL169c - yeast (Saccharomyces cerevisiae) ; (Z73525) ORF YPL169c [Saccharomyces cerevisiae] ; (X96770) P2520 protein [Saccharomyces cerevisiae]
23200	ENU06994	ANI61C539:2 64-83	021..1434	542-567	LINAP		g3915438	151	89	2.00E-17	31	62	hypothetical protein C10D6.08 in chromosome I ; (Z98951) hypothetical protein [Schizosaccharomyces pombe]
23201	ENU06995	ANI61C1360: 66-93	1..889	776-795	LINAP		g2244866	215	80	6.00E-23	35	13	(Z97337) hypothetical protein [Arabidopsis thaliana]
23202	ENU06996	ANI61C538:8 22-45	038..5666	758-781	LINAP		g1354473	2931	180	2.00E-90	67	21	(U53189) Os-1p [Neurospora crassa]
23203	ENU06997	ANI61C9831: 24-43	6221..5845	446-465	LINAP		g2132165	413	60	3.00E-17	54	51	hypothetical protein YPL051w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe21p [Saccharomyces cerevisiae] ; (AF017142) ADP-ribosylation factor-like protein 1 [Saccharomyces cerevisiae]